

Access DB# 76223

SEARCH REQUEST FORM

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Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
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	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	NA Sequence (#) _____	STN _____
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Date Searcher Picked Up: <u>9/22/02</u>	Bibliographic _____	Dr.Link _____
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Searcher Prep & Review Time: <u>15</u>	Fulltext _____	Sequence Systems <u>✓</u>
Clerical Prep Time: <u>20</u>	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:06:28 ; Search time 66.91 Seconds
(without alignments)
172.332 Million cell updates/sec

Title: US-09-803-918a-2_COPY_25_144

Perfect score: 631
Sequence: 1 DEPPQSPMDRYKDLATYVD.....LDPRQKKQEMELXROKVE 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: PIR.71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	631	100.0	267	1	LPHUAI
2	606	96.0	267	1	A26529
3	606	96.0	267	1	JS0079
4	556	88.1	266	1	LPDGA1
5	545	86.4	264	2	S31394
6	545	86.4	265	2	A46018
7	533	84.5	265	2	JT0672
8	521	82.6	265	2	A56888
9	521	82.6	266	1	LPRB12
10	517	81.9	265	1	LPRB12
11	516.5	81.9	241	2	A24998
12	495	78.4	231	2	J00704
13	481	76.2	262	2	J01237
14	481	76.2	262	2	S22420
15	479	75.9	259	2	A24700
16	329	52.1	264	1	LPCHA1
17	328	52.0	264	1	J05456
18	326	51.7	246	2	A61448
19	179	28.4	164	2	S21830
20	142	22.5	429	2	S39565
21	139	22.0	406	1	LPHUAI
22	138	21.9	491	2	A47141
23	125.5	19.9	391	2	LPRTA4
24	114	18.1	391	2	B40892
25	114	18.1	394	2	A45281
26	114	18.1	395	2	A40892
27	114	18.1	399	2	C40892
28	106	16.8	34	2	S67972
29	106	16.8	36	2	A56866

ALIGNMENTS

30	104	16.5	312	1	LPRTA	apolipoprotein E p
31	101.5	16.1	365	2	D71559	probable ABC ATRP
32	101	16.0	20	2	A05313	apolipoprotein A-I
33	98	15.5	298	2	S12635	apolipoprotein E p
34	98	15.5	311	2	JU0036	apolipoprotein E p
35	90	14.3	317	2	A28792	apolipoprotein E p
36	89	14.3	317	2	S03185	apolipoprotein E p
37	89	14.1	291	2	C60940	apolipoprotein E p
38	89	14.1	329	2	J05566	apolipoprotein E p
39	89	14.1	1138	2	T24635	hypothetical prote
40	88	13.9	258	2	JH0472	apolipoprotein A-I
41	87	13.8	317	2	S33450	apolipoprotein E -
42	86.5	13.7	911	2	S51441	hypothetical prote
43	86.5	13.7	1046	2	T42720	cytoplasmic linker
44	86	13.6	336	2	T03999	ATG1 protein homol
45	86	13.6	583	2	C84788	probable myosin he

RESULT 1

LPHUAI

apolipoprotein A-I precursor [validated] - human
N:Alternate names: apoA-I-2; apoA-I-4; preproapoA-I; prostacyclin stabilizing factor

C:Species: Homo sapiens (man)
C:Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text change 08-Dec-2000
C:Accession: A90947; B90947; S02373; A93465; A21147; A93519; B93519; A93472; A94010; 6197

R:Seilhamer, J.J.; Protter, A.A.; Frossard, P.; Levy-Wilson, B.
DNA 3, 309-317, 1984

A:Title: Isolation and DNA sequence of full-length cDNA and of the entire gene for hu
A:Reference number: A90947; MUID:85026665

A:Accession: A90947
A:Molecule type: DNA
A:Residues: 1-267 <SEI>

A:Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635
A:Accession: B90947
A:Molecule type: mRNA
A:Residues: 1-267 <SE2>

A:Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635
R:Karlides, S.C.; Ruiz-Opazo, N.; Hayden, M.; Nussbaum, A.L.; Breslow, J.L.; Zannis,
Eur. J. Biochem. 173, 465-471, 1988

A:Title: Sequence number and expression of Tangier apoA-I gene.
A:Reference number: S02373; MUID:88196137
A:Accession: S02373
A:Molecule type: DNA
A:Residues: 1-267 <MAK>

A:Cross-references: EMBL:X07496; NID:g28774; PIDN:CAA30377.1; PID:g296729
R:Shoulders, C.C.; Kornblith, A.R.; Munro, B.S.; Baralle, F.E.
Nucleic Acids Res. 11, 2827-2837, 1983

A:Title: Gene structure of human apolipoprotein A1.
A:Reference number: A93465; MUID:83220822
A:Accession: A93465
A:Molecule type: DNA
A:Residues: 1-267 <SHO>

A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:R01518;
R:Katharasis, S.K.; Zannis, V.I.; Breslow, J.L.
Proc. Natl. Acad. Sci. U.S.A. 80, 6147-6151, 1983

A:Title: Isolation and characterization of the human apolipoprotein A-I gene.
A:Reference number: A21147; MUID:84016011
A:Accession: A21147
A:Molecule type: DNA
A:Residues: 1-267 <KAR>

A:Cross-references: GB:J00098; GB:J03222; NID:g178765; PIDN:AAB59514.1; PID:g178768
R:Sharpe, C.R.; Sidoli, A.; Shelley, C.S.; Lucero, M.A.; Shoulders, C.C.; Baralle, F.
Nucleic Acids Res. 12, 3917-3932, 1984

A:Title: Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA abundant
A:Reference number: A93519; MUID:84221405
A:Accession: A93519
A:Molecule type: mRNA
A:Residues: 1-267 <SHA>

A:Cross-references: GB:X00566; NID:g28765; PIDN:CAA25232.1; PID:g732753

A:Accession: B93519
 A:Molecule type: DNA
 A:Residues: 1-24 <SH2>
 R:Cheung, P.; Chan, L.
 Nucleic Acids Res. 11, 3703-3715, 1983
 A:Title: Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.
 A:Reference number: A93472; MUID:83220772
 A:Accession: A93472
 A:Molecule type: mRNA
 A:Residues: 1-267 <CHD>
 A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J03222; GB:K01518; GB:R:Law, S.W.; Brewer Jr., H.B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 66-70, 1984
 A:Title: Nucleotide sequence and the encoded amino acids of human apolipoprotein A-I mRNA
 A:Reference number: A94010; MUID:84119464
 A:Accession: A94010
 A:Molecule type: mRNA
 A:Residues: 1-267 <LAW>
 A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J03222; GB:K01518; GB:R:Zammit, V.I.; Karathanasis, S.K.; Keutmann, H.T.; Goldberger, G.; Breslow, J.L.
 Proc. Natl. Acad. Sci. U.S.A. 80, 2574-2578, 1983
 A:Title: Intracellular and extracellular processing of human apolipoprotein A-I: secreted
 A:Reference number: A21118; MUID:83195100
 A:Accession: A21118
 A:Molecule type: protein
 A:Residues: 1-24 <ZAN>
 R:Brewer Jr., H.B.; Fairwell, T.; Kay, L.; Meng, M.; Ronan, R.; Law, S.; Light, J.A.
 Biochem. Biophys. Res. Commun. 113, 626-632, 1983
 A:Title: Human plasma proapo-A-I: isolation and amino-terminal sequence.
 A:Reference number: A90112; MUID:83256553
 A:Accession: A90112
 A:Molecule type: protein
 A:Residues: 19-27 <BRE>
 R:Brewer Jr., H.B.; Fairwell, T.; LaRue, A.; Ronan, R.; Houser, A.; Bronzert, T.J.
 Biochem. Biophys. Res. Commun. 80, 623-630, 1978
 A:Title: The amino acid sequence of human APOA-I, an apolipoprotein isolated from high density lipoproteins
 A:Reference number: A90209; MUID:78123731
 A:Accession: A90209
 A:Molecule type: protein
 A:Residues: 25-57, 'Q', '59', '169', '172-267 <BR2>
 R:Yul, Y.; Aoyama, T.; Morishita, H.; Takashashi, M.; Takatsu, Y.; Kawai, C.
 J. Clin. Invest. 82, 803-807, 1988
 A:Title: Serum prostacyclin stabilizing factor is identical to apolipoprotein A-I (Apo A-I)
 A:Reference number: A30516; MUID:88331387
 A:Accession: A30516
 A:Molecule type: protein
 A:Residues: 25-36 <TUI>
 R:Nichols, W.C.; Dwulet, F.E.; Liepnieks, J.; Benson, M.D.
 Biochem. Biophys. Res. Commun. 156, 762-768, 1988
 A:Title: Variant apolipoprotein AI as a major constituent of a human hereditary amyloid.
 A:Reference number: A31582; MUID:89050104
 A:Accession: A31582
 A:Molecule type: protein
 A:Residues: 25-49, 'R', '51-85', 'D', '87-107 <NIC>
 A:Note: variant sequence from patient with familial amyloidotic polyneuropathy type III
 R:Manjunath, P.; Marcel, Y.L.; Una, J.; Seidah, N.G.; Chretien, M.; Chappelaine, A.
 J. Biol. Chem. 264, 16853-16857, 1989
 A:Title: Apolipoprotein A-I binds to a family of bovine seminal plasma proteins.
 A:Reference number: A34409; MUID:89380318
 A:Accession: A34409
 A:Molecule type: protein
 A:Residues: 25-48 <MAN>
 R:Stoffel, W.; Binczek, E.
 Biol. Chem. Hoppe-Seyler 369, 1055-1063, 1988
 A:Title: Structural requirements of human preproapolipoprotein AI for translocation and
 A:Reference number: S02737; MUID:89149957
 A:Accession: S02737
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-6, 'AV', '9', '1V', '12-29 <STO>
 A:Note: part of this sequence, including the amino end of the mature protein, was confirmed
 R:Stoffel, W.; Binczek, E.
 Biol. Chem. Hoppe-Seyler 372, 481-488, 1991

A:Title: Transient expression of wild type and mutant human apolipoprotein AI in COS
 A:Reference number: S16197; MUID:92029676
 A:Contents: annotation; extension; studies in reference S02737
 R:Stoffel, W.; Kruger, E.; Deutzmann, R.
 Hoppe-Seyler's Z. Physiol. Chem. 364, 227-237, 1983
 A:Title: Cell-free translation of human liver apolipoprotein AI and AII mRNA processed
 A:Reference number: A19913; MUID:83236195
 A:Accession: B19913
 A:Molecule type: protein
 A:Residues: 1-6, 'X', '8-13', 'XXX', '17-18', 'XX', '21', 'X', '23-25', 'X', '27-29 <ST2>
 R:Phinholm, C.; Bozas, S.E.; Tenkanen, H.; Kitzbaum, L.; Metso, J.; Murphy, B.; Walke
 Biochim. Biophys. Acta 1086, 255-260, 1991
 A:Title: The apolipoprotein A-I binding protein of placenta and the SP-40.40 protein
 A:Reference number: A56815; MUID:92075698
 A:Accession: A56815
 A:Molecule type: protein
 A:Residues: 25-31, 'P', '33 <ENH>
 A:Experimental source: serum
 A:Note: sequence extracted from NCBI backbone (NCBIP:69759)
 A:Note: 32-Tp was also found
 R:Knittake, S.W.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
 Biochemistry 33, 1988-1993, 1994
 A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipoproteins
 A:Reference number: A54223; MUID:94162201
 A:Accession: A54223
 A:Molecule type: protein
 A:Residues: 25-39 <KUN>
 R:Mogulievsky, N.; Roobol, C.; Loriau, R.; Guillaume, J.P.; Jacobs, P.; Cravador, A.;
 DNA B. 429-436, 1989
 A:Title: Production of human recombinant proapolipoprotein A-I in Escherichia coli: p
 A:Reference number: I39476; MUID:89377481
 A:Accession: I39476
 A:Molecule type: mRNA
 A:Residues: 19-267 <RES>
 A:Cross-references: GB:M29068; MUID:9178774; PIDN:AAA51747.1; PID:9178775
 R:Hiigchi, K.; Law, S.W.; Hoeg, J.M.; Schumacher, U.K.; Meglin, N.; Brewer, H.B.
 J. Biol. Chem. 263, 18530-18536, 1988
 A:Title: Tissue-specific expression of apolipoprotein A-I (ApoA-I) is regulated by the
 A:Reference number: I39475; MUID:89054040
 A:Accession: I39475
 A:Molecule type: DNA
 A:Residues: 1-14 <RE2>
 A:Cross-references: GB:J04066; MUID:9178763; PIDN:AAA51746.1; PID:9553183
 R:Breslow, J.L.
 Annu. Rev. Biochem. 54, 699-727, 1985
 A:Title: Human apolipoprotein molecular biology and genetic variation.
 A:Reference number: A90042; MUID:85278004
 A:Contents: annotation; review of sequences, variants and gene location
 R:Hoeg, J.M.; Meng, M.S.; Ronan, R.; Fairwell, T.; Brewer Jr., H.B.
 J. Biol. Chem. 261, 3911-3914, 1986
 A:Title: Human apolipoprotein A-I. Post-translational modification by fatty acid acyl
 A:Reference number: A92577; MUID:86140194
 A:Contents: annotation; acylation with palmitate
 A:Note: an underdetermined serine or threonine is acylated by fatty acid; the acylating
 R:Law, S.W.; Brewer, H.B.
 J. Biol. Chem. 260, 12810-12814, 1985
 A:Title: Tangier disease: the complete mRNA sequence encoding for preproapo-A-I.
 A:Reference number: I55236; MUID:86008382
 A:Accession: I55236
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-143, 'D', '145-267 <RE2>
 A:Cross-references: GB:M11791; MUID:9178776; PIDN:AAA35545.1; PID:9178777
 C:Comment: Apolipoprotein A-I precursor is synthesized in the liver and small intestine
 C:Genetics: HDL in plasma.
 A:Gene: GDB:APOA1
 A:Cross-references: GDB:119684; OMIM:107680
 A:Map position: 11q23.3-11q23.3
 A:Introns: 15/1; 67/2
 C:Function:
 A:Description: participates in the reverse transport of cholesterol from tissues to the
 sterol acyltransferase (LCAT); noncovalently binds and stabilizes prostacyclin (PGI-2)

A: Molecule type: protein
 A: Residues: 25-56, '2', 1261-262, 'A', <NAK>
 C: Superfamily: apolipoprotein A-I
 C: Keywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid transport; lipid
 F: 1-18/Domain: signal sequence #status predicted <SIG>
 F: 19-24/Domain: propeptide #status predicted <PRO>
 F: 25-266/Product: apolipoprotein A-I #status experimental <MAT>

Query Match	88.1%	Score 556;	DB 1;	Length 266;
Best Local Similarity	88.1%;	Pred. No. 3.6e-36;		
Matches 104; Conservative	8;	Mismatches 6;	Indels 0;	Gaps 0

QY	2	EPPOSEMDRKYDLATYAYVVLKDSGDYDYSGCESGALKOLNKLKLNPNMVSYSFTEKRL	6
Db	25	DEPOSEMDRKYDLATYAYVVAVKDSGDYVADQEAASALCOLKLTLLDNPMOSISSTYIKLR	8
QY	62	EOLGPTVYQEFMDLLEKETEGRLROEMSKDLEFYKAAVQVYPLDDPOCKKQOEEMELTRYCKV	119
Db	85	EOLGPTVYQEFMDLLEKETLEVLROEMSKDLEFYKAAVQVYPLDDPOCKKQOEEMELTRYCKV	142

RESULT 5
S31394
apolipoprotein A-I - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C:Accession: S31394
R:Moehel, B.; Flisch, R.; Weiss, B.; Weller-Guettler, H.; Frey, A.; Zinke, H.; Gassen, H.
submitted to the EMBL Data Library, November 1992
A:Description: Genomic organization of the porcine apolipoprotein AI gene and study of
A:Reference number: S31394
A:Accession: S31394
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-264 <MOE>
A:Cross-references: EMBL:X69477; NID:g1889; PIDN:CAA45234.1; PID:g1890
C:Superfamily: apolipoprotein A-I

```

Query Match      86.4%; Score 545; DB 2; length 264;
Best Local Similarity 85.6%; Pred. No. 2,5e-35;
Matches 101; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY      2  EPPOSMDRYKDATATYYVDLKDSGHDYQSFSGSLGKOLNKLILNMWVSYSSTSKLR 61
      :  |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      25  DDQPSMDRYKDATATYYVDALINDSGDIYAQFEASALTKHLNKLILNMWSLGSSTFKV 84

QY      62  EQLGPTVTOEFWNLEKETEGLRQENSKDLEEVKAKVQPIYLDPOFKKQOEEMETLYRQV 119
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
      85  EQLGPTVTOEFWNLDLREKETEGLRQENSKDLEEVKAKVQPIYLDPOFKKQOEEMETLYRQ 142

```

RESULT 6
A46018
apolipoprotein AI - pig
C.Species: Sus scrofa domestica (domestic pig)
C.Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C.Accession: A46018
R.Birchbauer, A.; Knüpling, G.; Juritsch, B.; Aschauer, H.; Zechner, R.
Genomics 15, 643-652, 1993
A.Title: Characterization of the apolipoprotein AI and CIII genes in the domestic pig
A.Reference number: A46018; MUID:93224154
A.Accession: A46018
A.Status: preliminary
A.Molecule type: DNA; protein
A.Residues: 1-265 <BIR>
A.Cross-references: GB:L00626; NID:g164358; PIDN:AAA30992.1; PID:g164359
A.Note: sequence extracted from NCBI backbone (NCBIN:129509, NCBIIP:129511)
C.Superfamily: apolipoprotein A-I

```
Query Match      86.48; Score 545; DB 2; Length 265;
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Best Local Similarity 85.6%; Pred. No. 2.5e-35;
Matches 101; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

```

0Y 2 EPPSPMDRKDLATLAYVVLKMSGSDYVDSOEESGALGKLTMLTLDNMPDSTPSKLR 61
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 25 DDPGSPMDRKDEATYAYVDAIKDSGRDVAQGEASALGKHLTMLTLDNMPDSTGTFKRA 84
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
0Y 62 EQLSPYVQGEWMDLLEKETSGILQEMSKOLEFYKAAVQYVYLDLPCKQKQEMELLYROKV 119
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 85 EQLGSPYVQGEWMDLLEKETLALQEMSKOLEEYKAAVQYVYLDLPCKNKKQEMELTYRQML 142
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 7
J06072
apolipoprotein A-I - pig
N:Alternate names: apo-A-I
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 11-May-2000
C:Accession: J06072; P00471; A05311
R:Rieu, V.N.; Patel, B.; Zhan, R.; Black, D.D.
Gene 134, 267-270, 1993
A:Title: Sequence of the porcine apoA-I gene.
A:Reference number: J06072; MUID:94085789
A:Accession: J06072
A:Molecule type: DNA
A:Residues: 1-265 <TR>
A:Cross-references: EMBL:214124; MID:91893
A:Note: this translation is not annotated in GenBank entry SSAPOIG, release 111.0; t
R:Rieu, V.N.; Hasler-Rapacz, J.; Rapacz, J.; Black, D.D.
Gene 123, 173-179, 1993
A:Title: Sequences and expression of the porcine apolipoprotein A-I and C-II mRNAs.
A:Reference number: P00471; MUID:93154581
A:Accession: P00471
A:Molecule type: mRNA
A:Residues: 105-265 <TR2>
A:Experimental source: liver
R:Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.
Biochemistry 15, 1928-1933, 1976
A:Title: Characterization of the plasma lipoproteins and apoproteins of the Erythroce
A:Reference number: A90395; MUID:76184721
A:Accession: A05311
A:Molecule type: protein
A:Residues: 25-34 <MAH>
C:Comment: This protein is the major apolipoprotein of high-density lipoprotein and s
C:Genetics:
A:Gene: apoA-I
A:Introns: 15/1; 66/2
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid metabolism;
P:99/Region: ochre stop codon

Query Match	84.58;	Score 533;	DB 2;	Length 265;
Best Local Similarity	83.98;	Pred. No. 2.2e-34;		
Matches 99;	Conservative 7;	Mismatches 12;	Indels 0;	Gaps 0

[illegible]

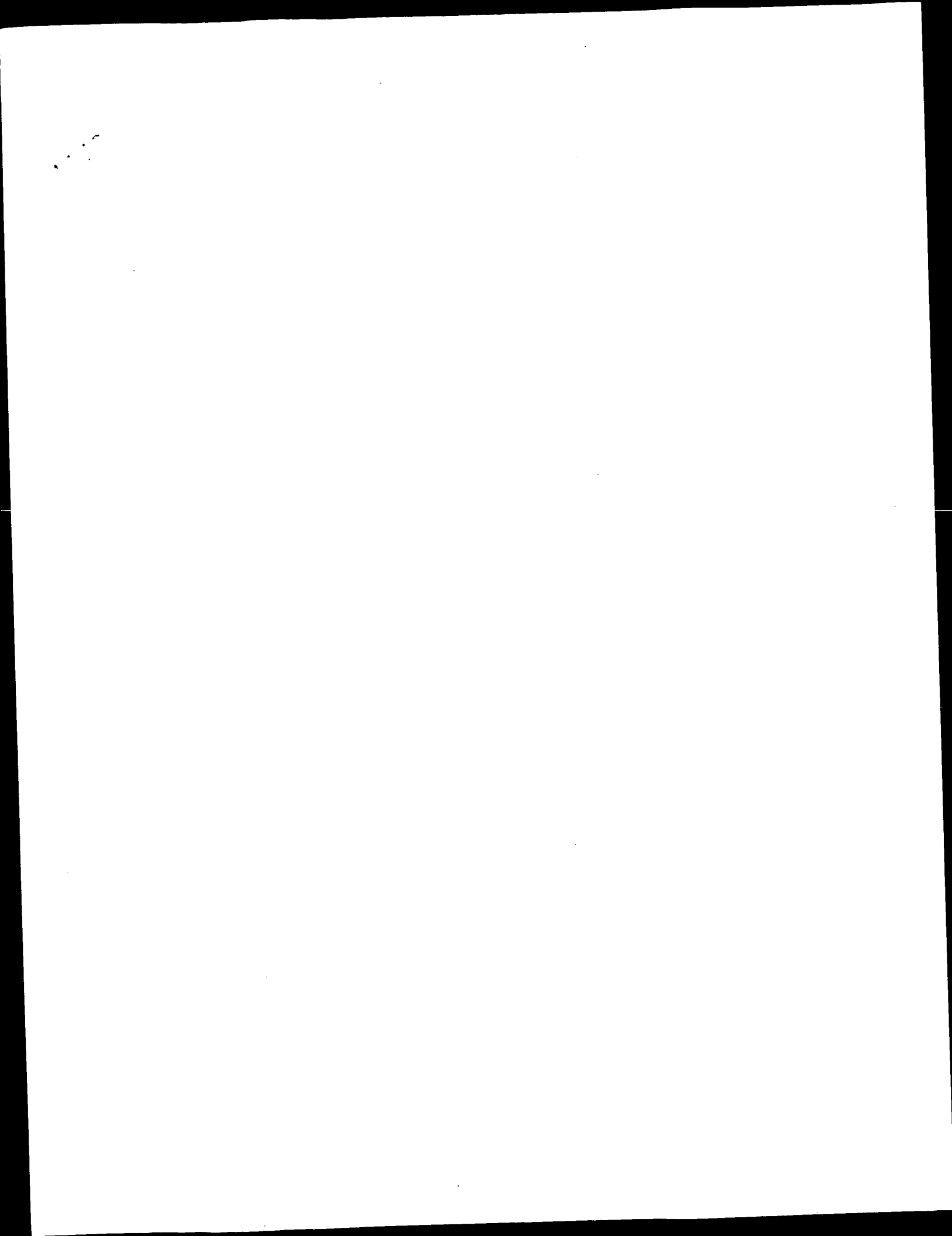
RESULT 8
A56858
apolipoprotein A-I precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 05-Jan-1996 #sequence.revision 23-Aug-1997 #text_change 13-Aug-1999
C:Accession: I45853; A56858; A34649
R:O'Ruigin, C.; Chan, L.; Li, W.
Mol. Biol. Evol. 7, 327-339, 1990

A:Accession: A05314
 A:Molecule type: Protein
 A:Residues: 1-18, 'X', 20-21, 'X', 23-28, 'X', 30-38, 'X', 40-41, 'X', 43-45 <GOR>
 C:Comment: This protein is synthesized in the liver and small intestine. The propeptide
 C:Genetics: This protein is a major component of the high density lipoproteins in plasma.
 A:Introns: 15/1; 66/2
 C:Superfamily: apolipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipoprotein; signal sequence #status experimental <SIG>
 F:18/Domain: propeptide #status experimental <PRO>
 F:19-24/Domain: propeptide #status experimental <PRO>
 F:25-259/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 75.9%; Score 479; DB 2; Length 259;
 Best Local Similarity 73.9%; Pred. No. 3.3e-30;
 Matches 88; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

OY	2	EPQSPMDRYKDLATYVYVNLKDSGRDYVSQFEGSALGKQLNLKLDNWDVSTFESKLR	61
Db	25	DEPQSQMDRYKDFATYVYVDAVAKDSGRDYVSQFESSTLGKQLNLKLDNWDVSTFESKLR	84
OY	62	EQIGPYTQEFWNLKEKETEGLEKQEMSKDLEEVKAKAVQPYLDDPQKQKQEMELYRQKE	120
Db	85	EOLGPYTOEFWNLKEKETDMLRNEKMKDLENVKQKQPHLDEFOEKWNEEYAYRQKE	143

Search completed: September 22, 2002, 12:06:29
 Job time: 324 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:22:17 ; Search time 35.02 Seconds
(without alignments)
132.677 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_144

Perfect score: 631
Sequence: 1 DERPOSPMWRVMDLAFVYD.....LDDFOKKQCEMEELTKRQVE 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	100.0	267	1	APAL_HUMAN
2	606	96.0	267	1	APAL_MACFA
3	556	88.1	266	1	APAL_CANFA
4	545	86.4	265	1	APAL_PIG
5	521	82.6	265	1	APAL_BOVIN
6	521	82.6	266	1	APAL_RABIT
7	481	76.2	264	1	APAL_MOUSE
8	479	75.9	259	1	APAL_RAT
9	463	73.4	265	1	APAL_TUPGB
10	329	52.1	264	1	APAL_CHICK
11	328	52.0	264	1	APAL_COTJA
12	326	51.7	264	1	APAL_ANAPL
13	142	22.5	429	1	APAL_MACFA
14	139	22.0	396	1	APAL_HUMAN
15	138	21.9	401	1	APAL_PAPAN
16	125.5	19.9	391	1	APAL_RAT
17	121	19.2	382	1	APAL_PIG
18	114.5	18.1	262	1	APAL_ONCMY
19	114	18.1	395	1	APAL_MOUSE
20	112.5	17.8	262	1	APAL_BRARE
21	108	17.1	281	1	APAL_BRARE
22	107	17.0	262	1	APAL_ONCMY
23	106.5	16.9	262	1	APAL_SALTR
24	104	16.5	312	1	APAL_RAT
25	101.5	16.1	365	1	RECF_CHLTR
26	101	16.0	20	1	APAL_ERIPA
27	98	15.5	298	1	APAL_CAVPO
28	98	15.5	311	1	APAL_MOUSE
29	95.5	15.1	260	1	APAL_SPAUV
30	90	14.3	317	1	APAL_MACFA
31	90	14.3	317	1	APAL_PAPAN
32	89	14.1	305	1	APAL_CANFA
33	88.5	14.0	539	1	MYS3_HYDAT

ALIGNMENTS

RESULT ID	APAL_HUMAN	STANDARD:	PRT:	267 AA.
AC	P02647;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Apolipoprotein A-I precursor (Apo-AI).			
GN	APOLI.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84221405; PubMed=6328445;			
RA	Shaper C.R., Sidoli A., Shelley C.S., Lucero M.A., Shoulders C.C.,			
RA	Baralle F.E.;			
RT	"Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA			
RT	abundance.";			
RL	Nucleic Acids Res. 12:3917-3932(1984).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=6502665; PubMed=6207999;			
RA	Sellhammer J.J., Proter A.A., Frossard P., Levy-Wilson B.;			
RT	"Isolation and DNA sequence of full-length cDNA and of the entire			
RT	gene for human apolipoprotein AI -- discovery of a new genetic			
RT	polymorphism in the apo AI gene.";			
RL	DNA 3:309-317(1984).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83220822; PubMed=6406984;			
RA	Shoulders C.C., Kornblith A.R., Munro B.S., Baralle F.E.;			
RT	"Gene structure of human apolipoprotein AI.";			
RL	Nucleic Acids Res. 11:2827-2837(1983).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83220772; PubMed=6304641;			
RA	Cheung P., Chan L.;			
RT	"Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.";			
RL	Nucleic Acids Res. 11:3703-3715(1983).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84119464; PubMed=6198645;			
RA	Lau S.W., Brewer H.B. Jr.;			
RT	"Nucleotide sequence and the encoded amino acids of human			
RT	apolipoprotein A-I mRNA.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 81:66-70(1984).			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86008382; PubMed=2995392;			
RA	Lau S.W., Brewer H.B. Jr.;			
RT	"Mangier disease. The complete mRNA sequence encoding for			
RT	preproapo-A-I.";			
RL	J. Biol. Chem. 260:12810-12814(1985).			
RN	[7]			

34	87	13.8	317	1	APE_PIG	P18650 sus scrofa
35	85	13.5	107	1	APE_MACMU	Q28502 macaca mula
36	85	13.5	258	1	APAL_SALSA	P27007 salmo salar
37	85	13.5	657	1	LAMA_CHICK	P13648 gallus gall
38	84	13.3	583	1	LAMI_XENLA	P09010 xenopus lae
39	83	13.2	107	1	APE_SALISC	Q28995 salmali sci
40	83	13.2	2663	1	GENE_HUMAN	Q02224 homo sapien
41	82.5	13.1	365	1	RECF_CHLMU	Q98K5 chlamydia m
42	82.5	13.1	512	1	K2C5_XENLA	P16878 xenopus lae
43	82.5	13.1	574	1	LAMC_MOUSE	P1516 mus musculu
44	82.5	13.1	664	1	LAMA_HUMAN	P02545 homo sapien
45	82.5	13.1	665	1	LAMA_MOUSE	P48678 mus musculu

- RP SEQUENCE FROM N.A.
RX MEDLINE=84016011; PubMed=6413973;
RA Karathanasis S.K., Zannis V.I., Breslow J.L.;
RT "Isolation and characterization of the human apolipoprotein A-I
RT gene."
RL Proc. Natl. Acad. Sci. U.S.A. 80:6147-6151(1983).
RN [18]
RP SEQUENCE FROM N.A.
RX MEDLINE=89377481; PubMed=2673706;
RA Mogullevsky N., Roobol C., Loriau R., Guillaume J.P., Jacobs P.,
RA Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,
RA Holmquist L., Carlson L.A., Bollen A.;
RT "Production of human recombinant proapolipoprotein A-I in *Escherichia*
RT coli: purification and biochemical characterization."
RL DNA 8:429-436(1989).
RN [9]
RP SEQUENCE FROM N.A. (VARIANT TANGIER).
RX MEDLINE=88196137; PubMed=3129297;
RA Makrides S.C., Ruiz-Opazo N., Hayden M., Nussbaum A.L., Breslow J.L.,
RA Zannis V.I.;
RT "Sequence and expression of Tangier apoa-I gene."
RL Eur. J. Biochem. 173:465-471(1988).
RN [10]
RP SEQUENCE OF 118-267 FROM N.A.
RX MEDLINE=83091059; PubMed=6294659;
RA Breslow J.L., Ross D., McPherson J., Williams H.W., Kurnit D.,
RA Nussbaum A.L., Karathanasis S.K., Zannis V.I.;
RT "Isolation and characterization of cDNA clones for human
RT apolipoprotein A-I."
RL Proc. Natl. Acad. Sci. U.S.A. 79:6861-6865(1982).
RN [11]
RP SEQUENCE OF 19-27,
RX MEDLINE=83256553; PubMed=6409108;
RA Brewer H.B. Jr., Fairwell T., Kay L., Meng M., Roman R., Law S.,
RA Light J.A.;
RT "Human plasma proapo-A-I: isolation and amino-terminal sequence."
RL Biochem. Biophys. Res. Commun. 113:626-632(1983).
RN [12]
RP SEQUENCE OF 25-267,
RX MEDLINE=78123731; PubMed=204308;
RA Brewer H.B. Jr., Fairwell T., Larue A., Roman R., Houser A.,
RA Bronzert T.J.;
RT "The amino acid sequence of human APOA-I, an apolipoprotein isolated
RT from high density lipoproteins."
RL Biochem. Biophys. Res. Commun. 80:623-630(1978).
RN [13]
RP SEQUENCE OF 25-267,
RX MEDLINE=75133493; PubMed=164450;
RA Baker H.N., Gatto A.M. Jr., Jackson R.L.;
RT "The primary structure of human plasma high density apolipoprotein
RT glutamine I (APOA-I). II. The amino acid sequence and alignment of
RT cyanoogen bromide fragments IV, II, and I."
RL J. Biol. Chem. 250:2725-2738(1975).
RN [14]
RP SEQUENCE OF 25-56,
RX MEDLINE=8831387; PubMed=3047170;
RA Yui Y., Aoyama T., Morishita H., Takahashi M., Takatsu Y., Kawai C.;
RT "Serum prostacyclin stabilizing factor is identical to apolipoprotein
RT A-I (Apo A-I). A novel function of Apo A-I."
RL J. Clin. Invest. 82:803-807(1988).
RN [15]
RP SEQUENCE OF 25-48,
RX MEDLINE=89380318; PubMed=2506184;
RA Manjunath P., Marcel Y.L., Uma J., Seidah N.G., Chretien M.,
RA Chappelaine A.;
RT "Apolipoprotein A-I binds to a family of bovine seminal plasma
RT proteins."
RL J. Biol. Chem. 264:16853-16857(1989).
RN [16]
RP SEQUENCE OF 25-43,
RX MEDLINE=88070603; PubMed=3120314;
RA Prioli R.P., Ordovas J.M., Rosenberg I., Schaeffer E.J.,
RA Pereira M.E.A.;
RT "Similarity of cruzin, an inhibitor of *Trypanosoma cruzi*
RT neuraminidase, to high-density lipoprotein."
RL Science 238:1417-1419(1987).
RN [17]
RP SEQUENCE OF 25-42,
RX TISSUE=Heart;
MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994."
RL Electrophoresis 15:1459-1465(1994).
RN [18]
RP PALMITOYLATION.
RX MEDLINE=86140194; PubMed=3005308;
RA Hoeg J.M., Meng M.S., Roman R., Fairwell T., Brewer H.B. Jr.;
RT "Human apolipoprotein A-I. Post-translational modification by fatty
RT acid acylation."
RL J. Biol. Chem. 261:3911-3914(1986).
RN [19]
RP PROCESSING.
RX MEDLINE=83195100; PubMed=6405383;
RA Zannis V.I., Karathanasis S.K., Keutmann H.T., Goldberger G.,
RA Breslow J.L.;
RT "Intracellular and extracellular processing of human apolipoprotein
RT A-I: secreted apolipoprotein A-I isoprotein 2 is a propeptide."
RL Proc. Natl. Acad. Sci. U.S.A. 80:2574-2578(1983).
RN [20]
RP STRUCTURE BY NMR OF 190-209,
RX MEDLINE=96270776; PubMed=8664326;
RA Wang G., Treleaen W.D., Cushman R.J.;
RT "Conformation of human serum apolipoprotein A-I(166-185) in the
RT presence of sodium dodecyl sulfate or dodecylphosphocholine by ¹H-NMR
RT and CD. Evidence for specific peptide-SDS interactions."
RL Biochim. Biophys. Acta 1301:174-184(1996).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (4.0 ANGSTROMS) OF 67-267,
RX MEDLINE=98024124; PubMed=9356442;
RA Borhani D.W., Rogers D.P., Engler J.A., Brouillette C.G.;
RT "Crystal structure of truncated human apolipoprotein A-I suggests a
RT lipid-bound conformation."
RL Proc. Natl. Acad. Sci. U.S.A. 94:12291-12296(1997).
RN [22]
RP VARIANT MILANO.
RX MEDLINE=83109095; PubMed=6401735;
RA Weisgraber K.H., Rall S.C. Jr., Bersot T.P., Mahley R.W.,
RA Franceschini G., Sirtori C.R.;
RT "Apolipoprotein A-I-Milano. Detection of normal A-I in affected
RT subjects and evidence for a cysteine for arginine substitution in the
RT variant A-I."
RL J. Biol. Chem. 258:2508-2513(1983).
RN [23]
RP VARIANT TANGIER.
RX MEDLINE=83300108; PubMed=6412234;
RA Schmitz G., Assmann G., Rall S.C. Jr., Mahley R.W.;
RT "Tangier disease: defective recombination of a specific Tangier
RT apolipoprotein A-I isoform (Pro-apo A-I) with high density
RT lipoproteins."
RL Proc. Natl. Acad. Sci. U.S.A. 80:6081-6085(1983).
RN [24]
RP VARIANT NORWAY.
RX MEDLINE=84289383; PubMed=6432779;
RA Rall S.C. Jr., Weisgraber K.H., Mahley R.W., Ogawa Y., Fielding C.J.,
RA Utermann G., Haas J., Steimetz A., Menzel H.J., Assmann G.;
RT "Abnormal lecithin:cholesterol acyltransferase activation by a human
RT apolipoprotein A-I variant in which a single lysine residue is
RT deleted."
RL J. Biol. Chem. 259:10063-10070(1984).
RN [25]
RP SEQUENCE OF 25-107 (VARIANT IOWA).
RX MEDLINE=89050104; PubMed=3124262;
RA Nichols W.C., Duvel F.E., Liepnieks J., Benson M.D.;
RT "Variant apolipoprotein AI as a major constituent of a human
RT hereditary amyloid.";

Query Match 100.0%; Score 631; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 5.2e-44;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DEPPSPMDRKVDLTVVVDVVKSGRDYVSQFESGALGKOLNKLNDMDSVTSFSKL 60
 DB 25 DEPPSPMDRKVDLTVVVDVVKSGRDYVSQFESGALGKOLNKLNDMDSVTSFSKL 84
 OY 61 RQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVAKVQPYLDDEQKKWQEMELYRQKVE 120
 DB 85 RQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVAKVQPYLDDEQKKWQEMELYRQKVE 144

RESULT 2
 APAL_MACFA STANDARD; PRT: 267 AA.

AC P15568: p17929; (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
 OS Papio hamadryas (Hamadryas baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541, 9557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=87191989; PubMed=3106152;
 RA Polites H.G., Melchior G.W., Castle C.K., Marotti K.R.;
 RT "The primary structure of cynomolgus monkey apolipoprotein A-I
 deduced from the cDNA sequence: comparison to the human sequence.";
 RL Gene 49:103-110(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=92305062; PubMed=1610902;
 RA Murray R.W., Marotti K.R.;
 RT "Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene
 and corresponding flanking regions.";
 RL Biochim. Biophys. Acta 1131:207-210(1992).
 RN [3]
 RP SEQUENCE OF 25-48.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=87185451; PubMed=3105581;
 RA Herbert P.N., Bausserman L.L., Lynch K.M., Saritelli A.L.,
 RA Kantor M.A., Nicolosi R.J., Shulman R.S.;
 RT "Homologues of the human C and A apolipoproteins in the Macaca
 fascicularis (cynomolgus) monkey.";
 RL Biochemistry 26:1457-1463(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas; TISSUE=Liver;
 RX MEDLINE=89232739; PubMed=2907746;
 RA Hixson J.E., Borenstein S., Cox L.A., Rainwater D.L., Vandeberg J.L.;
 RT "The baboon gene for apolipoprotein A-I: characterization of a cDNA
 clone and identification of DNA polymorphisms for genetic studies of
 cholesterol metabolism.";
 RL Gene 74:483-490(1988).
 RN [5]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC SPECIES=M.fascicularis;
 RA Sorci-Thomas M.;
 RT Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
 CC THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.

CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC EMBL: M15411; AAA36834.1; -
 DR EMBL: M83242; AAA36832.1; -
 DR EMBL: M83634; AAA35380.1; -
 DR EMBL: M69223; AAA36831.1; -
 DR PIR: A26529; A26529.
 DR PIR: A26627; A26627.
 DR PIR: J50079; J50079.
 DR PIR: S23135; S23135.
 DR HSSP: P02647; 10DR.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 DR Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 KW SIGNAL
 FT PROPEP 1 18
 FT CHAIN 25 267
 FT DOMAIN 68 267
 FT REPEAT 68 89
 FT REPEAT 90 111
 FT REPEAT 112 122
 FT REPEAT 123 144
 FT REPEAT 145 166
 FT REPEAT 167 188
 FT REPEAT 189 210
 FT REPEAT 211 232
 FT REPEAT 233 243
 FT REPEAT 244 267
 FT REPEAT 267 267
 FT CONFLICT 13 13
 FT SEQUENCE 267 AA; 30735 MW; 869955C024088E21 CRC64;
 L -> P (IN REF. 1).
 L 10 X APPROXIMATE TANDEM REPEATS.

Query Match 96.0%; Score 606; DB 1; Length 267;
 Best Local Similarity 95.0%; Pred. No. 5.3e-42;
 Matches 114; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 DEPPSPMDRKVDLTVVVDVVKSGRDYVSQFESGALGKOLNKLNDMDSVTSFSKL 60
 DB 25 DEPPSPMDRKVDLTVVVDVVKSGRDYVSQFESGALGKOLNKLNDMDSVTSFSKL 84
 OY 61 RQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVAKVQPYLDDEQKKWQEMELYRQKVE 120
 DB 85 RQGLPVTQEFWDNLEKETEGLRQEMSKDLEEVAKVQPYLDDEQKKWQEMELYRQKVE 144

RESULT 3
 APAL_CANFA STANDARD; PRT: 266 AA.

AC P02648:
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=90132271; PubMed=2515239;
 RA Luo C.-C., Li W.-H., Chan L.;

RT "Structure and expression of dog apolipoprotein A-I, E, and C-I
RT mRNAs: implications for the evolution and functional constraints of
RT apolipoprotein structure."
RL J. Lipid Res. 30:1735-1746(1989).
RN [2]
RP SEQUENCE OF 25-266.
RX MEDLINE=82142425; PubMed=6801039;
RA Chung H., Kandolph A., Reardon I., Heinrikson R.L.;
RT "The covalent structure of apolipoprotein A-I from canine high
RT density lipoproteins."
RL J. Biol. Chem. 257:2361-2367(1982).
RN [3]
RP SEQUENCE OF 25-57 AND 262-265.
RX MEDLINE=76210910; PubMed=179887;
RA Nakai T., Whayne T.F., Tang J.;
RT "The amino- and carboxyl-terminal sequences of canine apolipoprotein
RT A-I."
RL FEBS Lett. 64:409-411(1976).
RN [4]
RP SEQUENCE OF 25-37.
RX TISSUE=Heart;
MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins."
RL Electrophoresis 18:2795-2802(1997).
CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS. SYNTHESIZED IN THE LIVER AND SMALL INTESTINE.
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC PIR: A03092; LPDA1.
DR HSSP: P02647; IODR1.
DR HSC-2DPAGE: P02648; DOG.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein: 1.
KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
FT SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 24
FT CHAIN 25 266 APOLOPOPROTEIN A-I.
FT DOMAIN 67 266 10 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 67 88 1.
FT REPEAT 89 110 2.
FT REPEAT 111 121 3 (HALF-LENGTH).
FT REPEAT 122 143 4.
FT REPEAT 144 165 5.
FT REPEAT 166 187 6.
FT REPEAT 188 209 7.
FT REPEAT 210 231 8.
FT REPEAT 232 242 9 (HALF-LENGTH).
FT REPEAT 243 266 10.
FT CONFLICT 168 168 A -> G (IN REF. 2).
FT CONFLICT 202 202 E -> Q (IN REF. 2).
FT CONFLICT 235 235 E -> Q (IN REF. 2).
FT CONFLICT 264 266 NAO -> A (IN REF. 3).
SQ SEQUENCE 266 AA; 30196 MW; A3202620C28A869D CRC64;

Query Match 88.18; Score 556; DB 1; Length 266;
Best Local Similarity 88.18; Pred. No. 5,4e-38;
Matches 104; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 EPPSPMDRVKDLATVVDVLDKSGRDYVQFEGSALGKOLNKLIDNMSTSTSKLR 61
Db : |||||
Db 25 DEQSPMDRVKDLATVVDVLDKSGRDYVQFEGSALGKOLNKLIDNMSTSTSKLR 84
QY 62 EQGQVPTQEFMDNLEKTEGLRQEMSKDLEEVAKVQPYLDFFOKKWOEEMELYROKV 119
Db 85 EQIGPVTQEFMDNLEKTEGLRQEMSKDLEEVAKVQPYLDFFOKKWOEEMELYROKV 142

RESULT 4
AC APAL_PIG STANDARD; PRT; 265 AA.
ID APAL_PIG
AC P18648;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOL1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93224154; PubMed=8468059;
RA Birchbauer A., Knipping G., Juritsch B., Aschauer H., Zechner R.;
RT "Characterization of the apolipoprotein AI and CIII genes in the
RT domestic pig."
RL Genomics 15:643-652(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Brain;
RX MEDLINE=94125128; PubMed=8294940;
RA Moeckel B., Zinke H., Flach R., Weiss B., Weller-Guetler H.,
RA Gassen H.;
RT "Expression of apolipoprotein A-I in porcine brain endothelium in
RT vitro."
RL J. Neurochem. 62:788-798(1994).
RN [3]
RP SEQUENCE OF 34-265 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90132667; PubMed=2105375;
RA Weller-Guetler H., Sommerfeldt M., Papandriopoulou A., Mischek U.,
RA Bonitz D., Frey A., Grupe M., Scherer J., Gassen H.G.;
RT "Synthesis of apolipoprotein A-I in pig brain microvascular
RT endothelial cells."
RL J. Neurochem. 54:444-450(1990).
RN [4]
RP SEQUENCE OF 105-265 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93154581; PubMed=8428656;
RA Trier V.N., Hasler-Rapacz J., Rapacz J., Black D.D.;
RT "Sequences and expression of the porcine apolipoprotein A-I and C-III
RT mRNAs."
RL Gene 123:173-179(1993).
RN [5]
RP SEQUENCE OF 25-265.
RA Hasler-Rapacz J.O., Chaudhary R., Chowdhary B.P., Trier V.N.,
RA Jackson K., Gustavsson I., Rapacz J.;
RL Submitted (OCT-1995) to the SWISS-PROT data bank.
RN [6]
RP SEQUENCE OF 25-34.
RX MEDLINE=76184721; PubMed=178359;
RA Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;
RT "Characterization of the plasma lipoproteins and apoproteins of the
RT Erythrocytes pates monkey."
RL Biochemistry 15:1928-1933(1976).
CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS. SYNTHESIZED PREDOMINANTLY IN THE INTESTINE AND THE
CC LIVER.
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC -----
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RESULT 6
APAL_MOUSE STANDARD: PRT: 266 AA.
AC P09809;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22AP AI; TISSUE=Small intestine;
RA Paraskevopoulos T.B., Kritsis A., Zannis V.I.;
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine; PubMed=3121329;
RA Pan T.C., Hao Q.L., Yamin T.T., Dai P.H., Chen B.S., Chen S.L.,
RA Kiron P.A., Chao Y.S.;
RT "Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit
RT apolipoprotein A-I is synthesized in the intestine but not in the
RT liver."
RL Eur. J. Biochem. 170:99-104(1987).
RN [3]
RP SEQUENCE OF 25-266.
RX MEDLINE=87030294; PubMed=3095115;
RA Yang C., Yang T., Pownall H.J., Gotto A.M. Jr.;
RT "The primary structure of apolipoprotein A-I from rabbit high-density
RT lipoprotein."
RL Eur. J. Biochem. 160:427-431(1986).
CC -I- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -I- SUBCELLULAR LOCATION: Extracellular.
CC -I- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC -I- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC -----
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CC -----
DR EMBL: X15908; CAA34024.1; -
DR EMBL: X06658; CAA29857.1; -
DR EMBL: X06659; CAA29858.1; -
DR PIR: S06064; LPRB12.
DR PIR: S00230; LPRB1B.
DR PIR: A24998; A24998.
DR HSSP: P02647; 1A71.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein; 1.
KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 266
FT DOMAIN 67 266
FT REPEAT 67 88
FT REPEAT 89 110
FT REPEAT 111 121
FT REPEAT 122 143
FT REPEAT 144 165
FT REPEAT 166 187
FT REPEAT 188 209

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FT REPEAT 210 231
FT REPEAT 232 242
FT REPEAT 243 266
FT REPEAT 18 18
FT CONFLICT 18 18
FT CONFLICT 44 44
FT CONFLICT 45 45
FT CONFLICT 107 107
FT CONFLICT 123 123
FT CONFLICT 147 147
FT CONFLICT 150 150
FT CONFLICT 191 191
FT CONFLICT 195 195
FT CONFLICT 211 211
FT CONFLICT 255 256
FT CONFLICT 256 256
SQ SEQUENCE 266 AA; 30591 MW; 0FF6DB386497C7D2 CRC64;

Query Match
Best Local Similarity 82.6%; Score 521; DB 1; Length 266;
Matches 94; Conservative 16; Mismatches 9; Indels 0; Gaps 0;

QY 2 EPPSPMDRVKDLATVYVDLKDGRDYVSOFEGSALGKOLNKLIDNMDSVTSFESKLR 61
Db 25 DEPRSSMDKIKDFATVYVDYKDSGRYVAOFESAGKOLNKLIDNMDSLSYSTSKLD 84
QY 62 EQLGPVQTEFMDNIEKETEGLEKDEBKAQVPIYLDFOKKWQEMELYSKVE 120
Db 85 EQLGPVQTEFMDNIEKETEGLEKDEBKAQVPIYLDFOKKWQEMELYSKVE 143

RESULT 7
APAL_MOUSE STANDARD: PRT: 264 AA.
AC Q00623;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92281682; PubMed=1596360;
RA Stoffel W., Mueller R., Binczek E., Hofmann K.;
RT "Mouse apolipoprotein AI. cDNA-derived primary structure, gene
RT organization and complete nucleotide sequence."
RN Biol. Chem. Hoppe-Seyler 373:187-193(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93122774; PubMed=1478650;
RA Janusz J.L., Azrolan N., O'Connell A., Aalto-Setälä K., Breslow J.L.;
RT "Characterization of the mouse apolipoprotein ApoA-1/ApoC-3 gene
RT locus: genomic, mRNA, and protein sequences with comparisons to other
RT species."
RL Genomics 14:1081-1088(1992).
CC -I- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -I- SUBCELLULAR LOCATION: Extracellular.
CC -I- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC -I- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC -----
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RESULT	9		
APAL_TUPGB			
ID	APAL_TUPGB	STANDARD;	PRT;
AC	018759;		265 AA.

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DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, last sequence update)
DT 30-MAY-2000 (Rel. 39, last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Tupia glis belangeri (Common tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.
OX NCBI_TaxID=9396;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Lu X., Chen B., Zhao Y., Wang K., Xue H., Zeng W.;
RU Submitted (May-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AF005638; AAB82326.1;
DR HSSP: P02647; IAV1.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein; 1.
KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
FT SIGNAL 1 18
FT PROPEP 19 24 BY SIMILARITY.
FT CHAIN 25 265 APOLIPOPROTEIN A-I.
FT DOMAIN 67 265 10 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 67 88 1.
FT REPEAT 89 110 2.
FT REPEAT 111 121 3 (HALF-LENGTH).
FT REPEAT 122 143 4.
FT REPEAT 144 165 6.
FT REPEAT 166 187 7.
FT REPEAT 188 209 8.
FT REPEAT 210 231 9 (HALF-LENGTH).
FT REPEAT 232 242 10.
FT REPEAT 243 265 10.
SQ SEQUENCE 265 AA; 30332 MW; 60076BC39FAEAL65 CRC64;
Query Match 73.4% Score 463; DB 1; Length 265;
Best Local Similarity 69.7% Pred. No. 1.6e-30;
Matches 83; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

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OY 2 EPPSPMDRVKDLATVYVDVLDKSGROYVSQFESALGKOLNKLDDNMSVSTPSKLR 61
OY : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 DEPOSSMDRVADLANVYDAVAKSGREVSQLEASALGKOLNKLVDNMDTLSTTEQKH 84
OY 62 EQLGPVTQVEFNDLEKETEGRLQMSKDLQEVKAKVQPYLDPPQKKQGEEMELYRQVE 120
OY : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 EHLSPVAQEEFWEKLEKETELRREINRDLQVROKTPFLDEIQKKQEDLEKRYKQVE 143

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DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88049703; PubMed=3118875;
RA Byrnes L., Luo C.-C., Li W.-H., Yang C.-Y., Chan L.;
RT "Chicken apolipoprotein A-I: cDNA sequence, tissue expression and
RT evolution."
RL Biochem. Biophys. Res. Commun. 148:485-492(1987).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=88152500; PubMed=3126099;
RA Ferrari S., Tarugi P., Drusiani E., Calandra S., Fregni M.;
RT "The complete sequence of chick apolipoprotein A-I mRNA and its
RT expression in the developing chick."
RL Gene 60:39-46(1987).
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE=8722301; PubMed=3108248;
RA Rajavashisth T.B., Dawson P.A., Williams D.L., Shackelford J.E.,
RA Leberer H., Lusis A.J.;
RT "Structure, evolution, and regulation of chicken apolipoprotein A-I."
RL J. Biol. Chem. 262:7058-7065(1987).
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=92381402; PubMed=1512510;
RA Lamou-Fava S., Sastri R., Ferrari S., Rajavashisth T.B.,
RA Lusis A.J., Karathanasis S.K.;
RT "Evolutionary distinct mechanisms regulate apolipoprotein A-I gene
RT expression: differences between avian and mammalian apoA-I gene
RT transcription control regions."
RL J. Lipid Res. 33:831-842(1992).
RN [5]
RP SEQUENCE OF 25-44.
RX MEDLINE=83213468; PubMed=6406496;
RA Shackelford J.E., Leberer H.G.;
RT "Synthesis and secretion of apolipoprotein AI by chick breast
RT muscle."
RL J. Biol. Chem. 258:7175-7180(1983).
CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC -----
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC -----
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CC -----
DR EMBL: M17961; AAA48593.1;
DR EMBL: M18746; AAA48594.1;
DR EMBL: M25559; AAA48592.1;
DR EMBL: M96012; AAA48597.1;
DR PIR: S01453; LPCHA1.
DR PIR: JH0471; JH0471.
DR HSSP: P02647; IODR.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein; 1.
KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
FT SIGNAL 1 18
FT PROPEP 19 24

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DR EMBL; D85133; BAI4729.1; -.
DR HSSP; P02647; IGM4.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
FT SIGNAL
FT PROPEP 1 19 24
FT CHAIN 25 264 APOLOPROTEIN A-1.
FT DOMAIN 67 264 10 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 67 88 1.
FT REPEAT 89 110 2.
FT REPEAT 111 121 3 (HALF-LENGTH).
FT REPEAT 122 143 4.
FT REPEAT 144 165 5.
FT REPEAT 166 187 6.
FT REPEAT 188 209 7.
FT REPEAT 210 231 8.
FT REPEAT 232 242 9 (HALF-LENGTH).
FT REPEAT 243 264 10.
SQ SEQUENCE 264 AA; 30753 MW; 8781DE213C3F863F CRC64;

Query Match          52.0%; Score 328; DB 1; Length 264;
Best Local Similarity 50.8%; Pred. No. 1,1e-19;
Matches   60; Conservative 29; Mismatches 29; Indels 0; Gaps 0;

QY      2 EPPOSFMDRVDLATVYDVLKDSGRDYVSQPSGALCKOLNTKLIDNWDSTFSFKLR 61
       : - - - - - | - - - - - | - - - - - | - - - - - | - - - - - |
DB      25 DPQPPLRIIRIMDLVYETWAKSKDAISQESSAVGKLDLKIDLADLTLSAAAKLR 84
       : - - - - - | - - - - - | - - - - - | - - - - - | - - - - - |
QY      62 EQLGVTOEPFMNLKEETEGLEQMSKALAEYKAKVQPYLDLPFOKMQEEMELRYKY 119
       : - - - - - | - - - - - | - - - - - | - - - - - | - - - - - |
DB      85 EDMTPIYREVRMMLKTDEALRAELTKLDELVEYKRIREFLDQSAKWEEVGYQRRL 142
       : - - - - - | - - - - - | - - - - - | - - - - - | - - - - - |

RESULT 12
APAL ANAPL
ID APAL ANAPL STANDARD; PRT; 264 AA.
AC O42296;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eleutherozoa; Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_taxid=8839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEKIN BREED; TISSUE=Liver;
RA Chen B., Lu X., Wang K., Xue H., Zeng W., Zhu D., Chi L.;
RL Submitted (JAN-1997) to the EMBL/Genbank/DDJJ databases.
CC -! FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -! SUBCELLULAR LOCATION: Extracellular.
CC -! TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN CHYLOMICRONS.
CC -! SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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CC -----

DR EMBL: U86131; AAB64381.1; -

DR HSSP: P02647; 10DR.

DR InterPro: IPR000074; Apolipoprotein.

DR Pfam: PF01442; Apolipoprotein.1.

KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.

FT SIGNAL 1 18 BY SIMILARITY.

FT PROPEP 19 24 APOLIPOPROTEIN A-1.

FT CHAIN 25 264 APOLIPOPROTEIN A-1.

FT DOMAIN 67 264 10 X APPROXIMATE TANDEM REPEATS.

FT REPEAT 67 88 1.

FT REPEAT 89 110 2.

FT REPEAT 111 121 3 (HALF-LENGTH).

FT REPEAT 122 143 4.

FT REPEAT 144 165 5.

FT REPEAT 166 187 6.

FT REPEAT 188 209 7.

FT REPEAT 210 231 8.

FT REPEAT 232 242 9 (HALF-LENGTH).

FT REPEAT 243 264 10.

FT REPEAT 264 AA; 30659 MM; 7546F4BAF2846900 CRC64;

SEQUENCE

Query Match Best Local Similarity 51.7%; Score 326; DB 1; Length 264; Matches 60; Conservative 28; Mismatches 30; Indels 0; Gaps 0;

OY 2 EPPQSPMDVRDLATVYVYDLKDSGRDVSQFEGSALGKLNKLLDNMDSVTSTFSKLR 61
 DB 25 DEQAPDLRLDLVDVYLETYKASGKDAIQEASVNGKQDLNLDLNGAANKR 84
 OY 62 EQLGAVQGEFMDNLEKTEGRLROEMSKDLEEVAKVOPYLDDFOKKMOEMELYRQKV 119
 DB 85 EDMAVYKEVEMMLKTESLRALRTKDLVEKIRPFLDQFSKWTETELEYRQRL 142

RESULT 13
 ID AP04_MACFA STANDARD; PRT; 429 AA.
 AC P33621;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV).
 GN APOA4.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE=93192330; PubMed=8448212;
 RA Osada J., Pocovi M., Nicolosi R.J., Schaefer E.J., Ordovas J.M.;
 RT "Nucleotide sequences of the Macaca fascicularis apolipoprotein C-III
 and A-IV genes.";
 RL Biochim. Biophys. Acta 1172:335-339(1993).
 CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
 CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
 LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
 CC COMPONENT OF HDL AND CHYLOMICRONS.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SECRETED IN PLASMA.
 CC -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
 CC WERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
 CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
 CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LEGITIM:CHOLESTEROL
 CC ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.

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 CC or send an email to license@sb-sib.ch).

DR EMBL: X68361; CAA48421.1; -

DR PIR: S29565; S29565.

DR PIR: S30195; S30195.

DR HSSP: P02649; INFO.

DR InterPro: IPR000074; Apolipoprotein.

DR Pfam: PF01442; Apolipoprotein.1.

KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal.

FT SIGNAL 1 20 BY SIMILARITY.

FT CHAIN 21 429 APOLIPOPROTEIN A-IV.

FT DOMAIN 33 330 13 X 22 AA APPROXIMATE TANDEM REPEATS.

FT REPEAT 33 54 1.

FT REPEAT 60 81 2.

FT REPEAT 82 103 3.

FT REPEAT 105 126 4.

FT REPEAT 137 158 5.

FT REPEAT 159 180 6.

FT REPEAT 181 202 7.

FT REPEAT 203 224 8.

FT REPEAT 225 246 9.

FT REPEAT 247 268 10.

FT REPEAT 269 286 11.

FT REPEAT 287 308 12.

FT REPEAT 309 330 13.

FT DOMAIN 372 420 GLU/GLN-RICH.

FT SEQUENCE 429 AA; 49876 MM; 3D458F51DD00B60C CRC64;

Query Match Best Local Similarity 22.5%; Score 142; DB 1; Length 429; Matches 32; Conservative 29; Mismatches 51; Indels 0; Gaps 0;

OY 9 DRVKDLATVYVYVYDLKDSGRDVSQFEGSALGKLNKLLDNMDSVTSTFSKLRQGLGYT 68
 DB 25 DQVAVYMDYFESQLSNNAKEVHLLQKSELTQQNALPQDKRGVNTYAGDLQKLVFPA 84
 OY 69 QEFMDNLEKTEGRLROEMSKDLEEVAKVOPYLDDFOKKMOEMELYRQKV 120
 DB 85 TELHERLAKDSEKLEKEIRKELEEVARLPLHANEVSKIGENVRLEQRL 136

RESULT 14
 ID AP04_HUMAN STANDARD; PRT; 396 AA.
 AC P06727;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV).
 GN APOA4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=89194198; PubMed=2930771;
 RA Yang C., Gu Z.W., Xiong W., Rosseneu M., Yang H.X., Lee B.M.,
 RT Goltso A.M., Jr., Chan L.;
 RL "The primary structure of human apolipoprotein A-IV.";
 RN Biochim. Biophys. Acta 1002:231-237(1989).
 CC [2]
 CC SEQUENCE FROM N.A.
 RX MEDLINE=87041474; PubMed=3095836;
 RA Karathanasis S.K., Oetting P., Haddad I.A., Antonarakis S.E.;

RT "Structure, evolution, and polymorphisms of the human apolipoprotein
RT A4 gene (APOA4).";
RN Proc. Natl. Acad. Sci. U.S.A. 83:8457-8461(1986).
[13]
RX SEQUENCE FROM N.A.
RX MEDLINE=86296629; PubMed=3755616;
RA Karathanasis S.K., Yunis I.;
RT "Structure, evolution, and tissue-specific synthesis of human
RT apolipoprotein AIV.";
RN Biochemistry 25:3962-3970(1986).
[14]
RX SEQUENCE FROM N.A.
RX MEDLINE=87250378; PubMed=3036793;
RA Elshourbagy N.A., Walker D.W., Paik Y.K., Boguski M.S., Freeman M.,
RT Gordon J.I., Taylor J.M.;
RT "Structure and expression of the human apolipoprotein A-IV gene.";
RN J. Biol. Chem. 262:7973-7981(1987).
[15]
RX SEQUENCE OF 21-396 FROM N.A.
RX MEDLINE=86111885; PubMed=3080432;
RA Elshourbagy N.A., Walker D.W., Boguski M.S., Gordon J.I., Taylor J.M.;
RT "The nucleotide and derived amino acid sequence of human
RT apolipoprotein A-IV mRNA and the close linkage of its gene to the
RT genes of apolipoproteins A-I and C-III.";
RN J. Biol. Chem. 261:1998-2002(1986).
[16]
RX SIGNAL SEQUENCE CLEAVAGE SITE.
RX MEDLINE=84161950; PubMed=6706947;
RA Gordon J.I., Bisgaler C.L., Sims H.F., Sachdev O.P., Glickman R.M.,
RA Strauss A.W.;
RT "Biosynthesis of human preapolipoprotein A-IV.";
RN J. Biol. Chem. 259:468-474(1984).
[17]
RX REVIEW ON POLYMORPHISM.
RX Lohse P., Brewer H.B. Jr.;
RT "Genetic polymorphism of apolipoprotein A-IV.";
RN Curr. Opin. Lipidol. 2:90-95(1991).
[18]
RX VARIANT A-IV*2.
RX MEDLINE=90277616; PubMed=2351649;
RA Lohse P., Kindt M.R., Rader D.J.;
RT "Genetic polymorphism of human plasma apolipoprotein A-IV is due to
RT nucleotide substitutions in the apolipoprotein A-IV gene.";
RN J. Biol. Chem. 265:10061-10064(1990).
[19]
RX VARIANTS A-IV*0 AND A-IV*3.
RX MEDLINE=90324273; PubMed=1973689;
RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
RT "Human plasma apolipoproteins A-IV-0 and A-IV-3. Molecular basis for
RT two rare variants of apolipoprotein A-IV-1.";
RN J. Biol. Chem. 265:12734-12739(1990).
[10]
RX VARIANTS.
RX MEDLINE=91310615; PubMed=1677358;
RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
RT "Three genetic variants of human plasma apolipoprotein A-IV: apoA-IV-
RT 1(Thr-347->Ser), apoA-IV-0(Lys-167->Glu, Gln-360->His), and apoA-IV-
RT 3(Glu-165->Lys).";
RN J. Biol. Chem. 266:13513-13518(1991).
[11]
RX ERRATUM.
RX Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
RN J. Biol. Chem. 266:19866-19866(1991).
[12]
RX VARIANT MET-13.
RX MEDLINE=92238494; PubMed=1349197;
RA von Eckardstein A., Funke H., Schulte M., Erren M., Schulte H.,
RA Assmann G.;
RT "Nonsynonymous polymorphic sites in the apolipoprotein (apo) A-IV
RT gene are associated with changes in the concentration of apo B- and
RT apo A-I-containing lipoproteins in a normal population.";
RN Am. J. Hum. Genet. 50:1115-1128(1992).
[13]

RP VARIANT SER-147.
RX MEDLINE=92144647; PubMed=1737067;
RA Tenkansen H., Koskinen P., Metso J., Baumann M., Lukka M.,
RA Kauppinen-Makelin R., Kontula R., Taskinen M.R., Manttari M.,
RA Manninen V., Enholm C.;
RT "A novel polymorphism of apolipoprotein A-IV is the result of an
RT asparagine to serine substitution at residue 127.";
RN Biochim. Biophys. Acta 1138:27-33(1992).
[14]
RX VARIANT A-IV*5.
RX MEDLINE=93138374; PubMed=1487136;
RA Kamboh M.I., Williams E.R., Law J.C., Aston C.E., Bunker C.H.,
RA Ferrell R.E., Pollitzer W.S.;
RT "Molecular basis of a unique African variant (A-IV 5) of human
RT apolipoprotein A-IV and its significance in lipid metabolism.";
RN Genet. Epidemiol. 9:379-388(1992).
[15]
RX VARIANTS LYS-44 (BUDAPEST-2); CYS-305 AND SER-367 (BUDAPEST-1).
RX MEDLINE=95245341; PubMed=7728150;
RA Menzel H.J., Dieplinger H., Sandholzer C., Karadi I., Utermann G.,
RA Gaszdar A.;
RT "Apolipoprotein A-IV polymorphism in the Hungarian population: gene
RT frequencies, effect on lipid levels, and sequence of two new
RT variants.";
RN Hum. Mutat. 5:58-65(1995).
[16]
RX VARIANTS FCHL SEATTLE SER-161; LEU-178 AND GLN-264.
RX MEDLINE=97114287; PubMed=8956036;
RA Deeb S.S., Nevin D.N., Iwasaki L., Brunzell J.D.;
RT "Two novel apolipoprotein A-IV variants in individuals with familial
RT combined hyperlipidemia and diminished levels of lipoprotein lipase
RT activity.";
RN Hum. Mutat. 8:319-325(1996).
-1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
CATAROLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
COMPONENT OF HDL AND CHYLOMICRONS.
-1- SUBCELLULAR LOCATION: EXTRACELLULAR.
-1- TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE INTESTINE.
-1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN-CHOLESTEROL
ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
-1- POLYMORPHISM: EIGHT ALLELES HAVE BEEN CHARACTERIZED (APOA-IV*0
TO APOA-IV*7). APOA-IV*1 IS THE MAJOR ALLELE (90%), IV*2 IS ALSO
COMMON (8%), THE OTHERS ARE RARE ALLELES.
-1- DISEASE: DEFECTS IN APOA4 MAY CONTRIBUTE, ALONG WITH DEFECTS IN
OTHER GENES OR ENVIRONMENTAL FACTORS, TO THE DEVELOPMENT OF
FAMILIAL COMBINED HYPERLIPIDEMIA (FCHL).
-1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.

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CC or send an email to license@sib-sib.ch).

CC EMBL: M14642; AAA51745.1; -;
CC EMBL: X13629; CAA31955.1; -;
CC EMBL: M14566; AAA51748.1; -;
CC EMBL: J02758; AAA96731.1; -;
CC EMBL: M13654; AAA51744.1; -;
CC PIR: A26481; LPB004.
CC PIR: A24449; A24449.
CC PIR: A29330; A29330.
CC PIR: A26280; A26280.
CC PIR: S02715; S02715.
CC HSP: P02649; INFO.

DR SWISS-2DPAGE: P06727; HUMAN.
 DR MIM: 107690; -.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein, 1.
 DR Plasma, lipid transport; HDL; Chylomicron; Repeat; Signal;
 KW Disease mutation; Polymorphism.
 FT SIGNAL 1 20
 FT CHAIN 21 396
 FT DOMAIN 33 330
 FT REPEAT 33 54
 FT REPEAT 60 81
 FT REPEAT 82 103
 FT REPEAT 115 136
 FT REPEAT 137 158
 FT REPEAT 159 180
 FT REPEAT 181 202
 FT REPEAT 203 224
 FT REPEAT 225 246
 FT REPEAT 247 268
 FT REPEAT 269 286
 FT REPEAT 287 308
 FT REPEAT 309 330
 FT DOMAIN 372 389
 FT VARIANT 13 13
 FT VARIANT 44 44
 FT VARIANT 147 147
 FT VARIANT 161 161
 FT VARIANT 161 161
 Query Match
 Best Local Similarity 22.0%; Score 139; DB 1; Length 396;
 Matches 30; Conservative 32; Mismatches 50; Indels 0; Gaps 0;
 OY 9 DRVKDLATVYDVVKDSGRDVSQFSGALGKLNKLLDWMDSVTSTFSKLRQLGPGVT 68
 DB 25 DQVATVMDYFQSLSNNKKEAVEHLQKSELTOQLNALFDQKLGENVYAGDLQKLVFA 84
 OY 69 QEFWNLKEKETGLRQEMSKDLEEVKAKVOPYLDDFOKKQEMELRYOKVE 120
 DB 85 TELHRLAKDSKKLEETIRKELEEVRLRLPHANEVSQKIDNRLRELQORLE 136
 RESULT 15
 AP04_PAPAN STANDARD; PRT; 401 AA.
 AC Q28758;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, last sequence update)
 DT 15-DEC-1998 (Rel. 37, last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV) (Fragment).
 GN APOA4.
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OC NCBI_TaxID=9555;
 RN [1]
 RP TISSUE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=93340170; PubMed=8101842;
 RA Hixson J.E., Kammerer C.M., Mott G.E., Britten M.L., Birnbaum S.,
 RA Powers P.K., Vandenberg J.L.;
 RT "Baboon apolipoprotein A-IV. Identification of Lys-76-->Glu that
 RT distinguishes two common isoforms and detection of length
 RT polymorphisms at the carboxyl terminus.";
 RL J. Biol. Chem. 268:15667-15673(1993).
 CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
 CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
 CC LIPASE BY APOC-II, POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
 CC COMPONENT OF HDL AND CHYLOMICRONS.

CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE INTESTINE.
 CC SECRETED IN PLASMA.
 CC -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
 CC 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
 CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
 CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
 CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL
 CC ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
 CC -1- POLYMORPHISM: THERE ARE TWO COMMON APOA-IV ISOFORMS, I (SHOWN
 CC HERE) AND E. THE I ISOFORM IS ASSOCIATED WITH HIGHER LEVELS OF
 CC HIGH DENSITY LIPOPROTEIN-C ON A HIGH CHOLESTEROL, SATURATED FAT
 CC DIET.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----
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 CC -----
 DR EMBL: L13174; AAA35379.1; -.
 DR HSSP: P02649; INFO.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein, 1.
 DR Plasma, lipid transport; HDL; Chylomicron; Repeat; Signal;
 KW Polymorphism.
 FT NON_TER 1 1
 FT SIGNAL <1 4
 FT CHAIN 5 401
 FT DOMAIN 17 314
 FT REPEAT 17 38
 FT REPEAT 44 65
 FT REPEAT 66 87
 FT REPEAT 99 120
 FT REPEAT 121 142
 FT REPEAT 143 164
 FT REPEAT 165 186
 FT REPEAT 187 208
 FT REPEAT 209 230
 FT REPEAT 231 252
 FT REPEAT 253 270
 FT REPEAT 271 292
 FT REPEAT 293 314
 FT DOMAIN 356 394
 FT VARIANT 80 80
 FT SEQUENCE 401 AA; 46538 MW; 0A/6D1284AA9837F CRC64;
 Query Match
 Best Local Similarity 21.9%; Score 138; DB 1; Length 401;
 Matches 31; Conservative 30; Mismatches 51; Indels 0; Gaps 0;
 OY 9 DRVKDLATVYDVVKDSGRDVSQFSGALGKLNKLLDWMDSVTSTFSKLRQLGPGVT 68
 DB 9 DQVATVMDYFQSLSNNKKEAVEHLQKSELTOQLNALFDQKLGENVYAGDLQKLVFA 84
 OY 69 QEFWNLKEKETGLRQEMSKDLEEVKAKVOPYLDDFOKKQEMELRYOKVE 120
 DB 69 TELHRLAKDSKKLEETIRKELEEVRLRLPHANEVSQKIDNRLRELQORLE 120

Search completed: September 22, 2002, 12:22:18
 Job time: 1018 sec

Sun Sep 22 12:10:25 2002

us-09-803-918a-2_copy_25_144.rsp

Page 13

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:21:36 (Search time 111.17 Seconds
(without alignments)
186.736 Million cell updates/sec

Title: US-09-803-918a-2_COPY_25_144

Perfect score: 631
Sequence: 1 DEPPQSPWMDVKLATVYD.....LDDFOKKQWEMELRQKVE 120

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

SPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	80.5	264	11	Q9Z2L4
2	481	76.2	263	11	Q09042
3	481	76.2	263	11	Q08855
4	464	73.5	258	11	Q09054
5	464	73.5	258	11	Q08877
6	411	65.1	241	6	Q9T549
7	247	39.1	56	6	Q02762
8	217	34.4	82	6	Q29248
9	141	22.3	26	4	Q9UC78
10	139	22.0	174	13	Q9DF03
11	125.5	19.9	366	13	Q93601
12	119.5	18.9	244	4	Q13784
13	114	18.1	263	13	Q98766
14	114	18.1	435	11	Q01488
15	110	17.4	395	11	Q91X78
16	108.5	17.2	259	13	Q98765

17	107	17.0	395	11	Q9DBN0
18	106	16.8	34	13	Q9PRR6
19	105.5	16.7	259	13	Q98764
20	104.5	16.6	259	13	Q98761
21	103.5	16.4	174	13	Q98813
22	102.5	16.2	259	13	Q98763
23	101	16.0	30	11	Q9QV04
24	100.5	15.9	259	13	Q98762
25	100.5	15.9	363	4	Q9UBR3
26	99	15.7	313	6	Q9GIC0
27	96.5	15.3	275	13	Q9P702
28	91	14.4	178	2	P72564
29	90	14.3	138	2	Q9S613
30	89	14.1	1138	5	Q22276
31	88.5	14.0	1138	5	Q9KHL8
32	88.5	14.0	1814	5	Q9BLM9
33	88	13.9	317	6	Q9GLM8
34	87.5	13.9	1174	4	Q96D05
35	87	13.8	317	6	Q9GLM7
36	87	13.8	317	6	Q9GLM6
37	86.5	13.8	911	3	Q06704
38	86.5	13.7	1046	11	Q9Z0H8
39	86.5	13.7	1047	11	Q9EP81
40	86.5	13.7	1047	11	Q9EP81
41	86	13.6	336	10	Q9T0F4
42	86	13.6	583	10	Q9Z0C5
43	85	13.5	662	5	Q61096
44	85	13.5	967	5	Q9NGX2
45	85	13.5	980	5	Q96246

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	264 AA.
Q9Z2L4	Q9Z2L4			
ID	Q9Z2L4			
AC	Q9Z2L4			
DC	01-MAY-1999 (TREMBL)	10, Created		
DT	01-MAY-1999 (TREMBL)	10, Last sequence update		
DT	01-JUN-2001 (TREMBL)	17, Last annotation update		
DE	APOLIPROTEIN A-I.			
GN	APOLI.			
OS	Mesocricetus auratus (Golden hamster).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC	Mesocricetus.			
OX	NCBI_TaxID=10036;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=GOLDEN STRAIN; TISSUE=INTESTINE;			
RX	MEDLINE=99061559; PubMed=9843713;			
RA	WU J.Y.J., Reeves S.K., Wang Y.R., Wu Y., Lei P.P., Lei K.Y.;			
RT	"Zinc deficiency decreases plasma level and hepatic mRNA abundance of			
RT	apolipoprotein A-I in rats and hamsters.";			
RL	Am. J. Physiol. 275:CI516-CI525(1998).			
DR	EMBL; AF046919; AAC98484.1; .			
DR	HSSP; P02647; IAVI.			
DR	InterPro; IPR000074; Apolipoprotein.			
KW	pfam: PF01442; Apolipoprotein; I.			
SO	Lipoprotein.			
	SEQUENCE 264 AA; 30739 MW; 280B22F4C0F0B129 CRC64;			

Query Match 80.5%; Score 508; DB 11; Length 264;
Best Local Similarity 79.0%; Pred. No. 5.6e-36;
Matches 94; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 2 DEPPQSPWMDVKLATVYDVKLSGRDVSQFEGSALGKQINLKLDNMDSVSTSKLR 61
DB 25 DEPPQSPWMDVKLATVYDVKLSGRDVSQFEGSALGKQINLKLDNMDSVSTSKLR 84
QY 62 EQLPVTQEFWNLKEKTEGLRQENSKDLEVKAKVQYLDLDDFOKKQWEMELRQKVE 120

Db 85 EOLGPTVTOEFMDNLEKETEGRLROEMKDLAEVAKVQPYLDDFOKKQWEMELRYOKV 143

RESULT 2

ID 009042 PRELIMINARY; PRT; 263 AA.

DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE APOLIPROTEIN A-I.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ICR AND BALB/C, AND C3H; TISSUE=SPLEEN;

RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U79575; AAB58427.1; -

DR EMBL; U79572; AAB58424.1; -

DR HSSP; P02647; IAVI.

DR InterPro: IPR000074; Apolipoprotein.

DR Pfam: PF01442; Apolipoprotein; 1.

KW Lipoprotein.

SEQUENCE 263 AA; 30516 MW; E245DF7483A5A0DD CRC64;

Query Match 76.2%; Score 481; DB 11; Length 263;

Best Local Similarity 72.9%; Pred. No. 1.2e-33;

Matches 86; Conservative 21; Mismatches 11; Indels 0; Gaps 0;

QY 2 EPPQSPMDRVKDLATVYVDLKDGRDYVSQFEGSALGKQLNKLIDNMDVSTFSKRL 61

Db 25 DEPOSQMDRVKDLATVYVDLKDGRDYVSQFEGSALGKQLNKLIDNMDVSTFSKRL 61

QY 62 EOLGPTVTOEFMDNLEKETEGRLROEMKDLAEVAKVQPYLDDFOKKQWEMELRYOKV 119

Db 85 ERLGPTVTOEFMDNLEKETEGRLROEMKDLAEVAKVQPYLDDFOKKQWEMELRYOKV 142

RESULT 3

ID 008855 PRELIMINARY; PRT; 263 AA.

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DE APOLIPROTEIN A-I.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=SPLEEN;

RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U79575; AAB58427.1; -

DR HSSP; P02647; IAVI.

DR InterPro: IPR000074; Apolipoprotein.

DR Pfam: PF01442; Apolipoprotein; 1.

KW Lipoprotein.

SEQUENCE 263 AA; 30544 MW; 7825DF7483A5B24A CRC64;

Query Match 76.2%; Score 481; DB 11; Length 263;

Best Local Similarity 72.9%; Pred. No. 1.2e-33;

Matches 86; Conservative 21; Mismatches 11; Indels 0; Gaps 0;

QY 2 EPPQSPMDRVKDLATVYVDLKDGRDYVSQFEGSALGKQLNKLIDNMDVSTFSKRL 61

Db 25 DEPOSQMDRVKDLATVYVDLKDGRDYVSQFEGSALGKQLNKLIDNMDVSTFSKRL 61

QY 62 EOLGPTVTOEFMDNLEKETEGRLROEMKDLAEVAKVQPYLDDFOKKQWEMELRYOKV 119

Db 85 ERLGPTVTOEFMDNLEKETEGRLROEMKDLAEVAKVQPYLDDFOKKQWEMELRYOKV 142

RESULT 4

ID 009054 PRELIMINARY; PRT; 258 AA.

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DE APOLIPROTEIN A-I.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=WKY AND SHRSP; TISSUE=SPLEEN;

RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U79578; AAB58430.1; -

DR HSSP; P02647; IAVI.

DR InterPro: IPR000074; Apolipoprotein.

DR Pfam: PF01442; Apolipoprotein; 1.

KW Lipoprotein.

SEQUENCE 258 AA; 29918 MW; 093BE6FE2629CD08 CRC64;

Query Match 73.5%; Score 464; DB 11; Length 258;

Best Local Similarity 72.5%; Pred. No. 3.2e-32;

Matches 87; Conservative 14; Mismatches 17; Indels 2; Gaps 1;

QY 1 DEPOSQMDRVKDLATVYVDLKDGRDYVSQFEGSALGKQLNKLIDNMDVSTFSKRL 60

Db 25 DEPOSQMDRVKDLATVYVDLKDGRDYVSQFEGSALGKQLNKLIDNMDVSTFSKRL 60

QY 61 EOLGPTVTOEFMDNLEKETEGRLROEMKDLAEVAKVQPYLDDFOKKQWEMELRYOKV 120

Db 83 ERLGPTVTOEFMDNLEKETEGRLROEMKDLAEVAKVQPYLDDFOKKQWEMELRYOKV 142

RESULT 5

ID 008877 PRELIMINARY; PRT; 258 AA.

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DE APOLIPROTEIN A-I.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SHR; TISSUE=SPLEEN;

RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U79576; AAB58428.1; -

DR HSSP; P02647; IAVI.

RESULT	9		
Q9UC78			
ID	Q9UC78	PRELIMINARY;	PRT; 26 AA.
AC	Q9UC78;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)		
DE	SPERM ACTIVATING PROTEIN SUBUNIT I, APOLIPOPROTEIN A1, SPAP SUBUNIT I		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=91369902; PubMed=190988;		
RA	Akerlof E., Jorntvall H., Slotte H., Pousette A.;		

RT "Identification of apolipoprotein AI and immunoglobulin as components
 of a serum complex that mediates activation of human sperm motility."
 RL Biochemistry 30:8986-8990(1991).
 SO SEQUENCE 26 AA; 2930 MW; 64921A333E768D27 CRC64;

Query Match 22.3%; Score 141; DB 4; Length 26;
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEPPSPMDRVKDLATVYVDLKDSCG 26
 DB 1 DEPPSPMDRVKDLATVYVDLKDSCG 26

RESULT 10
 Q9DFQ3 PRELIMINARY; PRT; 174 AA.
 AC Q9DFQ3:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE APOLIPROTEIN A-IV (FRAGMENT).
 OS *Gillichthys mirabilis* (Long-jawed mudsnucker).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorphi; Acanthopterygii; Perciformi; Perciformes; Gobioidi;
 CC Gobiidae; Gillichthys.
 OC NCBI_TaxID=8222;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=21117151; PubMed=11172064;
 RA Gracey A.V., Troil J.V., Somero G.N.;
 RT "Hypoxia-induced gene expression profiling in the euryoxic fish
Gillichthys mirabilis."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1993-1998(2001).
 DR EMBL; AF266179; AAG13299.1; -;
 KW Lipoprotein.
 FT NON_TER 174
 FT SEQUENCE 174 AA; 19342 MW; 3440836F5EDC863B CRC64;

Query Match 22.0%; Score 139; DB 13; Length 174;
 Best Local Similarity 27.1%; Pred. No. 0.00015;
 Matches 32; Conservative 25; Mismatches 61; Indels 0; Gaps 0;

QY 2 EPPSPMDRVKDLATVYVDLKDSCGGRVYQFEGSALGKQLNKLIDNMDSVTSPFSKLK 61
 DB 21 EPPSPMDRVKDLATVYVDLKDSCGGRVYQFEGSALGKQLNKLIDNMDSVTSPFSKLK 80
 QY 62 EOLGPVTOEFMDLKEKETEGTLEKROEMSKDLEEVKAKVQPYLDLPQKKOEMELRYQKV 119
 DB 81 TQAGPISQDLITQITQOTETLKSRLTELSAVANANLOPIAEOVLADLOTKMDALKADV 138

RESULT 11
 Q93601 PRELIMINARY; PRT; 366 AA.
 AC Q93601:
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE APOLIPROTEIN AIV.
 GN APOAIV.
 OS *Gallus gallus* (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98221191; PubMed=9553114;

RA Steimerz A., Hermann M., Nimpf J., Aebersold R., Ducret A.,
 RA Weinberg R.B., Schneider W.J.;
 RT "Expression and conservation of apolipoprotein AIV in an avian
 RT species."
 RL J. Biol. Chem. 273:10543-10549(1998).
 DR EMBL; Y16534; CAA76273.1; -;
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 FT SEQUENCE 366 AA; 40852 MW; B47DB49F3E8D91CE CRC64;

Query Match 19.9%; Score 125.5; DB 13; Length 366;
 Best Local Similarity 29.4%; Pred. No. 0.0053;
 Matches 30; Conservative 26; Mismatches 45; Indels 1; Gaps 1;
 QY 6 SPMDRVKDLATVYVDLKDSCGRVYQFEGSALGKQLNKLIDNMDSVTSPFSKLREOLG 65
 DB 22 SP-DQVATVLMRYETELSGSSAKETVDOQAETIKQLNTLQSLNSNSVAEELQRLV 80
 QY 66 PYQGEFMDLKEKETEGTLEKROEMSKDLEEVKAKVQPYLDLPQKK 107
 DB 81 PFATLEQALVQDSQRLKQIQQLQELQAKLAPYADEVHQ 122

RESULT 12
 Q13784 PRELIMINARY; PRT; 244 AA.
 AC Q13784:
 ID Q13784:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE APOA4 PROTEIN (FRAGMENT).
 GN APOA4.
 OS *Homo sapiens* (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=86016704; PubMed=3931073;
 RA Karathanasis S.K.;
 RT "Apolipoprotein multigene family: tandem organization of human
 apolipoprotein AI, CIII, and AIV genes."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6374-6378(1985).
 DR EMBL; M10373; AAB59516.1; -;
 DR HSSP; P02649; 1B24.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 FT NON_TER 1
 FT SEQUENCE 244 AA; 28157 MW; 01616ACB53F12734 CRC64;

Query Match 18.9%; Score 119.5; DB 4; Length 244;
 Best Local Similarity 25.9%; Pred. No. 0.011;
 Matches 30; Conservative 31; Mismatches 46; Indels 9; Gaps 2;

QY 11 VKDLATVYVDLKDSCGRVYQFEGSALGKQLNKLIDNMDSVTSPFSKLREOLGPTVQ 70
 DB 82 VEELRSLAPYADPTQELKHOLEGLTFQMKKNNEELK--ARISASAEELRQRLAPLAE 139
 QY 71 FMDLKEKETEGTLEKROEMSKDLEEVKAKVQPYLDLPQKKOEMELRYQKV 119
 DB 140 VRGNLKGNTBGLQSLAELGHDQOQVEFRFRVEYGENFNALVOQMDOLRKL 195

RESULT 13
 Q98TG6 PRELIMINARY; PRT; 263 AA.
 AC Q98TG6:
 ID Q98TG6:
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)


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DE 01-061-2001 (Tremblrel. 18, last annotation update)
DE 28KDA-2 Apolipoprotein.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguillidae; Anguilla.
OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE=21175592; PubMed=11278178;
RA Kondo H., Kawazoe I., Nakaya M., Kikuchi K., Aida K., Watabe S.;
RT "The novel sequences of major plasma apolipoproteins in the eel
RL Anguilla japonica."
RL Blochum. Biophys. Acta 1531:132-142(2001).
DR EMBL; AB046203; BAB40960.1; -
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein; 1.
KW Lipoprotein.
SQ SEQUENCE 263 AA; 30087 MW; DB8CB0AF30EB6B1 CRC64;

Query Match 18.1%; Score 114; DB 13; Length 263;
Best Local Similarity 24.5%; Pred. No. 0.034;
Matches 35; Conservative 34; Mismatches 50; Indels 24; Gaps 5;

QY 1 DEF-POSPMDRVKDIATVYVDVLDKSGRDYSQFEGSALGKQLNLKLDN----- 49
DB 24 DAVAPVQLEHVAAYVTLQVKEAQKALEHDDTEY-KDYKRLQSQSDNTQGTQS 82
QY 50 -----WDSYTFPSKIREQLGPTVDFEWNLEKETEGLEKQEM---SKDLEEVKAVY 97
DB 83 ASALSPYTDVAVSSQFMELTKDMRKIQADVQLKQPRDELKEVYQKHIDEYRAKL 142
QY 98 OPTLDFQKKQOEEMELRYOKVE 120
DB 143 EPLVKEYTEKHQKQEMELKTKIQ 165

RESULT 14
Q01488 PRELIMINARY; PRT; 435 AA.
AC Q01488;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE VARIANT APOLIPOPROTEIN A-IV PRECURSOR (APOA-IV).
GN APOA-4.
OS Mus musculus castaneus (southeastern Asian house mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91286309; PubMed=1648102;
RA Reue K., Leete T.H.;
RT "Genetic variation in mouse apolipoprotein A-IV due to insertion and
RT deletion in a region of tandem repeats."
RL J. Biol. Chem. 266:12715-12721(1991).
CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
CC LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
CC COMPONENT OF HDL AND CHYLOMICRONS. IT MAY PLAY A ROLE IN THE
CC INTRAVASCULAR METABOLISM OF HDL. POTENTIAL ROLE IN CELLULAR
CC CHOLESTEROL EFFLUX.
CC -1- TISSUE SPECIFICITY: INTESTINE, LIVER, AND PLASMA.
CC -1- MISCELLANEOUS: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS
CC (EACH 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A & B, RELATED 11-
CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
CC HELICAL. 6 MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH
CC LECTININ:CHOLESTEROL ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
CC -1- MISCELLANEOUS: THE APOA-IV POLYMORPHISMS ARE CLASSIFIED BASED ON

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CC THE OCCURRENCE OF THREE, FOUR, OR FIVE E-Q-A-Q/ E-Q-Q-Q/ E-Q-V-Q
CC REPEAT UNITS.
DR EMBL: M64250; AAA37216.1; -
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein; 1.
KW Lipid transport; HDL; VLDL; Chylomicron; Repeat; Signal; Liver;
KW Plasma; Multigene family; Polymorphism; Cholesterol metabolism.
FT SIGNAL 1 20
FT CHAIN 21 435
FT DOMAIN 374 393
FT REPEAT 377 378
FT REPEAT 378 381
FT REPEAT 382 385
FT REPEAT 386 389
FT REPEAT 390 393
SQ SEQUENCE 435 AA; 49254 MW; B2AF55EEBA8E456B2 CRC64;

Query Match 18.1%; Score 114; DB 11; Length 435;
Best Local Similarity 21.4%; Pred. No. 0.064;
Matches 24; Conservative 37; Mismatches 51; Indels 0; Gaps 0;

QY 9 DRVKDIATVYVDVLDKSGRDYSQFEGSALGKQLNLKLDNMDVSTFSKIREQLGPTV 68
DB 25 DOVANVWDVFTHLSSNAKEAEAEQFKTDVYQQLSTLFQDKLGDASTYADGVRNKLVPV 84
QY 69 QEFWDNLEKETEGLEKQEMSKDLEEVKAVVOPYLDFQKKQOEEMELRYOKVE 120
DB 85 VOLSGHLAKETERYKVEIKLEELDRDMMPHANKVTOTFEENQKQLEHLK 136

RESULT 15
Q01488 PRELIMINARY; PRT; 395 AA.
AC Q01488;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:18592).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-KIDNEY;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010769; AAH10769.1; -
SQ SEQUENCE 395 AA; 45029 MW; C48BE32EED441F71 CRC64;

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Query Match 17.4%; Score 110; DB 11; Length 395;
Best Local Similarity 20.5%; Pred. No. 0.12;
Matches 23; Conservative 38; Mismatches 51; Indels 0; Gaps 0;

QY 9 DRVKDIATVYVDVLDKSGRDYSQFEGSALGKQLNLKLDNMDVSTFSKIREQLGPTV 68
DB 25 DOVANVWDVFTHLSSNAKEAEAEQFKTDVYQQLSTLFQDKLGDASTYADGVRNKLVPV 84
QY 69 QEFWDNLEKETEGLEKQEMSKDLEEVKAVVOPYLDFQKKQOEEMELRYOKVE 120
DB 85 VOLSGHLAKETERYKVEIKLEELDRDMMPHANKVTOTFEENQKQLEHLK 136

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Search completed: September 22, 2002, 12:21:37
 Job time: 1117 sec

Sun Sep 22 12:10:26 2002

us-09-803-918a-2_copy_25_144.rspt

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:06:28 ; Search time 66.91 Seconds
(without alignments)
244.137 Million cell updates/sec

Title: US-09-803-918a-2_COPY_25_194
Perfect score: 885

Sequence: 1 DEPPQSPMDRVRKDLATVYVD.....RARAHVDALRTHLADYSDEL 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pIR1:*
2: pIR2:*
3: pIR3:*
4: pIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	885	100.0	267	1	LPHUAI apolipoprotein A-I
2	842	95.1	267	1	A26529 apolipoprotein A-I
3	842	95.1	267	1	JS0079 apolipoprotein A-I
4	758	85.6	266	1	LPGAI1 apolipoprotein A-I
5	737	83.3	265	2	A46018 apolipoprotein A-I
6	730	82.5	265	2	JT0672 apolipoprotein A-I
7	728.5	82.3	264	2	S31394 apolipoprotein A-I
8	728.5	82.3	264	1	LPHI12 apolipoprotein A-I
9	708	80.0	265	2	A56858 apolipoprotein A-I
10	704	79.5	265	1	LPHR18 apolipoprotein A-I
11	701.5	79.3	241	2	A24998 apolipoprotein A-I
12	678.5	76.7	231	2	J00704 apolipoprotein A-I
13	655	74.0	262	2	JC1237 apolipoprotein A-I
14	655	74.0	264	2	S22420 apolipoprotein A-I
15	573	64.7	259	2	A24700 apolipoprotein A-I
16	471	53.2	246	2	A61448 apolipoprotein A-I
17	471	53.2	264	1	LPCHA1 apolipoprotein A-I
18	454	51.3	264	2	JC5456 apolipoprotein A-I
19	370	41.8	164	2	S21830 apolipoprotein A-I
20	214	24.2	429	2	S29565 apolipoprotein A-I
21	213	23.1	396	1	LPHUAI apolipoprotein A-I
22	210	23.7	401	2	A47141 apolipoprotein A-I
23	181	20.5	391	1	LPHUAI apolipoprotein A-I
24	175	19.8	391	1	B40892 apolipoprotein A-I
25	175	19.8	394	2	A25281 apolipoprotein A-I
26	175	19.8	395	2	A40892 apolipoprotein A-I
27	175	19.8	399	2	C40892 apolipoprotein E p
28	156.5	17.7	311	2	JU0036 apolipoprotein E p
29	156.5	17.7	312	1	LPHUAI apolipoprotein E p

ALIGNMENTS

RESULT 1

LPHUAI apolipoprotein A-I precursor [validated] - human

N:Alternate names: apoA-I-2; apoA-I-4; preproapoA-I; prostacyclin stabilizing factor

C:Species: Homo sapiens (man)

C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 08-Dec-2000

C:Accession: A90947; B90947; S02373; A93465; A21147; A93519; B93519; A93472; A94010; 6197

R:Seilhammer, J.J.; Protter, A.A.; Frossard, P.; Levy-Wilson, B.

DNA 3, 309-317, 1984

A:Title: Isolation and DNA sequence of full-length cDNA and of the entire gene for hu

A:Reference number: A90947; MUID:85026655

A:Accession: A90947

A:Molecule type: DNA

A:Residues: 1-267 <SEI>

A:Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635

A:Accession: B90947

A:Molecule type: mRNA

A:Residues: 1-267 <SE2>

A:Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635

R:Markrides, S.C.; Ruiz-Opazo, N.; Hayden, M.; Nussbaum, A.L.; Breslow, J.L.; Zannis,

Eur. J. Biochem. 173, 465-471, 1988

A:Title: Sequence and expression of Tangier apoA-I gene.

A:Reference number: S02373; MUID:88196137

A:Accession: S02373

A:Molecule type: DNA

A:Residues: 1-267 <MAK>

A:Cross-references: EMBL:X07496; NID:g28774; PIDN:CAA30377.1; PID:g296729

R:Shoulders, C.C.; Kornblith, A.R.; Munro, B.S.; Baralle, F.E.

Nucleic Acids Res. 11, 2827-2837, 1983

A:Title: Gene structure of human apolipoprotein AI.

A:Reference number: A93465; MUID:83220822

A:Accession: A93465

A:Molecule type: DNA

A:Residues: 1-267 <SHO>

A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518;

R:Karathanasis, S.K.; Zannis, V.I.; Breslow, J.L.

Proc. Natl. Acad. Sci. U.S.A. 80, 6147-6151, 1983

A:Title: Isolation and characterization of the human apolipoprotein A-I gene.

A:Reference number: A21147; MUID:84016011

A:Accession: A21147

A:Molecule type: DNA

A:Residues: 1-267 <KAR>

A:Cross-references: GB:J00098; GB:J03222; NID:g17875; PIDN:AAB59514.1; PID:g178768

R:Shaper, C.R.; Sidoti, A.; Shelley, C.S.; Lucero, M.A.; Shoulders, C.C.; Baralle, F.

Nucleic Acids Res. 12, 3917-3932, 1984

A:Title: Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA abundance

A:Reference number: A93519; MUID:84221405

A:Accession: A93519

A:Molecule type: mRNA

A:Residues: 1-267 <SHA>

A:Cross-references: GB:X00566; NID:g28765; PIDN:CAA25232.1; PID:g732753

A:Accession: B93519
 A:Molecule type: DNA
 A:Residues: 1-24 <SH2>
 R:Cheung, P.; Chan, L.
 Nucleic Acids Res. 11, 3703-3715, 1983
 A:Title: Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.
 A:Reference number: A93472; MUID:83220772
 A:Accession: A93472
 A:Molecule type: mRNA
 A:Residues: 1-267 <CHE>
 A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GB:Proc Natl. Acad. Sci. U.S.A. 81, 66-70, 1984
 R:Law, S.W.; Brewer Jr., H.B.
 A:Title: Nucleotide sequence and the encoded amino acids of human apolipoprotein A-I mRNA
 A:Reference number: A94010; MUID:84119464
 A:Accession: A94010
 A:Molecule type: mRNA
 A:Residues: 1-267 <LAN>
 A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GB:Proc Natl. Acad. Sci. U.S.A. 80, 2574-2578, 1983
 R:Zannis, V.I.; Karathanasis, S.K.; Keutmann, H.T.; Goldberger, G.; Breslow, J.L.
 A:Title: Intracellular and extracellular processing of human apolipoprotein A-I: secreted
 A:Reference number: A21118; MUID:83195100
 A:Accession: A21118
 A:Molecule type: protein
 A:Residues: 1-24 <ZAN>
 R:Brewer Jr., H.B.; Fairwell, T.; Kay, L.; Meng, M.; Roman, R.; Law, S.; Light, J.A.
 Biochem. Biophys. Res. Commun. 113, 626-632, 1983
 A:Title: The amino acid sequence of human APOA-I, an apolipoprotein isolated from high density lipoprotein
 A:Reference number: A90112; MUID:83256553
 A:Accession: A90112
 A:Molecule type: protein
 A:Residues: 19-27 <BRE>
 R:Brewer Jr., H.B.; Fairwell, T.; Lakke, A.; Roman, R.; Houser, A.; Bronzert, T.J.
 Biochem. Biophys. Res. Commun. 80, 623-630, 1978
 A:Title: The amino acid sequence of human APOA-I, an apolipoprotein isolated from high density lipoprotein
 A:Reference number: A90209; MUID:78123731
 A:Accession: A90209
 A:Molecule type: protein
 A:Residues: 25-57 'Q', 59-169 'Q', 172-267 <BR2>
 R:Yui, Y.; Aoyama, T.; Morishita, H.; Takahashi, M.; Takatsu, Y.; Kawai, C.
 J. Clin. Invest. 82, 803-807, 1988
 A:Title: Serum prostacyclin stabilizing factor is identical to apolipoprotein A-I (Apo A-I)
 A:Reference number: A30516; MUID:88331387
 A:Accession: A30516
 A:Molecule type: protein
 A:Residues: 25-56 <YUI>
 R:Nichols, W.C.; Duvallet, F.E.; Liepmanns, J.; Benson, M.D.
 Biochem. Biophys. Res. Commun. 156, 762-768, 1988
 A:Title: Variant apolipoprotein AI as a major constituent of a human hereditary amyloid.
 A:Reference number: A31582; MUID:89050104
 A:Accession: A31582
 A:Molecule type: protein
 A:Residues: 25-49 'R', 51-85 'P', 87-107 <NIC>
 R:Manjunath, P.; Marcel, Y.L.; Uma, U.; Seidah, N.G.; Chretien, M.; Chapdelaine, A.
 J. Biol. Chem. 264, 16853-16857, 1989
 A:Title: Apolipoprotein A-I binds to a family of bovine seminal plasma proteins.
 A:Reference number: A34409; MUID:89380318
 A:Accession: A34409
 A:Molecule type: protein
 A:Residues: 25-48 <MAN>
 R:Stoffel, W.; Binczek, E.
 Biol. Chem. Hoppe-Seyler 369, 1055-1063, 1988
 A:Title: Structural requirements of human preproapolipoprotein AI for translocation and secretion
 A:Reference number: S02737; MUID:89149957
 A:Accession: S02737
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-6, 'AV', '9', 'LV', '12-29 <STO>
 A:Note: part of this sequence, including the amino end of the mature protein, was confirmed by Stoffel, W.; Binczek, E.
 Biol. Chem. Hoppe-Seyler 372, 481-488, 1991

A:Title: Transient expression of wild type and mutant human apolipoprotein AI in COS cells
 A:Reference number: S16197; MUID:92029676
 A:Contents: annotation; extension in reference S02737
 R:Stoffel, W.; Kruger, E.; Deutzmann, R.
 Hoppe-Seyler's Z. Physiol. Chem. 364, 227-237, 1983
 A:Title: Cell-free translation of human liver apolipoprotein AI and AII mRNA processed in vitro
 A:Reference number: A19913; MUID:8326195
 A:Accession: A19913
 A:Molecule type: protein
 A:Residues: 1-6, 'X', 8-13, 'XXX', 17-18, 'XX', 21, 'X', 23-25, 'X', 27-29 <ST2>
 R:Enholm, C.; Bozas, S.E.; Tenkannen, H.; Kirsbaum, L.; Metsio, J.; Murphy, B.; Walke, B.
 Biochim. Biophys. Acta 1086, 255-260, 1991
 A:Title: The apolipoprotein A-I binding protein of placenta and the SP-40,40 protein
 A:Reference number: A56815; MUID:92073698
 A:Accession: A56815
 A:Molecule type: protein
 A:Residues: 25-31, 'P', 33 <EHN>
 A:Experimental source: serum
 A:Note: sequence extracted from NCBI backbone (NCBIP:69759)
 R:Kunitake, S.T.; Garilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
 Biochemistry 33, 1988-1993, 1994
 A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipoproteins
 A:Reference number: A54223; MUID:94162201
 A:Accession: A54223
 A:Molecule type: protein
 A:Residues: 25-39 <KUN>
 R:Mogul'sky, N.; Roobol, C.; Lortiu, R.; Guillaume, J.P.; Jacobs, P.; Cravador, A.; Dina, R.
 J. Biol. Chem. 269, 429-436, 1994
 A:Title: Production of human recombinant proapolipoprotein A-I in *Escherichia coli*: pAPOL
 A:Reference number: I39476; MUID:89377481
 A:Accession: I39476
 A:Molecule type: mRNA
 A:Residues: 19-267 <RES>
 A:Cross-references: GB:M20068; MUID:9178774; PIDN:AA51747.1; PID:9178775
 R:Ilqich, K.; Law, S.W.; Hoeg, J.M.; Schumacher, U.K.; Meglun, N.; Brewer, H.B.
 J. Biol. Chem. 263, 18530-18536, 1988
 A:Title: Tissue-specific expression of apolipoprotein A-I (ApoA-I) is regulated by the APOA1 gene
 A:Reference number: I39475; MUID:89050400
 A:Accession: I39475
 A:Molecule type: DNA
 A:Residues: 1-14 <RE2>
 A:Cross-references: GB:J04066; MUID:9178765; PIDN:AA51746.1; PID:9553183
 R:Breslow, J.L.
 Annu. Rev. Biochem. 54, 699-727, 1985
 A:Title: Human apolipoprotein molecular biology and genetic variation.
 A:Reference number: A90042; MUID:85278004
 A:Contents: annotation; review of sequences, variants and gene location
 R:Hoeg, J.M.; Meng, M.S.; Roman, R.; Fairwell, T.; Brewer Jr., H.B.
 J. Biol. Chem. 261, 3911-3914, 1986
 A:Title: Human apolipoprotein A-I. Post-translational modification by fatty acid acyl groups
 A:Reference number: A92577; MUID:86140194
 A:Contents: annotation; acylation with palmitate
 A:Note: an undetermined serine or threonine is acylated by fatty acid; the acylating R:Law, S.W.; Brewer, H.B.
 J. Biol. Chem. 260, 12810-12814, 1985
 A:Title: Tangier disease: the complete mRNA sequence encoding for preproapo-A-I.
 A:Reference number: I55236; MUID:86008382
 A:Accession: I55236
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-143, 'D', 145-267 <RE3>
 A:Cross-references: GB:M11791; MUID:9178776; PIDN:AA53545.1; PID:9178777
 C:Comment: Apolipoprotein A-I precursor is synthesized in the liver and small intestine (HDI) in plasma.
 A:Gene: GDB:APOA1
 A:Cross-references: GDB:119684; OMIM:107680
 A:Map position: 11q23.3-11q23.3
 A:Introns: 15/1; 67/2
 C:Function:
 A:Description: participates in the reverse transport of cholesterol from tissues to the liver and stabilizes prostacyclin (PGI-2)

C:Superfamily: apolipoprotein A-I
 C:Keywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid binding; lipi
 F:1-18/Domain: signal sequence #status experimental <SIG>
 F:19-24/Domain: propeptide #status experimental <PPO>
 F:25-267/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 100.0%; Score 885; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 4,7e-49;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DEPPSPMDRVKDLATVYVDVLDKSGRDYVSGFEGSALGKQNLKLDNMDSVTSFESKL 60
 |||||
 DB 25 DEPPSPMDRVKDLATVYVDVLDKSGRDYVSGFEGSALGKQNLKLDNMDSVTSFESKL 84
 |||||
 OY 61 REOLGPVTOEFWNLKEKETEGRLQEMSKDLEEVKAKVQPYLDPFQKKWQEMELYRQKVE 120
 |||||
 DB 85 REOLGPVTOEFWNLKEKETEGRLQEMSKDLEEVKAKVQPYLDPFQKKWQEMELYRQKVE 144
 |||||
 OY 121 PLRAELQEGAROKLHELQEKLSPLGSEMRDARAHVDALRTHLAPYSDEL 170
 |||||
 DB 145 PLRAELQEGAROKLHELQEKLSPLGSEMRDARAHVDALRTHLAPYSDEL 194
 |||||

RESULT 2

Apolipoprotein A-I precursor - crab-eating macaque

C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 30-Sep-1989 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999

C:Accession: A26529; A26627; S23135; A57766
 R:Polites, H.G.; Melchior, G.W.; Castle, C.K.; Marottili, K.R.

Gene 49, 103-110, 1986

A:Title: The primary structure of cynomolgus monkey apolipoprotein A-I deduced from the
 A:Reference number: A26529; MUID:87191989
 A:Accession: A26529

A:Molecule type: mRNA

A:Residues: 1-267 <PPO>

A:Cross-references: GB:M5411; NID:9342074; PIDN:AAA3634.1; PID:9342075

R:Herbert, P.N.; Bauserman, L.L.; Lynch, K.M.; Sartelli, A.L.; Kantor, M.A.; Nicolosi,
 Biochemistry 26, 1457-1463, 1987

A:Title: Homologues of the human C and A apolipoproteins in the Macaca fascicularis (cyn
 A:Reference number: A26627; MUID:87185451
 A:Accession: A26627

A:Molecule type: protein

A:Residues: 25-48 <HER>

R:Murray, R.W.; Marottili, K.R.

Biochim. Biophys. Acta 1131, 207-210, 1992

A:Title: Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene and corre
 A:Reference number: S23135; MUID:92305062

A:Accession: S23135

A:Molecule type: DNA

A:Residues: 1-12, 'L', 14-267 <MUR>

A:Cross-references: GB:M83242; NID:9342070; PIDN:AAA3632.1; PID:9342071

R:Sorci-Thomas, M.; Kearns, M.W.

J. Biol. Chem. 266, 18045-18050, 1991

A:Title: Transcriptional regulation of the apolipoprotein A-I gene.
 A:Reference number: A57766; MUID:92011532

A:Accession: A57766

A:Molecule type: DNA

A:Residues: 1-10 <RES>

A:Cross-references: GB:M69223; NID:9342066; PIDN:AAA36831.1; PID:9553820

C:Comment: The precursor is synthesized in the liver and small intestine. The propeptide
 C:Comment: ApoA-I makes up about 70% of the protein of the high density lipoproteins (HD
 Y promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin

C:Genetics: 15/1; 67/2

C:Superfamily: apolipoprotein A-I

C:Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem repe
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PPO>
 F:25-267/Product: apolipoprotein A-I #status predicted <MAT>

Query Match 95.1%; Score 842; DB 1; Length 267;
 Best Local Similarity 94.1%; Pred. No. 2,4e-46;
 Matches 160; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 DEPPSPMDRVKDLATVYVDVLDKSGRDYVSGFEGSALGKQNLKLDNMDSVTSFESKL 60
 |||||
 DB 25 DEPPSPMDRVKDLATVYVDVLDKSGRDYVSGFEGSALGKQNLKLDNMDSVTSFESKL 84
 |||||
 OY 61 REOLGPVTOEFWNLKEKETEGRLQEMSKDLEEVKAKVQPYLDPFQKKWQEMELYRQKVE 120
 |||||
 DB 85 REOLGPVTOEFWNLKEKETEGRLQEMSKDLEEVKAKVQPYLDPFQKKWQEMELYRQKVE 144
 |||||
 OY 121 PLRAELQEGAROKLHELQEKLSPLGSEMRDARAHVDALRTHLAPYSDEL 170
 |||||
 DB 145 PLRAELQEGAROKLHELQEKLSPLGSEMRDARAHVDALRTHLAPYSDEL 194
 |||||

RESULT 3

Apolipoprotein A-I precursor - baboon

C:Species: Papio sp. (baboon)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Jun-1997

C:Accession: JS0079

R:Hixon, J.E.; Borenstein, S.; Cox, L.A.; Rainwater, D.L.; Vandenberg, J.L.
 Gene 74, 483-490, 1988

A:Title: The baboon gene for apolipoprotein A-I: characterization of a cDNA clone and
 A:Reference number: JS0079; MUID:89232739
 A:Accession: JS0079

A:Molecule type: mRNA

A:Residues: 1-267 <HIX>

A:Experimental source: liver

C:Comment: This protein is the principal protein component of high density lipoprotei
 C:Comment: This protein serves as a cofactor for lecithin cholesterol acyltransferase

C:Comment: This protein contains a region of repeated amino acids which form amphipat
 C:Genetics: 1

A:Gene: apoA1

C:Superfamily: apolipoprotein A-I

C:Keywords: HDL; lipid binding; lipoprotein

F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-267/Product: apolipoprotein A-I #status predicted <PPO>

F:123-144,145-166,167-188,189-210,211-223,223-254/Region: tandem repeats

Query Match 95.1%; Score 842; DB 2; Length 267;
 Best Local Similarity 94.1%; Pred. No. 2,4e-46;
 Matches 160; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 DEPPSPMDRVKDLATVYVDVLDKSGRDYVSGFEGSALGKQNLKLDNMDSVTSFESKL 60
 |||||
 DB 25 DEPPSPMDRVKDLATVYVDVLDKSGRDYVSGFEGSALGKQNLKLDNMDSVTSFESKL 84
 |||||
 OY 61 REOLGPVTOEFWNLKEKETEGRLQEMSKDLEEVKAKVQPYLDPFQKKWQEMELYRQKVE 120
 |||||
 DB 85 REOLGPVTOEFWNLKEKETEGRLQEMSKDLEEVKAKVQPYLDPFQKKWQEMELYRQKVE 144
 |||||
 OY 121 PLRAELQEGAROKLHELQEKLSPLGSEMRDARAHVDALRTHLAPYSDEL 170
 |||||
 DB 145 PLRAELQEGAROKLHELQEKLSPLGSEMRDARAHVDALRTHLAPYSDEL 194
 |||||

RESULT 4

LipidGAL
 Apolipoprotein A-I precursor - dog

C:Species: Canis lupus familiaris (dog)
 C:Date: 17-Dec-1982 #sequence_revision 14-Jul-1994 #text_change 07-May-1999

C:Accession: A60940; A03092; A61418

R:Luo, C.C.; Li, W.H.; Chan, L.

J. Lipid Res. 30, 1735-1746, 1989

A:Title: Structure and expression of dog apolipoprotein A-I, E, and C-I mRNAs: implic
 A:Reference number: A60940; MUID:90132271
 A:Accession: A60940

A:Molecule type: mRNA

A:Residues: 1-266 <LUO>

Db 1 VKDEAYVYDAIKDSGRDYVAOFFASAI GKHI NI KI LDNDWDSI GSTETTKYBEQI CQVYTOE 50

61 FWDNLEKETFEALROKMSKDIFFYKKKKVOPYI DDEONKWOEFMEYDPM-DI CAEEECB 110

```

db      120 ROKVOELOEKSPLAEELRDBRLAHVAALBOHVAPYSDDL 159
      |||:|||||||:|||||||:|||||||:

```

RESOLUT 13
JC1237

```
C;Accession: JCI1237
c,date: 30-Sep-1993 #sequence_revision 30-Sep-1993
c,date: 30-Sep-1993 #text_change 31-Dec-1993
```

A; Reference number: JCI1237; MUID:92347700

A;Cross-references: GB:M77801

C:Superfamily: apolipoprotein A-I

[illegible]

Matches	120;	Conservative	28;	Mismatches	21;	Indels	0;	Gaps	0;
---------	------	--------------	-----	------------	-----	--------	----	------	----

d5 DEPOSQWDXKDFANVYDAVKDSGRDYSQFESSLGQNLNLLNNWDTLGSTVSQD 84

Dö 85 ERLGPIITRDFWINDJEKETDWARQEMNKDLLEEVKQVOPYLIDFEQKKKKEDVELYRQKAP 144

Db 145 LGAEIÖESARÖKLÖELÖGRSLPVAEEFRDMRTHVDSLRTÖLAPHSEÖM 193

apolipoprotein A-T precursor - mouse
S22420

C/Accession: S22420; S22421; A44364
R:Stoffel, W.; Mueller, R.; Binczek, E.; Hofmann, K

A:Reference number: S22420; MUID:92281682
A:Accession: S22420

A; Residues: 1-264 <STO>
A; Cross-references: EMBL:X64262: NTD:q50014: PTD:CAA45560.1: PTD:q50014:

A;Molecule type: DNA
A;Residues: 1-264 <ST2>

Qy	2	EPQSPMDRKYDADATYVYDVLKDGSGROYVSPESALGOKNLKLDNDNDVSTFSFKLR	61
Qy	25	DEPQSQMDRYKDFATYVYDAVKDGSROYVYQFESTLKGKLNLTLDNDNDVTLSGVGKQ	84
Db	62	EOGLPPTQFPMNLKEFEGELROEMSKDLEBYAKVQPYLDDFOKKWOEMELYRQKVER	121
Qy	85	EOGLPPTQFPMNLKEFEGELROEMSKDLEBYAKVQPYLDDFOKKWOEMELYRQKVER	144
Db	122	LRKLEDEGAROKLHLEQKLSPLGCEEMKDRBARAHVADALRTHLAPYSDEL	170

Search completed: September 22, 2002, 12:06:28
Job time: 323 sec

Sun Sep 22 12:10:31 2002

us-09-803-918a-2_copy_25_194.rpt

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2002, 12:22:16 ; Search time 35.02 seconds
(without alignments)
187.959 Million cell updates/sec

Title: US-09-803-918a-2_COPY_25_194

Perfect score: 885
Sequence: 1 DEPPQSPMDRVKDLATVYD.....RAAHVDAIRTHIAEYDEL 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	885	100.0	267 1 APAL_HUMAN	P02647 homo sapien
2	842	95.1	267 1 APAL_MACFA	P15568 macaca fasc
3	758	85.6	266 1 APAL_CANFA	P02648 canis fami1
4	742	83.8	265 1 APAL_PIG	P18648 sus scrofa
5	711	80.3	266 1 APAL_RABIT	P09809 oryctolagus
6	703	79.4	265 1 APAL_BOVIN	P15497 bos taurus
7	655	74.0	264 1 APAL_MOUSE	Q00623 mus musculu
8	637	72.0	265 1 APAL_TUGB	O18739 tupia glis
9	573	64.7	259 1 APAL_RAT	P04639 rattus norv
10	471	53.2	264 1 APAL_ANAPL	O42256 anas platyr
11	471	53.2	264 1 APAL_CHICK	P08250 gallus gall
12	454	51.3	264 1 APAL_CORTA	P32918 coturnix co
13	214	24.2	429 1 APAL_MACFA	P33621 macaca fasc
14	210	23.7	401 1 APAL_PAPAN	Q28758 papio anubi
15	209	23.6	396 1 APAL_HUMAN	P06727 homo sapien
16	192	21.7	382 1 APAL_PIG	O46409 sus scrofa
17	184.5	20.8	262 1 APAL_ONCMY	O57523 oncorhynch
18	182	20.6	281 1 APAL_BRARE	O42364 brachydanio
19	181	20.5	391 1 APAL_RAT	P02651 rattus norv
20	177.5	20.1	262 1 APAL_SALTR	Q91488 salmo trutt
21	175	19.8	262 1 APAL_ONCMY	O57524 oncorhynch
22	175	19.6	395 1 APAL_MOUSE	P06728 mus musculu
23	173.5	19.6	262 1 APAL_BRARE	O42363 brachydanio
24	156.5	17.7	311 1 APAL_MOUSE	P08226 mus musculu
25	156.5	17.7	312 1 APAL_RAT	P02650 rattus norv
26	154.5	17.5	260 1 APAL_SPAU	O42175 sparus auro
27	153	17.3	258 1 APAL_SALSA	P27007 salmo salar
28	138.5	15.6	317 1 APAL_PIG	P18650 sus scrofa
29	135.5	15.3	305 1 APAL_CANFA	P18649 canis fami1
30	133	15.0	298 1 APAL_CAVRO	P23529 canis porce
31	125	14.1	317 1 APAL_MACFA	P10517 macaca fasc
32	125	14.1	317 1 APAL_PAPAN	P05770 papio anubi
33	119.5	13.5	317 1 APAL_HUMAN	P02649 homo sapien

34	119.5	13.5	896 1	EP15_HUMAN	P42566 homo sapien
35	118.5	13.4	897 1	EP15_MOUSE	P42567 mus musculu
36	115	13.0	180 1	VE76_AOUAE	P47453 aequifex aeo
37	113	12.8	316 1	APL_BOVIN	O03247 bos taurus
38	111.5	12.6	539 1	MY53_HYDAT	P39922 hydra atten
39	110.5	12.5	520 1	RECNA_AOUAE	O66834 aequifex aeo
40	109	12.3	311 1	APL_RABIT	P18287 oryctolagus
41	108	12.2	2230 1	G0G4_HUMAN	Q13439 homo sapien
42	107.5	12.1	1938 1	MY5_AEOIR	P24733 aequipecten
43	106	12.0	429 1	SEP6_MOUSE	O941t4 mus musculu
44	106	12.0	664 1	LAMA_HUMAN	P02545 homo sapien
45	105.5	11.9	365 1	RECFC_CHLTR	O84077 chlamydia t

ALIGNMENTS

RESULT ID	APAL_HUMAN	STANDARD;	PRT;	267 AA.
AC	P02647;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Apolipoprotein A-I precursor (Apo-AI).			
GN	APOA1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84221405; PubMed=6328445;			
RA	Shapiro C.R., Sidoli A., Shelley C.S., Lucero M.A., Shoulders C.C.,			
RA	Barralle F.E.;			
RT	"Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA			
RT	abundance."			
RL	Nucleic Acids Res. 12:3917-3932(1984).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8502665; PubMed=6207999;			
RA	Sellhammer J.J., Protter A.A., Frossard P., Levy-Wilson B.;			
RA	Shoulders C.C., Kornblith A.R., Munro B.S., Barralle F.E.;			
RT	"Gene structure of human apolipoprotein AI -- discovery of a new genetic			
RT	polymorphism in the apo AI gene."			
RL	DNA 3:309-317(1984).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83220822; PubMed=6406984;			
RA	Shoulders C.C., Kornblith A.R., Munro B.S., Barralle F.E.;			
RT	"Gene structure of human apolipoprotein AI."			
RL	Nucleic Acids Res. 11:2827-2837(1983).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83220772; PubMed=6304641;			
RA	Cheung P., Chan L.;			
RT	"Nucleotide sequence of cloned cDNA of human apolipoprotein A-I."			
RL	Nucleic Acids Res. 11:3703-3715(1983).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84119464; PubMed=6198645;			
RA	Law S.W., Brewer H.B. Jr.;			
RT	"Nucleotide sequence and the encoded amino acids of human			
RT	apolipoprotein A-I mRNA."			
RL	Proc. Natl. Acad. Sci. U.S.A. 81:66-70(1984).			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86008382; PubMed=2993932;			
RA	Law S.W., Brewer H.B. Jr.;			
RT	"Angier disease. The complete mRNA sequence encoding for			
RT	preproapo-A-I."			
RL	J. Biol. Chem. 260:12810-12814(1985).			
RN	[7]			

- RP SEQUENCE FROM N.A.
 RX MEDLINE=84016011; PubMed=6413973;
 RA Karathanasis S.K., Zannis V.I., Breslow J.L.;
 RT "Isolation and characterization of the human apolipoprotein A-I
 gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:6147-6151(1983).
 RN [18]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89377481; PubMed=2673706;
 RA Mogulovsky N., Roobol C., Loriau R., Guillaume J.P., Jacobs P.,
 RA Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,
 RA Holmquist L., Carlson L.A., Bollen A.;
 RT "Production of human recombinant proapolipoprotein A-I in *Escherichia*
 coli: purification and biochemical characterization.";
 RL DNA 8:429-436(1989).
 RN [9]
 RP SEQUENCE FROM N.A. (VARIANT TANGIER).
 RX MEDLINE=88196137; PubMed=3129297;
 RA Makrides S.C., Ruiz-Opazo N., Hayden M., Nussbaum A.L., Breslow J.L.,
 RA Zannis V.I.;
 RT "Sequence and expression of Tangier apoA-I gene.";
 RL Eur. J. Biochem. 173:465-471(1988).
 RN [10]
 RP SEQUENCE OF 118-267 FROM N.A.
 RX MEDLINE=83091059; PubMed=6294659;
 RA Breslow J.L., Ross D., McPherson J., Williams H.W., Kurnit D.,
 RA Nussbaum A.L., Karathanasis S.K., Zannis V.I.;
 RT "Isolation and characterization of cDNA clones for human
 apolipoprotein A-I.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6861-6865(1982).
 RN [11]
 RP SEQUENCE OF 19-27,
 RX MEDLINE=83256553; PubMed=6409108;
 RA Brewer H.B. Jr., Fairwell T., Kay L., Meng M., Roman R., Law S.,
 RA Light J.A.;
 RT "Human plasma proapoA-I: isolation and amino-terminal sequence.";
 RL Biochem. Biophys. Res. Commun. 113:626-632(1983).
 RN [12]
 RP SEQUENCE OF 25-267,
 RX MEDLINE=78123731; PubMed=204308;
 RA Brewer H.B. Jr., Fairwell T., Larue A., Roman R., Houser A.,
 RA Bronzert T.J.;
 RT "The amino acid sequence of human apoA-I, an apolipoprotein isolated
 from high density lipoproteins.";
 RL Biochem. Biophys. Res. Commun. 80:623-630(1978).
 RN [13]
 RP SEQUENCE OF 25-267,
 RX MEDLINE=75133493; PubMed=164450;
 RA Baker H.N., Gotto A.M. Jr., Jackson R.L.;
 RT "The primary structure of human plasma high density apolipoprotein
 glutamine I (apoA-I). II. The amino acid sequence and alignment of
 cyanoogen bromide fragments IV, III, and I.";
 RL J. Biol. Chem. 250:2725-2738(1975).
 RN [14]
 RP SEQUENCE OF 25-56,
 RX MEDLINE=88331387; PubMed=3047170;
 RA Yui Y., Aoyama T., Morishita H., Takahashi M., Takatsu Y., Kawai C.;
 RT "Serum prostaticin stabilizing factor is identical to apolipoprotein
 A-I (apo A-I). A novel function of Apo A-I.";
 RL J. Clin. Invest. 82:803-807(1988).
 RN [15]
 RP SEQUENCE OF 25-48,
 RX MEDLINE=89380318; PubMed=2506184;
 RA Manjunath P., Marcel Y.L., Uma J., Seidah N.G., Chretien M.,
 RA Chappelain A.;
 RT "Apolipoprotein A-I binds to a family of bovine seminal plasma
 proteins.";
 RL J. Biol. Chem. 264:16853-16857(1989).
 RN [16]
 RP SEQUENCE OF 25-43,
 RX MEDLINE=88070603; PubMed=3120314;
 RA Pridmore R.P., Ordovas J.M., Rosenberg I., Schaeffer E.J.,
 RA Pereira M.E.A.;
 RT "Similarity of cruzin, an inhibitor of Trypanosoma cruzi
 neuraminidase, to high-density lipoprotein.";
 RL Science 238:1417-1419(1987).
 RN [17]
 RP SEQUENCE OF 25-42,
 RX TISSUE=Heart;
 RA MEDLINE=95203287; PubMed=7895732;
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
 RT "The human myocardial two-dimensional gel protein database: update
 1994.";
 RL Electrophoresis 15:1459-1465(1994).
 RN [18]
 RP PALMITOYLATION.
 RX MEDLINE=86140194; PubMed=3005308;
 RA Hoeg J.M., Meng M.S., Roman R., Fairwell T., Brewer H.B. Jr.;
 RT "Human apolipoprotein A-I. Post-translational modification by fatty
 acid acylation.";
 RL J. Biol. Chem. 261:3911-3914(1986).
 RN [19]
 RP PROCESSING.
 RX MEDLINE=83195100; PubMed=6405383;
 RA Zannis V.I., Karathanasis S.K., Keutmann H.T., Goldberger G.,
 RA Breslow J.L.;
 RT "Intracellular and extracellular processing of human apolipoprotein
 A-I: secreted apolipoprotein A-I isoprotein 2 is a propeptide.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2574-2578(1983).
 RN [20]
 RP STRUCTURE BY NMR OF 190-209,
 RX MEDLINE=96270776; PubMed=8664326;
 RA Wang G., Trelaevan W.D., Cushman R.J.;
 RT "Conformation of human serum apolipoprotein A-I(166-185) in the
 presence of sodium dodecyl sulfate or dodecylphosphocholine by ¹H-NMR
 and CD. Evidence for specific peptide-SDS interactions.";
 RL Biochim. Biophys. Acta 1301:174-184(1996).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (4.0 ANGSTROMS) OF 67-267,
 RX MEDLINE=98024124; PubMed=9356442;
 RA Borhani D.W., Rogers D.P., Engler J.A., Brouillette C.G.;
 RT "Crystal structure of truncated human apolipoprotein A-I suggests a
 lipid-bound conformation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12291-12296(1997).
 RN [22]
 RP VARIANT MILANO.
 RX MEDLINE=83109095; PubMed=6401735;
 RA Weisgraber K.H., Rall S.C. Jr., Bersot T.P., Mahley R.W.,
 RA Franceschini G., Sirtori C.R.;
 RT "Apolipoprotein A-I-Milano. Detection of normal A-I in affected
 subjects and evidence for a cysteine for arginine substitution in the
 variant A-I.";
 RL J. Biol. Chem. 258:2508-2513(1983).
 RN [23]
 RP VARIANT TANGIER.
 RX MEDLINE=83300108; PubMed=6412234;
 RA Schmitz G., Assmann G., Rall S.C. Jr., Mahley R.W.;
 RT "Tangier disease: defective recombination of a specific Tangier
 apolipoprotein A-I isoform (pro-apo A-I) with high density
 lipoproteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:6081-6085(1983).
 RN [24]
 RP VARIANT NORWAY.
 RX MEDLINE=84289383; PubMed=6432779;
 RA Rall S.C. Jr., Weisgraber K.H., Mahley R.W., Ogawa Y., Fielding C.J.,
 RA Oterman G., Haas J., Steinmetz A., Menzel H.J., Assmann G.;
 RT "Abnormal lecithin:cholesterol acyltransferase activation by a human
 apolipoprotein A-I variant in which a single lysine residue is
 deleted.";
 RL J. Biol. Chem. 259:10063-10070(1984).
 RN [25]
 RP SEQUENCE OF 25-107 (VARIANT IOWA).
 RX MEDLINE=89050104; PubMed=3142462;
 RA Nichols W.C., Duvellet F.E., Liepiens J., Benson M.D.;
 RT "Variant apolipoprotein AI as a major constituent of a human
 hereditary amyloid.";

CC	Eukarchota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX	NCBI_TaxId=9615;
RN	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RX	MEDLINE=90132271; PubMed=2515239;
RA	Luo C.-C., Li W.-H., Chan L.;
RT	"Structure and expression of dog apolipoprotein A-I, E, and C-II
RT	mRNAs: implications for the evolution and functional constraints of
RT	apolipoprotein structure.";
RL	J. Lipid Res. 30:1735-1746(1989).
RN	(2)
RP	SEQUENCE OF 25-266.
RX	MEDLINE=82142425; PubMed=6801039;
RA	Chung H., Randolph A., Reardon I., Heinrikson R.L.;
RT	"The covalent structure of apolipoprotein A-I from canine high
RT	density lipoproteins.";
RL	J. Biol. Chem. 257:2961-2967(1982).
RN	(3)
RP	SEQUENCE OF 25-57 AND 262-265.
RX	MEDLINE=76210910; PubMed=179887;
RA	Nakai T., Whayne T.F., Tang J.;
RT	"The amino- and carboxyl-terminal sequences of canine apolipoprotein
RT	A-I.";
RL	FEBS Lett. 64:409-411(1976).
RN	[4]
RP	SEQUENCE OF 25-37.
RC	TISSUE=Heart;
RX	MEDLINE=98163340; PubMed=9504812;
RA	Dunn M.J., Corbett J.M., Wheeler C.H.;
RT	"Hsc-ZPPAGE and the two-dimensional gel electrophoresis database of
RT	dog heart proteins.";
RL	Electrophoresis 18:2795-2802(1997).
CC	-I- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC	CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC	CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COPACITOR FOR
CC	THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC	-I- SUBCELLULAR LOCATION: Extracellular.
CC	-I- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC	CYLIOMICRONS. SYNTHESIZED IN THE LIVER AND SMALL INTESTINE.
CC	-I- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
DR	PfIR: A03092; LPDGL.
DR	HSPSP; P02647; IODR.
DR	HSC-ZDPAGE; P02648; DOG.
DR	InterPro: IPRO00074; Apolipoprotein.
PFam:	PF01442; Apolipoprotein; 1.
KW	Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal
FT	SIGNAL
FT	PROPEP
FT	CHAIN
FT	DOMAIN
FT	REPEAT
FT	REPEAT
FT	REPEAT
FT	REPEAT
FT	REPEAT
FT	REPEAT
FT	REPEAT
FT	REPEAT
FT	REPEAT
FT	CONFLICT
FT	CONFLICT
FT	CONFLICT
FT	CONFICT
QO	SEQUENCE

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Dd	25	DEQOSPMDRKDLDLAVIYDAKDSGRDYVAQFERSALGQGLNKLLDMMDSISTSVTKR
Oy	62	EQLGPVTOEFWNLKEKETEGLEROEMSKDLEEVAKVQPYILDPOFKMOEENELROKVP
Dd	85	EOIGPVTOEFWMNLKEKETETVLROEMSKDLEEVAKQKQPYILDDPOFKMOEEVELRLQVAP
Oy	122	LRRLEOEGARKOLHHLQCKLSPLCEBMRDRAAHVDALRTHLAPYSDEL
Dd	145	LGSELEGARQKLOELQEKISPLAEEDLRARTRHVADLRQAAPYSDDL
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RESULT 4		
ID	APAL_PIG	STANDARD; PRT; 265 AA.
AC	P18648;	
DT	01-NOV-1990 (Rel. 16, Created)	
DT	01-FEB-1994 (Rel. 28, Last sequence update)	
DE	16-OCT-2001 (Rel. 40, Last annotation update)	
DF	Apolipoprotein A-I precursor (apo-AI).	
GN	AF0A1.	
OS	Sus scrofa (Pig),	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Euteria; Cetartiodactyla; Suina; Suidae; Sus.	
OX	NCBI_TaxID=9623;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=93224154; PubMed=8468059;	
RA	Birchbauer A., Knipping G., Jurtisch B., Aschauer H., Zechner R.,	
RT	"Characterization of the apolipoprotein AI and CIII genes in the	
RT	domestic pig.";	
RL	Genomics 15:643-652(1993).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Liver, and Brain:	
RX	MEDLINE=94125128; PubMed=8294940;	
RA	Moeckel B., Zinke H., Flach R., Weiss B., Weller-Guetler H.,	
RA	Gassen H.;	
RT	"Expression of apolipoprotein A-I in porcine brain endothelium in	
RT	vitro.";	
RL	J. Neurochem. 62:788-798(1994).	
RN	[3]	
RP	SEQUENCE OF 34-265 FROM N.A.	
RC	TISSUE=Brain;	
RX	MEDLINE=90132667; PubMed=2105375;	
RA	Weller-Guetler H., Sommerfeldt M., Papandriakopoulou A., Mischek U.,	
RA	Bonitz D., Frey A., Grube M., Scheerer J., Gassen H.G.;	
RT	"Synthesis of apolipoprotein A-I in pig brain microvascular	
RT	endothelial cells.";	
RL	J. Neurochem. 54:444-450(1990).	
RN	[4]	
RP	SEQUENCE OF 105-265 FROM N.A.	
RC	TISSUE=Liver;	
RX	MEDLINE=93154581; PubMed=8428656;	
RA	Trieu V.N., Hasler-Rapacz J., Rapacz J., Black D.D.;	
RT	"Sequences and expression of the porcine apolipoprotein A-I and C-IIII	
RT	mRNAs.";	
RL	Gene 123:173-179(1993).	
RN	[5]	
RP	SEQUENCE OF 25-265.	
RA	Hasler-Rapacz J.O., Chaudhary R., Chowdhary B.P., Trieu V.N.,	
RA	Jackson K., Gustavsson I., Rapacz J.;	
RL	Submitted (OCT-1995) to the SWISS-PROT data bank.	
RN	[6]	
RP	SEQUENCE OF 25-34.	
RX	MEDLINE=76184721; PubMed=178359;	
RA	Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;	
RT	"Characterization of the plasma lipoproteins and apoproteins of the	
RT	Erythrocebus patas monkey.";	
RL	Biochemistry 15:1928-1933(1976).	
CC	-I- FUNCTION: APOA-I PARTICIPATES IN THE REVERSE TRANSPORT OF CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING	

RP SEQUENCE FROM N.A.
 RX MEDLINE=92281682; PubMed=1596360;
 RA Stoffel W., Mueller R., Binczek E., Hofmann K.;
 RT "Mouse apolipoprotein A-I, cDNA-derived primary structure, gene
 RT organisation and complete nucleotide sequence.";
 RN Biol. Chem. Hoppe-Seyler 373:187-193(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93122774; PubMed=1478650;
 RA Janusz J.L., Azrolan N., O'Connell A., Aalto-Setälä K., Breslow J.L.;
 RT "Characterization of the mouse apolipoprotein A-I/ApoC-3 gene
 RT locus: genomic, mRNA, and protein sequences with comparisons to other
 RT species.";
 RL Genomics 14:1081-1088(1992).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC -----
 CC EMBL: X64262; CAA45560.1; -;
 CC EMBL: X64263; CAA45561.1; -;
 CC EMBL: L04149; -; NOT_ANNOTATED_CDS.
 CC EMBL: L04151; -; NOT_ANNOTATED_CDS.
 CC PIR: S22420; S22420.
 CC PIR: A44364; A44364.
 CC HSP: P02647; IAVI.
 CC SWISS-2DPAGE: Q00623; MOUSE.
 CC MGI: 88049; APOA1.
 CC InterPro: IPR000074; Apolipoprotein.
 CC Pfam: PF01442; Apolipoprotein. 1.
 CC Plasma: Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 CC SIGNAL: 1 18
 CC PROPEP 19 24
 CC CHAIN 25 264
 CC DOMAIN 67 264
 CC REPEAT 67 88
 CC REPEAT 89 110
 CC REPEAT 111 121
 CC REPEAT 122 143
 CC REPEAT 144 165
 CC REPEAT 166 187
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 CC REPEAT 208 229
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 CC SEQUENCE 264 AA; 30587 MW; C453FF2019634AAC CRC64;
 QY 2 EPPSPMDRVKDLATVYVDVLDKSGRDYVSQFEGSALGKQLNKLKLDNMDSVTSFSKLR 61
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 QY 62 EQLGAPVQGFEMDNLKETEGLRQEMSKDLEEVAKAVQPYLDLDFQKKQOEEMELTRQKVEP 121
 Db 85 ERLGAPLRLDRWDNLKETEGLRQEMSKDLEEVAKAVQPYLDLDFQKKQOEEMELTRQKVEP 144
 QY 122 LRAELGAGAROKLHELOEKLSPLEEMRDRARAHDALRTHLAPYSDEL 170

Query Match 74.0%; Score 655; DB 1; Length 264;
 Best Local Similarity 71.0%; Pred. No. 3.3e-36;
 Matches 120; Conservative 28; Mismatches 21; Indels 0; Gaps 0;

Db 145 LRAELGAGAROKLHELOEKLSPLEEMRDRARAHDALRTHLAPYSDEL 193
 RESULT 8
 ID APOA1.TUPGB STANDARD; PRT; 265 AA.
 AC 018759;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Tupaiia glis belangeri (Common tree shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
 OX NCBI_Taxid=9396;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RL In X, Chen B., Zhao Y., Wang K., Xue H., Zeng W.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC -----
 CC EMBL: AF005638; AAB82326.1; -;
 CC HSP: P02647; IAVI.
 CC InterPro: IPR000074; Apolipoprotein.
 CC Pfam: PF01442; Apolipoprotein. 1.
 CC Plasma: Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 CC SIGNAL: 1 18
 CC PROPEP 19 24
 CC CHAIN 25 265
 CC DOMAIN 67 265
 CC REPEAT 67 88
 CC REPEAT 89 110
 CC REPEAT 111 121
 CC REPEAT 122 143
 CC REPEAT 144 165
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 QY 62 EQLGAPVQGFEMDNLKETEGLRQEMSKDLEEVAKAVQPYLDLDFQKKQOEEMELTRQKVEP 121
 Db 85 ERLGAPLRLDRWDNLKETEGLRQEMSKDLEEVAKAVQPYLDLDFQKKQOEEMELTRQKVEP 144

Query Match 72.0%; Score 637; DB 1; Length 265;
 Best Local Similarity 68.0%; Pred. No. 4.8e-35;
 Matches 115; Conservative 30; Mismatches 24; Indels 0; Gaps 0;


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RL J Lipid Res. 33:831-842(1992).
RN [5]
RP SEQUENCE OF 25-44.
RA MEDLINE=83213468; PubMed=6406496;
RX Shackelford J.E., Leberer H.G.;
RT "Synthesis and secretion of apolipoprotein A1 by chick breast muscle."
RT
RL J. Biol. Chem. 258:7175-7180(1983).
CC CC
CC -1- FUNCTION: APOA1 PARTICIPATES IN THE REVERSE TRANSPORT OF CHOLESTEROL EFFLUX FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING THE LECTITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC CC
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC CC
CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN CHROMIOMERONS.
CC CC
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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CC CC
CC EMBL; M17961; AAA48593.1; -.
DR DR
DR EMBL; M18746; AAA48594.1; -.
DR DR
DR EMBL; M25559; AAA48592.1; -.
DR DR
DR EMBL; M96012; AAA48597.1; -.
DR DR
DR PIR; S01453; LPCHAL.
DR DR
DR PIR; JH0471; JH0471.
DR DR
DR HSSP; P02647; IODR.
DR DR
DR InterPro: IPRO00074; Apolipoprotein.
DR DR Pfam: PF01442; Apolipoprotein; 1.
DR KV Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
FT FT SIGNAL 1 18
FT FT PROPEP 19 24
FT FT CHAIN 25 264
FT FT DOMAIN 67 264
FT FT REPEAT 67 88
FT FT REPEAT 89 110
FT FT REPEAT 111 121
FT FT REPEAT 122 143
FT FT REPEAT 144 165
FT FT REPEAT 166 187
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FT FT REPEAT 210 231
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FT FT CONFLICT 148 148
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Query Match 53.2%; Score 471; DB 1; Length 264;
Best local Similarity 51.5%; Pred. No. 2,9e-24;
Matches 87; Conservative 39; Mismatches 43; Indels 0; Gaps 0.

OY 2 EPQPSWDKDKLATAYVYVDKDSGDYVSOPGSLGKLNKLIDNDMSVTSFSKLR 61
DB 25 DEFOPTDLRIKRDWADVLLLETVKASGRDAIAOFSSAVGKDLKLKDNDITLSAAAKLR 84
OY 62 EOQPGVTOEFMDLIEKETEGLRQEMSKDLEEVAKVQPYLDDEFOKKQOEEMELYRKVEP 121
DB 85 EDMAPIYGVKEBWMMLDTEALRAELIKLDEEVKEKTRIFPDIFSASWTETLEQYRORLP 144
OY 122 LRAELGGAROKLHELOEKSPLEGEMPRDRAHVADLRNHLAPYSDEL 170
DB 145 VADELKELTKOKVELMQAKLTPLVAEEARDRLRGHVEELRNKLAPYSDEL 193

RESULT 12
APAL_COTUA
```

ID APA1_COTJA STANDARD; PRT; 264 AA.
 AC P32918;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Coturnix.
 NC NCBL_TaxID=93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Oku H., Toda T., Nagata J., Ishikawa M., Neyazaki K., Shinryo C.,
 RA Chinen I.;
 RT "Apolipoprotein A-I of Japanese quail: cDNA sequence and modulation of
 RT tissue expression by cholesterol feeding."
 RT Biosci. Biotechnol. Biochem. 61:286-290(1997).
 RN [2]
 RP SEQUENCE OF 25-60.
 RX MEDLINE=93213845; PubMed=8461329;
 RA Oku H., Ishikawa M., Nagata J., Toda T., Chinen I.;
 RT "Lipoprotein and apoprotein profile of Japanese quail."
 RT Biochim. Biophys. Acta 1167:22-28(1993).
 CC -1- FUNCTION: APOA-I PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF VLDL, HDL, LDL AND IN
 CC CHYLOMICRONS. EXPRESSED IN A NUMBER OF TISSUES INCLUDING LIVER,
 CC SMALL INTESTINE, LUNG, KIDNEY, HEART AND MUSCLE WITH HIGHEST
 CC EXPRESSION IN LIVER AND SMALL INTESTINE.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D85133; BAA12729.1; -
 DR HSSP: P02647; IGM4
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 264
 FT DOMAIN 67 264
 FT REPEAT 67 88
 FT REPEAT 89 110
 FT REPEAT 111 121
 FT REPEAT 122 143
 FT REPEAT 144 165
 FT REPEAT 166 187
 FT REPEAT 188 209
 FT REPEAT 210 231
 FT REPEAT 232 242
 FT REPEAT 243 264
 FT REPEAT 264 264
 SO SEQUENCE 264 AA; 30753 MW; 8781DE213C3F663F CRC64;

Query Match 51.3%; Score 454; DB 1; Length 264;
 Best Local Similarity 50.3%; Pred. No. 3.7e-23;
 Matches 85; Conservative 40; Mismatches 44; Indels 0; Gaps 0;
 2 EPPQSPWDRKDLATVYVVDIKSGRDYVSQFEGSALGKOLNKLIDNMDSVTSFSSKLIR 61

Db 25 DDQPLDRIKMDLVLETVKASGKAISQFESSAVGKQDLKLDNDTTSMAAKR 84
 QY 62 EQLGPVQFQWMDNLEKETGLROEMSKDLEEVAKVQPYDDPOKKMOEMELYRQKVP 121
 Db 85 EDMTPYRREWMKLTQALRAELFTKDLFEVEKIRPFLDQSAKTEVEEYRRLAP 144
 QY 122 LRNELGCAQKRLHELEKLSPLGEEMKRRARAHVDAALTHLAPYSDEL 170
 Db 145 VAQELKDTQKVELMQLKLPVAEEVRDLRQVEELRNKLAPYSSEL 193
 RESULT 13
 ID APA4_MACFA STANDARD; PRT; 429 AA.
 AC P33621;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV).
 GN APOA4.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NC NCBL_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE=93192330; PubMed=8448212;
 RA Osada J., Pocovi M., Nicolosi R.J., Schaefer E.J., Ordovas J.M.;
 RT "Nucleotide sequences of the Macaca fascicularis apolipoprotein C-III
 RT and A-IV genes."
 RT Biochim. Biophys. Acta 1172:335-339(1993).
 CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
 CC LIPOLYSIS. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
 CC LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
 CC COMPONENT OF HDL AND CHYLOMICRONS.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SECRETED IN PLASMA.
 CC -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
 CC 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
 CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
 CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
 CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL
 CC ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----
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 CC -----
 DR EMBL: X68361; CAA48421.1; -
 DR PIR: S29565; S29565.
 DR PIR: S30195; S30195.
 DR HSSP: P02649; INFO.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 429
 FT DOMAIN 33 330
 FT REPEAT 33 54
 FT REPEAT 54 60
 FT REPEAT 60 81
 FT REPEAT 82 103
 FT REPEAT 103 115
 FT REPEAT 115 136
 FT REPEAT 137 158
 FT REPEAT 159 180
 FT REPEAT 181 202

FT REPEAT 203 224 8.
 FT REPEAT 225 246 9.
 FT REPEAT 247 268 10.
 FT REPEAT 269 286 11.
 FT REPEAT 287 308 12.
 FT REPEAT 309 330 13.
 FT DOMAIN 372 420 GLU/GLN-RICH.
 SQ SEQUENCE 429 AA; 49876 MW; 3DA58F551D0DB60C CRC64;

Query Match 24.2%; Score 214; DB 1; Length 429;
 Best Local Similarity 28.4%; Pred. No. 2.4e-07;
 Matches 46; Conservative 43; Mismatches 73; Indels 0; Gaps 0;

QY 9 DRKVDATVYVVDIKSGRHYVSOFESSALGKQLNKLDMNDSVTSFSKIREQLGPT 68
 DB 25 DQVATVMDYFSSQSSNAKEAVEHLQKSELTOQLNALFQDKLGEVNTYAGDLQKLTVPFA 84
 QY 69 QEFWDNLEKETEGIRQEMSKDLEEVKAKVQPYLDDEFQKQWQEMELYRQKVEPLRAELQ 128
 DB 85 TELHERLAKSEKKEIRKELEEVARLRLPHANEVSQKIGENVRELQORLEPYTDQLRT 144
 QY 129 GARQKLEHLEOKLSPGEMRDRARAHVDALRTHLAPYDEL 170
 DB 145 QVNTQTEQLRQLTPYAQRMERVLRNADSLQTSLRPHADQL 186

RESULT 14
 APA4_PAPAN STANDARD; PRT; 401 AA.
 ID APA4_PAPAN STANDARD; PRT; 401 AA.
 AC 028758;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV) (fragment).
 GN APOA4.
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 NC NCBI_TaxID=9555;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Intestine;
 RX MEDLINE=93340170; PubMed=8101842;
 RA Hixson J.E., Kammerer C.M., Mott G.E., Britten M.L., Birnbaum S.,
 RA Powers P.K., Vandenberg J.L.;
 RT "Baboon apolipoprotein A-IV. Identification of Lys-76-->Glu that
 RT distinguishes two common isoforms and detection of length
 RT polymorphisms at the carboxyl terminus.";
 RL J Biol Chem. 268:15667-15673(1993).

-I- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
 CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
 LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
 COMPONENT OF HDL AND CHYLOMICRONS.
 CC -I- SUBCELLULAR LOCATION: Extracellular.
 CC -I- TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE INTESTINE.
 CC SECRETED IN PLASMA.
 CC -I- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
 CC 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
 CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
 CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
 CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL
 CC ACITYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
 CC -I- POLYMORPHISM: THERE ARE TWO COMMON APOA-IV ISOFORMS, I (SHOWN
 CC HERE) AND E. THE I ISOFORM IS ASSOCIATED WITH HIGHER LEVELS OF
 CC HIGH DENSITY LIPOPROTEIN-C ON A HIGH CHOLESTEROL, SATURATED FAT
 CC DIET.
 CC -I- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.

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DR EMBL: L13174; AAA35379.1; -.
 DR HSSP: P02649; INFO.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal;
 KW Polymorphism.

FT SIGNAL 1 4
 FT CHAIN 5 401
 FT DOMAIN 17 314
 FT REPEAT 17 38
 FT REPEAT 44 65
 FT REPEAT 66 87
 FT REPEAT 99 120
 FT REPEAT 121 142
 FT REPEAT 143 164
 FT REPEAT 165 186
 FT REPEAT 187 208
 FT REPEAT 209 230
 FT REPEAT 231 252
 FT REPEAT 253 270
 FT REPEAT 271 292
 FT REPEAT 293 314
 FT DOMAIN 356 394
 FT VARIANT 80 80
 SQ SEQUENCE 401 AA; 46538 MW; 0A76D1284AA9837F CRC64;
 K -> E (IN ISOFORM E).

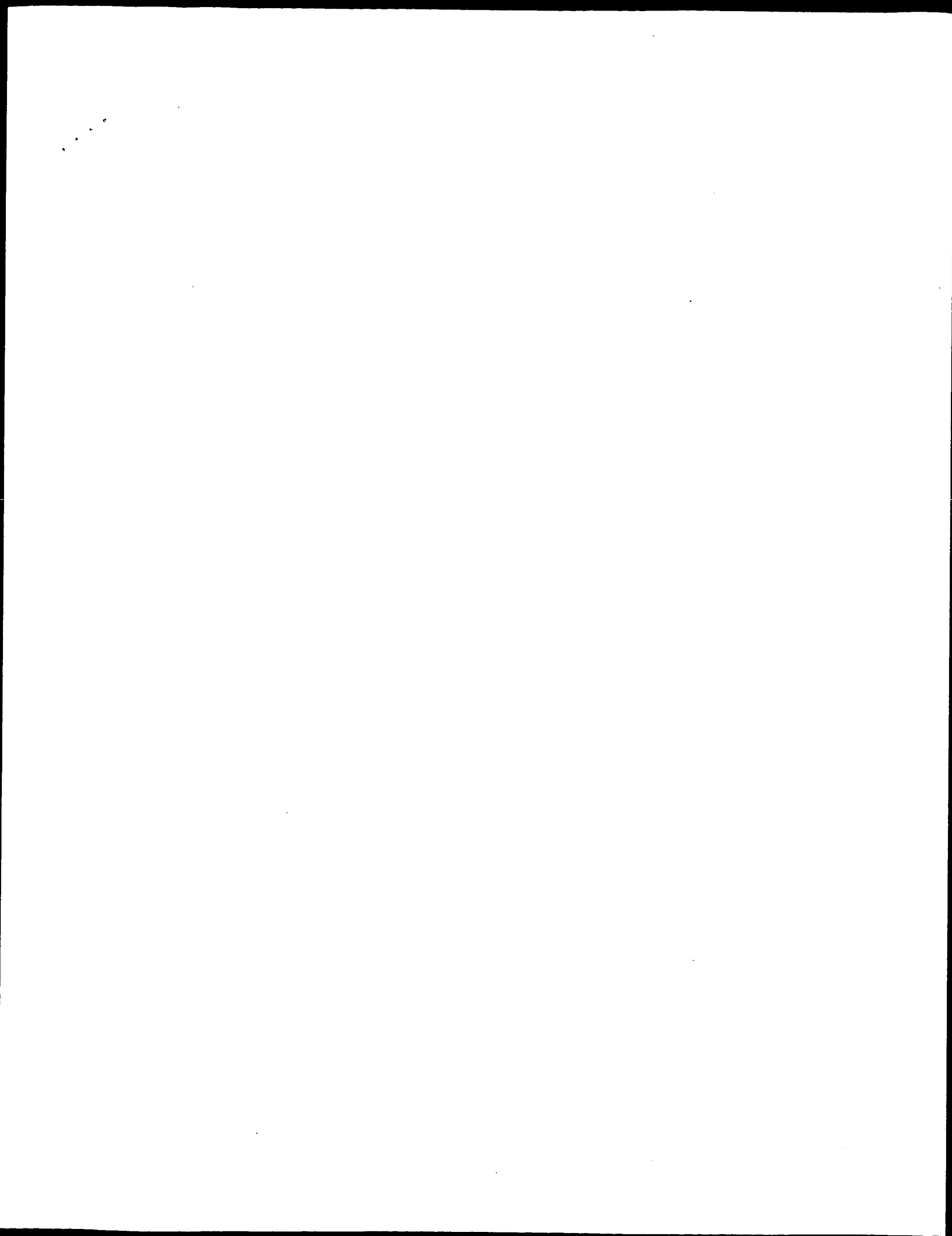
Query Match 23.7%; Score 210; DB 1; Length 401;
 Best Local Similarity 27.8%; Pred. No. 4e-07;
 Matches 45; Conservative 44; Mismatches 73; Indels 0; Gaps 0;

QY 9 DRKVDATVYVVDIKSGRHYVSOFESSALGKQLNKLDMNDSVTSFSKIREQLGPT 68
 DB 9 DQVATVMDYFSSQSSNAKEAVEHLQKSELTOQLNALFQDKLGEVNTYAGDLQKLTVPFA 68
 QY 69 QEFWDNLEKETEGIRQEMSKDLEEVKAKVQPYLDDEFQKQWQEMELYRQKVEPLRAELQ 128
 DB 69 TELHERLAKSEKKEIRKELEEVARLRLPHANEVSQKIGENVRELQORLEPYTDQLRT 128
 QY 129 GARQKLEHLEOKLSPGEMRDRARAHVDALRTHLAPYDEL 170
 DB 129 QVNTQTEQLRQLTPYAQRMERVLRNADSLQTSLRPHADQL 170

RESULT 15
 APA4_HUMAN STANDARD; PRT; 396 AA.
 ID APA4_HUMAN STANDARD; PRT; 396 AA.
 AC P06727;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV).
 GN APOA4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Intestine;
 RX MEDLINE=89194198; PubMed=2930771;
 RA Yang C., Gu Z.W., Xiong W., Rosseneu M., Yang H.X., Lee B.M.,
 RA Goto A.M. Jr., Chan L.;
 RT "The primary structure of human apolipoprotein A-IV.";
 RL Biochim. Biophys. Acta 1002:231-237(1989).
 RN [2]
 RP SEQUENCE FROM N.A.

RA MEDLINE=87041474; PubMed=3095836;
 RA Karathanasis S.K., Oettgen P., Haddad I.A., Antonarakis S.E.,
 RT "Structure, evolution, and polymorphisms of the human apolipoprotein
 RT A4 gene (APOA4).";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8457-8461(1986).
 RN [13]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86296629; PubMed=3755616;
 RA Karathanasis S.K., Yunis I.,
 RT "Structure, evolution, and tissue-specific synthesis of human
 RT apolipoprotein AIV";
 RL Biochemistry 25:3962-3970(1986).
 RN [14]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87250378; PubMed=3036793;
 RA Elshourbagy N.A., Walker D.W., Paik Y.K., Boguski M.S., Freeman M.,
 RA Gordon J.I., Taylor J.M.,
 RT "Structure and expression of the human apolipoprotein A-IV gene.";
 RL J. Biol. Chem. 262:7973-7981(1987).
 RN [15]
 RP SEQUENCE OF 21-396 FROM N.A.
 RX MEDLINE=86111885; PubMed=3080432;
 RA Elshourbagy N.A., Walker D.W., Boguski M.S., Gordon J.I., Taylor J.M.,
 RT "The nucleotide and derived amino acid sequence of human
 RT apolipoprotein A-IV mRNA and the close linkage of its gene to the
 RT genes of apolipoproteins A-I and C-III.";
 RL J. Biol. Chem. 261:1998-2002(1986).
 RN [16]
 RP SIGNAL SEQUENCE CLEAVAGE SITE.
 RX MEDLINE=84161950; PubMed=6706947;
 RA Gordon J.I., Bisgaler C.L., Sims H.F., Sachdev O.P., Glickman R.M.,
 RA Straus A.W.,
 RT "Biosynthesis of human preapolipoprotein A-IV";
 RL J. Biol. Chem. 259:468-474(1984).
 RN [17]
 RP REVIEW ON POLYMORPHISM.
 RA Lohse P., Brewer H.B. Jr.,
 RT "Genetic polymorphism of apolipoprotein A-IV";
 RL Curr. Opin. Lipidol. 2:90-95(1991).
 RN [18]
 RP VARIANT A-IV*2.
 RX MEDLINE=90277616; PubMed=2351649;
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.,
 RT "Genetic polymorphism of human plasma apolipoprotein A-IV is due to
 RT nucleotide substitutions in the apolipoprotein A-IV gene.";
 RL J. Biol. Chem. 265:10061-10064(1990).
 RN [19]
 RP VARIANTS A-IV*0 AND A-IV*3.
 RX MEDLINE=90324273; PubMed=1973689;
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.,
 RT "Human plasma apolipoproteins A-IV*0 and A-IV*3. Molecular basis for
 RT two rare variants of apolipoprotein A-IV-1";
 RL J. Biol. Chem. 265:12734-12739(1990).
 RN [10]
 RP VARIANTS.
 RX MEDLINE=91310615; PubMed=1677358;
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.,
 RT "Three genetic variants of human plasma apolipoprotein A-IV: apoA-IV-
 RT 1(Thr-347->Ser), apoA-IV-0(Lys-167->Glu, Gln-360->His), and apoA-IV-
 RT 3(Glu-165->Lys).";
 RL J. Biol. Chem. 266:13513-13518(1991).
 RN [11]
 RP ERRATUM.
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.,
 RL J. Biol. Chem. 266:19866-19866(1991).
 RN [12]
 RP VARIANT MET-13.
 RX MEDLINE=92238494; PubMed=1349197;
 RA von Eckardstein A., Funke H., Schulte M., Erren M., Schulte H.,
 RA Assmann G.,
 RT "Nononymous polymorphic sites in the apolipoprotein (apo) A-IV
 RT gene are associated with changes in the concentration of apo B- and
 RT apo A-I-containing lipoproteins in a normal population.";

RL Am. J. Hum. Genet. 50:1115-1128(1992).
 RN [13]
 RP VARIANT SER-147.
 RX MEDLINE=92144647; PubMed=1737067;
 RA Tenkanen H., Koskinen P., Metsu J., Baumann M., Lukka M.,
 RA Kauppinen-Makelin R., Kontula K., Taskiran M.R., Mantari M.,
 RA Manninen V., Ehnholm C.,
 RT "A novel polymorphism of apolipoprotein A-IV is the result of an
 RT asparagine to serine substitution at residue 127";
 RL Biochim. Biophys. Acta 1138:27-33(1992).
 RN [14]
 RP VARIANT A-IV*5.
 RX MEDLINE=93138374; PubMed=1487136;
 RA Kamboh M.I., Williams E.R., Law J.C., Aston C.E., Bunker C.H.,
 RA Ferrell R.E., Pollitzer W.S.,
 RT "Molecular basis of a unique African variant (A-IV 5) of human
 RT apolipoprotein A-IV and its significance in lipid metabolism";
 RL Genet. Epidemiol. 9:379-388(1992).
 RN [15]
 RP VARIANTS LYS-44 (BUDAPEST-2); CYS-305 AND SER-367 (BUDAPEST-1).
 RX MEDLINE=95245341; PubMed=7728150;
 RA Menzel H.J., Dieplinger H., Sandholzer C., Karadi I., Utermann G.,
 RA Csaszar A.,
 RT "Apolipoprotein A-IV polymorphism in the Hungarian population: gene
 RT frequencies, effect on lipid levels, and sequence of two new
 RT variants";
 RL Hum. Mutat. 5:58-65(1995).
 RN [16]
 RP VARIANTS FCGL, SEATTLE SER-161, LEU-178 AND GLN-264.
 RX MEDLINE=97114287; PubMed=8956036;
 RA Deeb S.S., Nevin D.N., Iwasaki L., Brunzell J.D.,
 RT "Two novel apolipoprotein A-IV variants in individuals with familial
 RT combined hyperlipidemia and diminished levels of lipoprotein lipase
 RT activity";
 RL Hum. Mutat. 8:319-325(1996).
 CC -1- FUNCTION: MAY HAVE A ROLE IN CHLOMICRONS AND VLDL SECRETION AND
 CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
 CC LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
 CC COMPONENT OF HDL AND CHYLOMICRONS.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE INTESTINE.
 CC SECRETED IN PLASMA.
 CC -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
 CC 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
 CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
 CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
 CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL
 CC ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
 CC -1- POLYMORPHISM: EIGHT ALLELES HAVE BEEN CHARACTERIZED (APOA-IV*0
 CC TO APOA-IV*7). APOA-IV*1 IS THE MAJOR ALLELE (90%), IV*2 IS ALSO
 CC COMMON (8%), THE OTHERS ARE RARE ALLELES.
 CC -1- DISEASE: DEFECTS IN APOA4 MAY CONTRIBUTE, ALONG WITH DEFECTS IN
 CC OTHER GENES OR ENVIRONMENTAL FACTORS, TO THE DEVELOPMENT OF
 CC FAMILIAL COMBINED HYPERLIPIDEMIA (FCHL).
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC -----
 CC EMBL: M14642; AAA51745.1; -
 CC EMBL: X13629; CAA31955.1; -
 CC EMBL: M14566; AAA51748.1; -
 CC EMBL: J02758; AAA96731.1; -
 CC EMBL: M13654; AAA51744.1; -
 CC EMBL: A26481; LPH04.
 CC PIR: A26449; A24449.
 CC PIR: A29330; A29330.
 CC PIR: A26280; A26280.



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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:21:36 ; Search time 111.17 Seconds
(without alignments)
264.542 Million cell updates/sec

Title: US-09-803-918a-2_COPY_25_194

Perfect score: 885
Sequence: 1 DEPPQSPMDRVKDLATVYVD.....KARAHVDALRTHLAFYSDEL 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_TREMBL_19:*
2: SP_archaea:*
3: SP_bacteria:*
4: SP_fungi:*
5: SP_human:*
6: SP_invertebrate:*
7: SP_mammal:*
8: SP_mmc:*
9: SP_organelle:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriophage:*
17: SP_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	700	79.1	264	11	Q92214 mesocricetus
2	645.5	72.9	263	11	Q09042 mus musculus
3	645.5	72.9	263	11	Q08855 mus musculus
4	565	63.8	241	6	Q9T849 Q9T849 erinaceus e
5	559	63.2	258	11	Q09054 ratius norv
6	559	63.2	258	11	Q08877 ratius norv
7	247	27.9	56	6	Q02762 ovis aries
8	217	24.5	82	6	Q02248 sus scrofa
9	195.5	22.1	366	13	Q93601 gallus gall
10	186	21.0	263	13	Q98T66 anguilla ja
11	175	19.8	435	11	Q01488 mus musculus
12	171	19.3	395	11	Q91XFB mus musculus
13	168	19.0	395	11	Q9B8N0 mus musculus
14	157.5	17.8	363	4	Q9UBJ3 homo sapien
15	154	17.4	67	4	Q9Y355 homo sapien
16	153	17.3	275	13	Q9PT02 oncorhynch

17	149.5	16.9	174	13	Q9DFQ3	Q9dfq3 gillichthys
18	146.5	16.6	313	6	Q9GLCO	Q9glco tupia glis
19	146	16.5	174	13	Q98SRT3	Q98srt3 cyprinus ca
20	144.5	16.3	244	4	Q13784	Q13784 homo sapien
21	144	16.3	367	11	Q9Q0H3	Q9q0h3 ratius norv
22	143.5	16.2	259	13	Q98T65	Q98t65 anguilla ja
23	141	15.9	26	4	Q9UCT8	Q9uct8 homo sapien
24	140.5	15.9	259	13	Q98T64	Q98t64 anguilla ja
25	140.5	15.9	259	13	Q98T62	Q98t62 anguilla ja
26	140.5	15.9	368	11	Q98P84	Q98p84 mus musculu
27	139.5	15.8	259	13	Q98T63	Q98t63 anguilla ja
28	139.5	15.8	368	11	Q91X90	Q91x90 mus musculu
29	136	15.4	259	13	Q98T61	Q98t61 anguilla ja
30	125.5	14.2	317	6	Q9GLM8	Q9glm8 gorilla gor
31	124.5	14.1	317	6	Q9GLM3	Q9glm3 pan troglod
32	124.5	14.1	317	6	Q9GLM6	Q9glm6 hylobates l
33	123.5	14.0	317	6	Q9GLM7	Q9glm7 pygma
34	119.5	13.5	1547	5	Q26471	Q26471 schistocerc
35	116.5	13.2	1708	5	Q9U0S6	Q9u0s6 mytilus gal
36	115	13.0	224	13	Q9PT73	Q9pt73 scophilthimu
37	114.5	12.9	1047	11	Q9EP81	Q9ep81 mus musculu
38	113	12.8	255	4	Q961V5	Q961v5 homo sapien
39	113	12.8	470	5	Q9XTH4	Q9xth4 caenorhabdi
40	113	12.8	1478	4	Q9BQ58	Q9bq58 homo sapien
41	112	12.7	1138	5	Q22276	Q22276 caenorhabdi
42	112	12.7	1411	4	Q15075	Q15075 homo sapien
43	112	12.7	1935	5	Q44934	Q44934 loligo peal
44	111.5	12.6	1046	11	Q9Z0H8	Q9z0h8 mus musculu
45	111.5	12.6	2779	5	Q9W4N7	Q9w4n7 drosophila

ALIGNMENTS

RESULT	ID	Q92214	PRELIMINARY	PRT	264 AA.
AC	Q92214	Q92214	Q92214		
DT	01-MAY-1999	(TREMUREL. 10, Created)			
DT	01-MAY-1999	(TREMUREL. 10, Last sequence update)			
DT	01-JUN-2001	(TREMUREL. 17, Last annotation update)			
DE	APOLIPROTEIN A-I.				
GN	APOLI.				
OS	Mesocricetus auratus (Golden hamster).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;				
CC	Mesocricetus.				
OX	NCBI_TaxID=10036;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-GOLDEN SYRIAN; TISSUE-INTESTINE;				
RX	MEPILN=99061559; PubMed=9843713;				
RA	Wu J.Y.J., Reeves S.K., Wang Y.R., Wu Y., Lei P.P., Lei K.Y.;				
RT	"Zinc deficiency decreases plasma level and hepatic mRNA abundance of				
RL	apolipoprotein A-I in rats and hamsters."				
DR	Am. J. Physiol. 275:C1516-C1525(1998).				
DR	EMBL: AF046919; AAC98484.1; .				
DR	HSSP: P02647; IAVI.				
DR	InterPro: IPR000074; Apolipoprotein.				
DR	Pfam: PF01442; Apolipoprotein. 1.				
KW	Lipoprotein.				
SC	SEQUENCE 264 AA; 30739 MW; 280822F4C0F0B129 CRC64;				

Query Match 79.1%; Score 700; DB 11; Length 264;

Best Local Similarity 76.9%; Pred. No. 1.1e-42;
Matches 130; Conservative 21; Mismatches 18; Indels 0; Gaps 0;

QY	2	EPPOSMDRVKDLATVYVDLTKSGRDVYSQFEGSALGKQLNLKLDNWDVSTFSKLR 61
DB	25	DDPQTPMDRVKDFATVYVDVAVKDSGREYVSQFETSAIGKQLNLNLEMDTLGISTVRLQ 84
QY	62	EDLGVTQDFWNLKEKEBGLRQEMSKDLEEVKAVQVYLDLDFQKKQEMELRQKVEP 121

DE 01-JUN-2001 (TREMblrel. 17, last annotation update)
 DT APOLipoprotein A-I.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WKY, AND SHRS; TISSUE=SPLEEN;
 RC Chiating A.N., Fan K.C., Shaw G.C., Yang U.C.;
 RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RL EMBL: U97578; AAB58430.1; -.
 DR EMBL: U97577; AAB58429.1; -.
 DR HSSP: P02647; IAVI.
 DR Interpro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 DR Lipoprotein
 KW SEQUENCE 258 AA; 29918 MW; 093E6FF2E629C0DC8 CRC64;
 SQ

[illegible]

```

RESULT      6
008877
ID      008877      PRELIMINARY;      PRT;      258 AA.
AC      008877.
DT      01-JUL-1997      (TREMBLrel. 04, Created)
DT      01-JUL-1997      (TREMBLrel. 04, Last sequence update)
DT      01-DEC-2001      (TREMBLrel. 19, Last annotation update)
DE      Apolipoprotein A-I.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sclurognathu; Muridae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=SHR; TISSUE=SPLEEN;
RC      MEDLINE=98077648; Pubmed=9415807;
RA      Chiang A.N., Pan K.C., Shaw G.C., Yang U.C.;
RT      "Repetitive elements in the third intron of murine apolipoprotein A-I
RT      gene.";
RL      Biochem. Mol. Biol. Int. 43:989-996(1997).
DR      EMBL; U79576; AAB58428.1; -.
DR      HSSP; P02647; IAVI.
DR      InterPro; IPR000074; Apolipoprotein.
DR      Pfam; PF01442; Apolipoprotein; 1.
KW      Lipoprotein.
SQ      SEQUENCE      258 AA;      29831 MW;      093FEB582E629CD08 CRC64;

```

	Query Match	63.2%	Score 559;	DB 11;	Length 258;
	Best Local Similarity	63.5%;	Pred. No.	1.3e-32;	
	Matches 108; Conservative	21;	Mismatches	35;	Indels 6; Gaps 2.
Oy	1 DEPPSPMDRKKDLATYVVDYLKDSGGDYVSQFSGSLIGKQLNLKLLDNDSDVTSSKRL	60			
Db	25 DDPSP--WDRAKDRAFTYVDANAKDSGRDYVSQSFSSTLIGKQLNLTLDNDMTDGSTVGRL	82			

[illegible]

RESULT	7			
ID	002762	PRELIMINARY;	PRF;	56 AA.
AC	002762.			
DT	01-JUL-1997	(TREMBLrel. 04, Created)		
DT	01-JUL-1997	(TREMBLrel. 04, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	APOLIPROTEIN AI (FRAGMENT).			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;			
OC	Bovidae; Caprinae; Ovis.			
OX	NCBI_TaxID=940;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99098454; PubMed=9883985;			
RA	Robertson J.A., Bhattacharya S., Ing N.H.;			
RT	"Tamoxifen up-regulates oestrogen receptor-alpha, c-fos and			
RT	glyoxaldehyde 3-phosphate-dehydrogenase mRNAs in ovine endometrium.";			
RL	J. Steroid Biochem. Mol. Biol. 67:285-292(1998).			
DR	EMBL; U94720; AAB57840.1; -.			
DR	HSSP; P02647; LAVI.			
KW	lipoprotein.			
FT	NON_TER	1	1	
FT	NON_TER	56	56	
SQ	SEQUENCE	56 AA;	6617 MW;	2AB38E08F1EBF1BC CRC64;

	Query Match	Best Local	Similarity	Matches	Conservative	Score	2d7	DB	6	Length	56
OY	47	LDNMDSVTSPFSKIREOLDGPGVTOEDFMDNLEKTEFGEKROEMSKTLEFVAKKVOYILD	82.18 <td>46 <td>3 <td>Mismatches <td>7 <td>Indels <td>0 <td>Gaps <td>0</td> </td></td></td></td></td></td></td>	46 <td>3 <td>Mismatches <td>7 <td>Indels <td>0 <td>Gaps <td>0</td> </td></td></td></td></td></td>	3 <td>Mismatches <td>7 <td>Indels <td>0 <td>Gaps <td>0</td> </td></td></td></td></td>	Mismatches <td>7 <td>Indels <td>0 <td>Gaps <td>0</td> </td></td></td></td>	7 <td>Indels <td>0 <td>Gaps <td>0</td> </td></td></td>	Indels <td>0 <td>Gaps <td>0</td> </td></td>	0 <td>Gaps <td>0</td> </td>	Gaps <td>0</td>	0
Db	1	LDNMDSVTSPFSKIREOLDGPGVTOEDFMDNLEKTEFGEKROEMSKTLEFVAKKVOYILD	82.18 <td>46 <td>3 <td>Mismatches <td>7 <td>Indels <td>0 <td>Gaps <td>0</td> </td></td></td></td></td></td></td>	46 <td>3 <td>Mismatches <td>7 <td>Indels <td>0 <td>Gaps <td>0</td> </td></td></td></td></td></td>	3 <td>Mismatches <td>7 <td>Indels <td>0 <td>Gaps <td>0</td> </td></td></td></td></td>	Mismatches <td>7 <td>Indels <td>0 <td>Gaps <td>0</td> </td></td></td></td>	7 <td>Indels <td>0 <td>Gaps <td>0</td> </td></td></td>	Indels <td>0 <td>Gaps <td>0</td> </td></td>	0 <td>Gaps <td>0</td> </td>	Gaps <td>0</td>	0

RESULT	8		
Q92948			
ID	Q92948	PRELIMINARY;	PRT: 82 AA.
AC	Q92948;		
DT	01-NOV-1996 (TREMBLrel, 01, Created)		
DT	01-NOV-1996 (TREMBLrel, 01, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel, 19, Last annotation update)		
DE	APOLIPROTEIN A-I (FRAGMENT).		
OS	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.		
CC	NCBI_TaxID=9823;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=SMALL INTESTINE;		
RX	MEDLINE=96337607; PubMed=8672129;		
RA	Winteroe A.K., Fredholm M., Davies W.;		
RT	"Evaluation and characterization of a porcine small intestine cDNA		
RT	library.";		
RL	Mamm. Genome 7:509-517(1996).		
DR	EMBL; F14858; CAA23298.1; -. Lipoprotein.		
KW	NON_TER	82	
FT			
SQ	SEQUENCE	82 AA;	9168 MW; 24625656SCEFFED8 CRC64;

Query Match 24.5%; Score 217; DB 6; Length 82;


```

SQ      SEQUENCE      363 AA;  40923 MW;  9E09CE97205D8A7D CRC64;

```

Query Match 17.8%; Score 157.5; DB 4; Length 363;

Best Local Similarity 26.1%; Pred. No. 0.0009; Matches 43; Conservative 40; Mismatches 61; Indels 21; Gaps 4;

OY 24 DSGRDVVSQFESSALGKQNLKLDNMDSVSTFSKLRQLGPTVQFWDNLEKETGLR 83
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 34 DKGR--VEQIHQKMARE-PATLKDSLLEDLNNMKNFLEKLRPLSGSEAPRLQDPVGM 90

OY 84 QEMSKDLEVKAKVOPYLDDFOKWOEMELYKQVEPIRAELOGAKOKLHELOEKLSP 143
: : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 91 KDLQEELEVKARLQPYMAEAHLELWNLGLRQOLKPYTMDLMEQVALRVQELQEOQLRV 150

OY 144 LSEEMR-----DRAAHVDALRTHLA-----PYSDEL 170
: | : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 151 VGEDTRKAQLGSGVDEAMALQGLQSGRVYHHTGRFKEKLFHYAEL 195

RESULT 15

ID Q9Y355 PRELIMINARY; PRT; 67 AA.

AC Q9Y355; 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE APOLIPROTEIN A1 (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99216322; PubMed=10198255;

RA Hamidi Asl K., Ilepniaks J.J., Nakamura M., Parker F., Benson M.D.,

RT "A novel apolipoprotein A-I variant, Arg173Pro, associated with

RT cardiac and cutaneous amyloidosis";

RL Biochem. Biophys. Res. Commun. 257:584-588(1999).

DR EMBL; AF148963; AAD34604.1; -.

DR HSSP; P02647; LAV1.

KW Lipoprotein.

FT NON_TER 1 1

FT 67 67

SQ SEQUENCE 67 AA; 7433 MW; 525E1FEB7BDD5AFB CRC64;

Query Match 17.4%; Score 154; DB 4; Length 67;

Best Local Similarity 100.0%; Pred. No. 0.00021;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 LSPLGEEMDRARAHDALRTHLAPYSDEL 170

DB 1 LSPLGEEMDRARAHDALRTHLAPYSDEL 30

Search completed: September 22, 2002, 12:21:36
Job time: 1116 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2002, 12:05:15 ; Search time 139.03 seconds
(without alignments)
135.816 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_194

Perfect score: 885
Sequence: 1 DEPOSFMDRKYDLATYVD.....RAAHVVALRTHLAPYSEL 170

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT.*
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9: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT.*
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11: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT.*
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20: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	885	100.0	243	9 AAP81082	Sequence of mature Apo-IIipoprotein AI
2	885	100.0	264	15 AAR56863	Apo-IIipoprotein AI
3	885	100.0	264	7 AAR56864	Assumed human apol
4	885	100.0	267	7 AAP61079	Entire human prepr
5	885	100.0	267	9 AAP82128	Sequence of apo AI
6	885	100.0	267	14 AAR34032	Human apo A-I incl
7	885	100.0	267	16 AAR72705	Human apolipoprote
8	885	100.0	267	20 AAY18675	Full length Apo-AI
9	885	100.0	267	22 AAB47620	Recombinant human
10	885	100.0	268	9 AAP80668	Novel human secret
11	878	99.2	299	22 AAU33170	

12	877	99.1	267	18 AAU08602	Human apolipoprote
13	739.5	83.6	244	22 AAU28184	Novel human secret
14	727	82.1	151	22 AAU02278	Human polypeptide
15	712	80.5	221	22 AAU29835	Novel human secret
16	647.5	78.2	166	22 AAU28372	Novel human secret
17	516.5	58.4	318	22 AAU30268	Novel human secret
18	501.5	56.7	154	22 AAU12095	Human polypeptide
19	479.5	54.2	119	22 AAU30468	Novel human secret
20	476.5	53.8	120	22 AAU30267	Novel human secret
21	476.5	53.8	120	22 AAU30469	Novel human secret
22	434	49.0	359	22 AAU30470	Novel human secret
23	218	24.6	42	13 AAR20164	Apo AI polypeptide
24	213	24.1	396	22 AAB90664	Human secreted pro
25	212.5	24.0	377	14 AAR39502	Human apolipoprote
26	210	23.7	333	14 AAR39497	Human apolipoprote
27	210	23.7	342	14 AAR39498	Human apolipoprote
28	209	23.6	183	14 AAR39482	Human apolipoprote
29	209	23.6	333	14 AAR39481	Human apolipoprote
30	209	23.6	333	14 AAR39490	Human apolipoprote
31	209	23.6	333	14 AAR39495	Human apolipoprote
32	209	23.6	337	14 AAR39492	Human apolipoprote
33	209	23.6	342	14 AAR39487	Human apolipoprote
34	209	23.6	342	14 AAR39491	Human apolipoprote
35	209	23.6	342	14 AAR39496	Human apolipoprote
36	209	23.6	346	14 AAR39493	Human apolipoprote
37	209	23.6	377	14 AAR39443	Human apolipoprote
38	209	23.6	377	14 AAR45242	Human apolipoprote
39	209	23.6	377	14 AAR45243	Human apolipoprote
40	208	23.6	377	14 AAR45244	Human apolipoprote
41	208	23.5	377	14 AAR39501	Human apolipoprote
42	207	23.4	337	14 AAR39494	Human apolipoprote
43	205	23.2	363	14 AAR39479	Human apolipoprote
44	205	23.2	373	14 AAR39486	Human apolipoprote
45	205	23.2	377	14 AAR39480	Human apolipoprote

ALIGNMENTS

RESULT 1	
AAU082	14-JAN-1991 (first entry)
AAU082	Sequence of mature human apolipoprotein AI (apoAI).
AAU082	Atherosclerosis; therapy; cardiovascular disease.
AAU082	Homo sapiens.
AAU082	W08803166-A.
AAU082	05-MAY-1988.
AAU082	21-OCT-1987; 87WO-EP00621.
AAU082	23-OCT-1986; 86GB-0025435.
AAU082	(FARM) FARMITALIA C ERBA SPA.
AAU082	Lorenzetti R, Monaco L, Soria M, Palomba R, Isacchi A, Sarmientos P;
AAU082	WPI: 1988-133240/19.
AAU082	N-PSDB: AAN80243.
AAU082	Recombinant human apolipoprotein AI -
AAU082	used to lower plasma cholesterol and/or tri glyceride levels and
AAU082	to combat atherosclerosis and cardiovascular diseases
AAU082	Disclosure; Fig 1; 51pp; English.

XX The protein comprising apo AI genetic variants may be used to lower
 CC plasma cholesterol and/or triglyceride levels. They may also be used to
 CC combat atherosclerosis and cardiovascular diseases such as coronary
 CC heart disease. Pref. Proteins are Met-apo AI, Met-apo AI-T6, Met-apo
 CC AI-MI and Met-apo AI-T6/MI.

XX Sequence 243 AA;

Query Match 100.0%; Score 885; DB 9; Length 243;
 Best Local Similarity 100.0%; Pred. No. 3.3e-66;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPSPMDRYKDLATVYVDVILKDSGRDYVSQFEGSALGKQLNLKLDNMDSVTSTFSKL 60
 Db 1 deppspmdrykdlatvyvdvilkdsgrdyvsqfegsalsgkqlnlkldnmdsvstfskl 60
 QY 61 REQLGPTVQEFWDLNLEKTEGLROEMSKDLEEVKAKVQPYLDLDFOKKQEMELYRQKVE 120
 Db 61 reqlgptvqefwldnleketeglrqemskdleevkakvqpyldldfokkqemelyrqkve 120
 QY 121 PLRAELQEGARQKHLHLEQKLSPLGEMDRARAHVDALRTHLAPYSDEL 170
 Db 121 plraelqegarqkhlhelqeklsplgeemdrarahvdalrthlapyssel 170

RESULT 2

AAR56863
 ID AAR56863 standard; Protein; 264 AA.

XX AAR56863;

DT 26-JAN-1995 (first entry)

XX Apo-lipoprotein AI-M.

XX Apo-lipoprotein AI-M; Apo AI-M; Escherichia coli; plasmid pKP683;
 KM vector; atherosclerosis; cardiovascular disease.

XX Homo sapiens.

XX WO9413819-A.

XX 23-JUN-1994.

XX 09-DEC-1993; 93WO-SE01061.

XX 11-DEC-1992; 92SE-0003753.

XX (KABI) KABI PHARMACIA AB.

PI Abrahamson L, Holmgren E, Kalderen C, Lake M, Mikaelsson A;
 PI Sejitz T;

XX WPI: 1994-217892/26.

DR N-PSDB; AA068357.

XX Expression vector for extracellular prodn of apo-lipoprotein AI-M
 PT in E. coli - includes inducible promoter and signal peptide
 PT sequences providing improved yield, useful in treating
 PT atherosclerosis and cardiovascular disease.

XX Disclosure; Fig. 3; 33pp; English.

XX Plasmid pKP683 encodes human apo-lipoprotein AI-M in E. coli. The
 CC NotI-HindIII segment of pKP683 and the deduced amino acid sequence
 CC of the translated Apo AI-M protein were determined. The plasmid
 CC provides high yields of extracellular Apo AI-M.

XX Sequence 264 AA;

Query Match 100.0%; Score 885; DB 15; Length 264;
 Best Local Similarity 100.0%; Pred. No. 3.6e-66;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPSPMDRYKDLATVYVDVILKDSGRDYVSQFEGSALGKQLNLKLDNMDSVTSTFSKL 60
 Db 22 deppspmdrykdlatvyvdvilkdsgrdyvsqfegsalsgkqlnlkldnmdsvstfskl 81
 QY 61 REQLGPTVQEFWDLNLEKTEGLROEMSKDLEEVKAKVQPYLDLDFOKKQEMELYRQKVE 120
 Db 82 reqlgptvqefwldnleketeglrqemskdleevkakvqpyldldfokkqemelyrqkve 141
 QY 121 PLRAELQEGARQKHLHLEQKLSPLGEMDRARAHVDALRTHLAPYSDEL 170
 Db 142 plraelqegarqkhlhelqeklsplgeemdrarahvdalrthlapyssel 191

RESULT 3

AAR56864
 ID AAR56864 standard; Protein; 264 AA.

XX AAR56864;

DT 26-JAN-1995 (first entry)

XX Apo-lipoprotein AI-M.

XX Apo-lipoprotein AI-M; Apo AI-M; Escherichia coli; plasmid pKP764;
 KM vector; atherosclerosis; cardiovascular disease.

XX Homo sapiens.

XX WO9413819-A.

XX 23-JUN-1994.

XX 09-DEC-1993; 93WO-SE01061.

XX 11-DEC-1992; 92SE-0003753.

XX (KABI) KABI PHARMACIA AB.

PI Abrahamson L, Holmgren E, Kalderen C, Lake M, Mikaelsson A;
 PI Sejitz T;

XX WPI: 1994-217892/26.

DR N-PSDB; AA068358.

XX Expression vector for extracellular prodn of apo-lipoprotein AI-M
 PT in E. coli - includes inducible promoter and signal peptide
 PT sequences providing improved yield, useful in treating
 PT atherosclerosis and cardiovascular disease.

XX Disclosure; Fig. 4; 33pp; English.

XX Plasmid pKP764 encodes human apo-lipoprotein AI-M in E. coli. The
 CC NotI-HindIII segment of pKP764 and the deduced amino acid sequence
 CC of the translated Apo AI-M protein were determined. The plasmid
 CC provides high yields of extracellular Apo AI-M.

XX Sequence 264 AA;

Query Match 100.0%; Score 885; DB 15; Length 264;
 Best Local Similarity 100.0%; Pred. No. 3.6e-66;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPSPMDRYKDLATVYVDVILKDSGRDYVSQFEGSALGKQLNLKLDNMDSVTSTFSKL 60
 Db 22 deppspmdrykdlatvyvdvilkdsgrdyvsqfegsalsgkqlnlkldnmdsvstfskl 81
 QY 61 REQLGPTVQEFWDLNLEKTEGLROEMSKDLEEVKAKVQPYLDLDFOKKQEMELYRQKVE 120
 Db 142 plraelqegarqkhlhelqeklsplgeemdrarahvdalrthlapyssel 191

Db 8c reqlgvgtgfwdnleketeglrqemskdleevkavqpylddfgkkgwgemelyrqkve 141
 QY 121 PLRAELQEGAROKLHLEQEKLSPLGEMDRARAHVDALRTHLAPYSDEL 170
 Db 142 plraelqegargklhelqeklsplgeemdrarahvdalrthlapydel 191

RESULT 4

AAP61079
 ID AAP61079 standard; Protein; 267 AA.
 AC AAP61079;
 XX
 XX

DT 07-OCT-1991 (first entry)
 XX
 XX

DE Assumed human apolipoprotein A-1 derivative gene product.
 XX
 XX

KW Hyperlipaemia; arteriosclerosis.
 XX
 XX

OS Homo sapiens.
 XX
 XX

PN JP61096998-A.
 XX
 XX

PD 15-MAY-1986.
 XX
 XX

PF 16-OCT-1984; 84JP-0216988.
 XX
 XX

PR 16-OCT-1984; 84JP-0216988.
 XX
 XX

PA (MITU) MITSUBISHI CHEM IND KK.
 XX
 XX

DR WPI; 1986-165025/26.
 XX
 XX

DR N-PSDB; AAN60886.
 XX
 XX

PT Human apo:lipoprotein A-1 (deriv.) prepn. - by providing DNA
 fragment in cloning site downstream of expression vector promoter
 PT and introducing into host microorganism.
 XX
 XX

PS Disclosure; Fig 2; 9pp; Japanese.
 XX
 XX

CC The human apolipoprotein may be produced by a suitable transformed
 host, it is effective in treating hyperlipaemia and arteriosclerosis.
 CC
 XX

XX Sequence 267 AA;
 SQ

Query Match 100.0%; Score 885; DB 7; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3.7e-66;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPMDRVKDLATVYVVDVLDKSGRDYVSOEFGSALGKQLNLKLDNMDSVTSTPSKL 60
 Db 25 deppqspmdrvkdlatvyvvdvldksgrdyvsqfegsalgkqlnlkldnmdsvtstfsl 84
 QY 61 REQLGPTQGEFMDNLEKETEGLEKROEMSKDLEEVKAKVQPYLDPOKKQWQEMELYRQKVE 120
 Db 85 reqlgptqgefwdnleketeglrqemskdleevkavqpylddfgkkgwgemelyrqkve 144

QY 121 PLRAELQEGAROKLHLEQEKLSPLGEMDRARAHVDALRTHLAPYSDEL 170
 Db 145 plraelqegargklhelqeklsplgeemdrarahvdalrthlapydel 194

RESULT 5

AAP82128
 ID AAP82128 standard; Protein; 267 AA.
 AC AAP82128;
 XX
 XX

DT 24-OCT-1990 (first entry)
 XX
 XX

DE Entire human preproapoprotein A1.
 DE
 XX

XX

KW human preproapoprotein A1; high density lipoprotein deficiency; ss.
 XX
 XX

OS synthetic.
 OS
 XX

PH Key Location/Qualifiers
 FT Peptide 1..18
 FT Peptide /label=precursor
 FT Peptide 19..24
 FT Peptide /label=propeptide
 FT Protein 25..267
 FT /label=mature apoprotein

EP293357-A.
 XX
 XX

PD 30-NOV-1988.
 XX
 XX

PF 24-MAY-1988; 88EP-0870095.
 XX
 XX

PR 28-MAY-1987; 87GB-0012540.
 XX
 XX

PA (UNIO) UCB SA.
 XX
 XX

PI Bollen A, Gobert J, Wulfert E;
 XX
 XX

DR WPI; 1988-339891/48.
 XX
 XX

DR N-PSDB; AAN82064.
 XX
 XX

PT New DNA encoding human preproapoprotein A1 -
 modified to eliminate hairpin structures
 PT
 XX

PS Disclosure; ; P; French.
 XX
 XX

CC The cDNA 878bp fragment encoding preproapoprotein A1 was detected
 in clone PUB1609 derived from human liver cells.
 CC
 XX

CC See also AAN81258.
 CC
 XX

XX Sequence 267 AA;
 SQ

Query Match 100.0%; Score 885; DB 9; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3.7e-66;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPMDRVKDLATVYVVDVLDKSGRDYVSOEFGSALGKQLNLKLDNMDSVTSTPSKL 60
 Db 25 deppqspmdrvkdlatvyvvdvldksgrdyvsqfegsalgkqlnlkldnmdsvtstfsl 84
 QY 61 REQLGPTQGEFMDNLEKETEGLEKROEMSKDLEEVKAKVQPYLDPOKKQWQEMELYRQKVE 120
 Db 85 reqlgptqgefwdnleketeglrqemskdleevkavqpylddfgkkgwgemelyrqkve 144

QY 121 PLRAELQEGAROKLHLEQEKLSPLGEMDRARAHVDALRTHLAPYSDEL 170
 Db 145 plraelqegargklhelqeklsplgeemdrarahvdalrthlapydel 194

RESULT 6

AAR34032
 ID AAR34032 standard; Protein; 267 AA.
 AC AAR34032;
 XX
 XX

DT 13-AUG-1993 (first entry)
 XX
 XX

DE Sequence of apo A1.
 DE
 XX

XX Lipoprotein; apoprotein; B-100; A-I; LDL; HDL; assay.
 XX
 XX

OS Homo sapiens.
 OS
 XX

PN W09307165-A.
 PN
 XX

PD 15-APR-1993.
 PD
 XX

XX

XX 09-OCT-1992; 92MO-US08634.
 PF
 XX
 PR 09-OCT-1991; 91US-0774633.
 PR 08-OCT-1992; 92US-055555.
 PR 28-JUN-1992; 92US-0901706.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Curtiss LK, Koduri KR, Smith RS, Wiltzium JL, Young SG;
 XX
 DR WPI: 1993-134378/16.
 DR N-PSDB; AAQ40030.
 PT Polypeptide mimic of native apo B-100 and native apo A-I - useful
 XX in assays for LDL and HDL in plasma samples
 XX
 PS Claim 19; Pages 105-106; 137pp; English.
 XX
 CC The inventors claim a portion of the polypeptide contg. apo B-100
 CC that immunoreacts with antibodies secreted by the hybridoma MB47
 CC having ATCC Accession No. 8746. Polypeptides specifically claimed
 CC include residues 217-297, 216-310, 216-331, 216-352, 216-377, 1-377,
 CC 205-297, 173-297, 140-297. DNA sequences encoding the polypeptides
 CC are also claimed. Also claimed are a fusion polypeptide that
 CC contains: (a) a first amino acid residue sequence up to 250 residues
 CC in length that includes residues 120-135 of apo A-I, (b) a second
 CC amino acid residue sequence up to 375 residues in length that
 CC includes residues 217-297 of apo B-100 and DNA encoding it.
 CC
 XX Sequence 267 AA:
 SQ
 Query Match 100.0%; Score 885; DB 14; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3.7e-66;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEPPQSPMDRVKDLATVYVDVLDKSGRDVYSQFEGSALGKQLKLDNMDSVTSTFSKL 60
 DB 25 deppqspmdrvkdlatvvdvldksgrdyvsqfegsalsgkqlkldnmdsvstfskl 84
 QY 61 REQLGPTVTOEFWDLKEKETEGILQEMSKDLEEVKAKVQPYLDFFOKKWOEMELYRQKVE 120
 DB 85 reqlgptvtefwdlkeketegilrqemskdleevkakvqpylddfqkkwgeemelyrqkve 144
 QY 121 PLRAELQEGAROKLHLEQEKLSPLGEMDRARAHVDALRTHLAPYSDEL 170
 DB 145 plraelqegargklhelqeklsplgeemdrarahvdalrthlapydel 194
 RESULT 7
 AAR72705
 ID AAR72705 standard; Protein: 267 AA.
 XX
 AC AAR72705;
 XX
 DT 31-OCT-1995 (first entry)
 XX
 DE Human apo A-I including signal and propeptide sequences.
 XX
 KW Apo A-I; LDL cholesterol; low density lipoprotein; lipid.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..18
 FT Peptide /label= presignal
 FT 19..24
 FT Peptide /label= propeptide
 FT 120..135
 FT Peptide /label= claimed
 FT /note="as part of fusion polypeptide"
 FT 19..240
 FT Peptide .

FT /label= claimed
 FT /note= "as part of fusion polypeptide"
 XX
 PN US5408038-A.
 XX
 PD 18-APR-1995.
 XX
 PF 09-OCT-1991; 91US-0774633.
 XX
 PR 09-OCT-1991; 91US-0774633.
 PR 18-JUN-1992; 92US-0901706.
 PR 08-OCT-1992; 92US-0959946.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Curtiss LK, Koduri KR, Smith RS, Wiltzium JL, Young SG;
 XX
 DR WPI: 1995-161146/21.
 DR N-PSDB; AAQ89634.
 XX
 PT New apo:lipoprotein B-100 peptide(s) and fusion peptide(s) - used
 XX in assay systems for detecting LDL and HDL cholesterol levels in
 XX body fluids.
 XX
 PS Claim 10; Fig 2; 41pp; English.
 XX
 CC AA89634 and AAR72705 depict the AA sequence of human apo A-I and its
 CC corresp. cDNA, including prestinal residues and propeptide
 CC residues, according to Seilhamer et al., DNA 3(4):309 (1984).
 CC A dispersible apo A-I/B-100 fusion polypeptide is claimed which
 CC contains a first AA sequence of apo A-I and that includes at
 CC least AA sequence positions 120-135 (see AAR72606) and which reacts
 CC with pan anti-apo AI antibodies such as: AI-4 ATCC HB8744; AI-7
 CC ATCC HB 8745; AI-9 ATCC HB 8741; AI-10 ATCC HB 9200; AI-11 ATCC
 CC HB 9201; AI-12 ATCC HB 9202; AI-13 ATCC HB 9203; AI-14 ATCC HB
 CC 9204; AI-18 ATCC HB 9507.
 CC
 XX Sequence 267 AA:
 SQ
 Query Match 100.0%; Score 885; DB 16; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3.7e-66;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DEPPQSPMDRVKDLATVYVDVLDKSGRDVYSQFEGSALGKQLKLDNMDSVTSTFSKL 60
 DB 25 deppqspmdrvkdlatvvdvldksgrdyvsqfegsalsgkqlkldnmdsvstfskl 84
 QY 61 REQLGPTVTOEFWDLKEKETEGILQEMSKDLEEVKAKVQPYLDFFOKKWOEMELYRQKVE 120
 DB 85 reqlgptvtefwdlkeketegilrqemskdleevkakvqpylddfqkkwgeemelyrqkve 144
 QY 121 PLRAELQEGAROKLHLEQEKLSPLGEMDRARAHVDALRTHLAPYSDEL 170
 DB 145 plraelqegargklhelqeklsplgeemdrarahvdalrthlapydel 194
 RESULT 8
 AAY18675
 ID AAY18675 standard; Protein: 267 AA.
 XX
 AC AAY18675;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE Human apolipoprotein AI protein sequence.
 XX
 KW Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder;
 KW ApoA-I; cardiovascular disease; atherosclerosis; restenosis; LCAT;
 KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.
 XX
 OS Homo sapiens.
 XX

PN W09916409-A2.
 XX 08-APR-1999.
 PD
 XX
 XX 28-SEP-1998; 98WO-US20329.
 PF
 XX 29-SEP-1997; 97US-0940136.
 PR
 XX
 XX (BUTT/) BUTTNER K.
 PA (CORN/) CORNUT I.
 PA (DASS/) DASSEUX J.
 PA (DUFO/) DUFOURCO J.
 PA (METZ/) METZ G.
 PA (SEKUL/) SEKUL R.
 XX
 XX Buttner K, Cornut I, Dasseux J, Dufourcq J, Metz G;
 PI Sekul R;
 PI
 XX WPI: 1999-254921/21.
 DR N-PSDB; AAH55971.
 DR

Nucleic acid encoding apolipoprotein A-I agonist peptides
 Example: Fig 1; 232pp; English.

The present invention describes a nucleic acid (A) encoding an apolipoprotein A-I (ApoA-I) agonist (B) that is a peptide, or analog, which forms an amphipathic alpha-helix in presence of lipids. (A), optionally as a complex with lipids, and host cells that contain (A), are useful for gene therapy, or prevention, of diseases associated with dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease, atherosclerosis, restenosis, HDL (high density lipoprotein) and ApoA-I deficiency, hypertriglyceridemia and metabolic syndrome, also to treat endotoxaemia (septic shock). Host cells containing (A) can also be used to study the role of ApoA-I in lipid metabolism. (B) can also be used diagnostically, e.g. to measure serum HDL (particularly its subpopulation involved in retrograde cholesterol transport) and for imaging the circulatory system or HDL accumulations at fatty streaks. The present sequence represents human ApoA-I.

Sequence 267 AA;

Query Match 100.0%; Score 885; DB 20; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3,7e-66;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSMRDKVLDATVYVDLKDSDGRVYSGESALGKOLNKLNDNDSTSTFSKL 60
 Db 25 deppqsmrDKVLDATVYVDLKDSDGRVYSGESALGKOLNKLNDNDSTSTFSKL 84
 QY 61 REQLGPTVTOEFWNLKETEGLKQEMSKDLEEVKAKVQPYLDDFOKKWDEMELYRQKVE 120
 Db 85 reqlgptvtgfwnlketeGLKQEMSKDLEEVKAKVQPYLDDFOKKWDEMELYRQKVE 144
 QY 121 PLRAELQEGAROKLHELOEKLSPLGEMMRDARAHVDAIRTHIAPYSDEL 170
 Db 145 plraelqegarklHELOEKLSPLGEMMRDARAHVDAIRTHIAPYSDEL 194

RESULT 9
 AAB47620
 ID AAB47620 standard; Protein; 267 AA.
 XX
 AC AAB47620;
 XX

21-JAN-2002 (first entry)
 DE Full length Apo-AI.
 XX

Apolipoprotein; Apo-AI; Apo-A-I fragment T-cell activation inhibitor;
 KW APT1; monocyte; IL-1; Interleukin 1; TNF; tumour necrosis factor;
 acute pancreatitis; Alzheimer's disease; asthma; cancer; fever;
 XX

KW inflammatory bowel disease; ischemia; multiple sclerosis; osteoporosis;
 KW Parkinson's disease; psoriasis; probe.
 XX

OS Homo sapiens.

PH Key Location/Qualifiers

FT Binding-site 44..65 /label= Helical lipid binding domain

FT Binding-site 220..241 /label= Helical lipid binding domain

FT Domain 74..111 /note= "Involved in lipoprotein-mediated cholesterol efflux from monocytes"

FT Binding-site 149..219 /label= Receptor binding domain

FT Domain 99..120 /label= Major antigenic epitope domain

FT Domain 99..143 /label= Hinged domain

FT Domain 66..120 /label= Phylogenetically conserved domain

FT Domain 90..111 /note= "Involved in lectin-cholesterol acyltransferase activity"

FT Domain 44..65 /label= Amphipathic helix

FT Domain 66..98 /label= Amphipathic helix

FT Domain 99..120 /label= Amphipathic helix

FT Domain 121..142 /label= Amphipathic helix

FT Domain 143..164 /label= Amphipathic helix

FT Domain 165..208 /label= Amphipathic helix

FT Domain 209..219 /label= Amphipathic helix

FT Domain 220..241 /label= Amphipathic helix

FT Domain 25..194 /label= Amphipathic helix

FT Peptide /label= APT1

FT Peptide /note= "18 KD N-terminal fragment"

FT Peptide /label= APT1

FT Peptide /note= "13 KD N-terminal fragment"

FT Peptide /label= APT1

FT Peptide /note= "13 KD C-terminal fragment"

PN W0200168852-A2.

XX 20-SEP-2001.

XX 13-MAR-2001; 2001WO-US07826.

XX 13-MAR-2000; 2000US-189008P.

XX (AMGE-) AMGEN INC.

XX Edwards CK, Burger D, Dayer J, Kohno T;

XX WPI: 2001-596908/67.

XX N-PSDB; AAH43623.

XX Apo-A-I fragment T-cell activation inhibitor (APT1) polynucleotides,

XX useful for treating, diagnosing, ameliorating diseases associated with

XX IL-1 and/or TNF activity, e.g. acute pancreatitis, Alzheimer's disease

XX and asthma -

XX Claim 1; Fig 1A; 132pp; English.

XX This sequence shows full length apolipoprotein (Apo-AI). Fragments

of Apo-A-I may be used as Apo-A-I fragment T-cell activation inhibitors (AFTI). These fragments are selected from an 18 kD N-terminal fragment (amino acids 25-194), a 13 kD N-terminal fragment (amino acids 25-144) and a 13 kD C-terminal fragment (amino acids 156-267). The AFTI polypeptides and polynucleotides are useful for regulating T-cell mediated activation of monocytes and for treating, diagnosing, ameliorating diseases associated with IL-1 and/or TNF activity. The diseases are acute pancreatitis, Alzheimer's disease, asthma, cancer, fever, inflammatory bowel disease, ischemia, multiple sclerosis, osteoporosis, Parkinson's disease or psoriasis. Numerous examples of other diseases are given in the specification. The AFTI nucleic acids are useful as hybridization probes in diagnostic assays to test for the presence of an AFTI or Apo-A-I DNA in mammalian tissue or bodily fluid samples.

Sequence 267 AA;

Query Match 100.0%; Score 885; DB 22; Length 267;
Best Local Similarity 100.0%; Pred. No. 3,7e-66;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPMDRVKDLATVYVDVLDKSGRDVYSGFEGSALGKQLNKLDDNWDSTSTFSKL 60
|||||
Db 25 deppqspmdrvkdlatvyydvldksgrdyvsqfegsalgkqlnklldnwdststfskl 84
QY 61 REQLGPVYQEFMDNLEKETEGLRQEMSKDLEEVKAKVOPYLDDFOKKWOEMELIRKQVE 120
|||||
Db 85 reqlgpyvtqefwldnleketeglrqemskdleevkakvopylddfqkwwgemelyrkqve 144
QY 121 PLRAELQEGAROKLHLEQELSLPLGEMDRARAHVDAIRTHLAPYSDEL 170
|||||
Db 145 plraelqegargklhelqeklsplgeemdrarahvdairthlapyssel 194

RESULT 10

AA080668
ID AAP80668 standard; protein; 268 AA.

AC AAP80668;

DT 24-OCT-1990 (first entry)

DE Recombinant human preproapoprotein A1.

DE human preproapoprotein A1; high density lipoprotein deficiency; ss.

KW synthetic.

OS Key Location/Qualifiers

FT 1..18 /label-precursor

FT Peptide 19..25 /label1=proprotein

FT Protein 26..268 /label=mature apoprotein A1

FT EP293357-A.

PD 30-NOV-1988.

PF 24-MAY-1988; 88EP-0870095.

PR 28-MAY-1987; 87GB-0012540.

XX (UNTO) UCB SA.

PI Bollen A, Gobert J, Wulfert E;

DR WPI; 1988-339891/48.

DR N-PSDB; AAN81258.

PT New DNA encoding human preproapoprotein A1 -

PT modified to eliminate hairpin structures

PS Claim 1; Page 12; 25pp; French.

CC Met at posn 19 is inserted as an extra amino acid c.f. wild-type

CC protein.

CC The DNA fragment used to replace the wild-type sequence encoding

CC amino acids -6 to +14 (= Arg 20 to Leu 39) modifies codons

CC corresponding to wild-type amino acids -6, -1, 1, 3, 4, 5, 6, 7,

CC 10, 11 and 14. The changed codons still encode the same amino acids

CC as in the wild-type protein but reduce formation of secondary

CC structures in mRNA.

CC See also AAN82064.

CC structures in mRNA.

CC See also AAN82064.

CC structures in mRNA.

CC See also AAN82064.

CC structures in mRNA.

CC See also AAN82064.

RESULT 11

AA033170
ID AA033170 standard; protein; 299 AA.

AC AA033170;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #3661.

DE Human; vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

PA (HYSE-) HYSED INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-611725/70.

PT Nucleic acids encoding a range of human polypeptides, useful in genetic

PT vaccination, testing and therapy -

XX Claim 20; Page 718; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for

CC determining the presence of or predisposition to a disease associated

CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptides. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukemias. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.

XX Sequence 299 AA;

Query Match 99.2%; Score 878; DB 22; Length 299;
 Best Local Similarity 99.4%; Pred. No. 1.6e-65;
 Matches 169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEPPSPMDRVKDLATVYVDVLDKSGRDVYSQFEGSALGKQLNKLDMDSVSTFSKL 60
 DB 57 deppspmdrvkdlatvyvdvldksgrdvysqfegsalsgqlnklldmwsvtfskl 116
 QY 61 RRLGPGVYQEFMDNLEKETEGRLRQEMSKDLEEVKAKVQPYLDFOKKQEMELYRQKVE 120
 DB 117 rrlgpgvyrqefmdnleketegrlrqemskdleevkakvpylddfqkkqemelyrqkve 176
 QY 121 PLRAELQEGARQKLHELOEKLSPGSEMRDRAHVAALRTHLAPYSDEL 170
 DB 177 plraelqegarqklhelqeklsplgeemrdrarahvalrthlapysgel 226

RESULT 12

AAU08602 standard; Protein; 267 AA.

XX AAU08602;

DT 04-SEP-1997 (first entry)

XX Human apolipoprotein A-1 variant "Paris" protein sequence.

XX Human: apolipoprotein A-1; variant; mutation; serum lipid; cholesterol;
 KW high density lipoprotein; triglyceride; symptom; cardiovascular disease;
 KW atherosclerosis; restenosis; myocardial infarct; angina; death; stroke;
 KW cardiac decompensation; metabolic deficit.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..24 /note= "prepro peptide"

FT Region 172..178 /note= "this sequence which contains the mutated amino

FT MISC-difference 175 /note= "acid residue is claimed - claim 2"

FT due to a C to T transition mutation"

XX WO9637608-A1.

XX 28-NOV-1996.

XX 20-MAY-1996; 96MO-FR00747.

XX 22-MAY-1995; 95FR-0006061.

PA (INSP) INST PASTEUR LITTLE.
 PA (RHON) RHONE POULENC RORER SA.
 PA (UYPA-) UNIV CURIE PARIS VI P 6 M.

XX Benoit P, Bruckert E, Deneffe P, Duverger N, Fruchart J;
 PI Luc G, Turping, Assmann G, Funke H;
 DR WPI: 1997-021218/02.
 DR N-PSDB: AAT43691.

PT New variant of human apoA-1 with Cys at position 151 - has
 PT anti-atherogenic activity for treatment and prevention of
 PT cardiovascular disease

PS Claim 2; Page -: 58pp; French.

CC This is the amino acid sequence of a human apolipoprotein A-1 variant
 CC designated the "Paris" variant which has a Cys replacing the Arg residue
 CC at position 151. The substitution is generated by a mutation of
 CC the C nucleotide at position 523 in the wild type gene to a T residue,
 CC changing the encoded residue from an Arg to a Cys. The gene was isolated
 CC from a patient with an unusual pattern of serum lipids i.e. low levels of
 CC apoA-1 and high density lipoprotein (HDL)-cholesterol and high
 CC triglycerides, but showing symptoms of atherosclerosis. The new variant
 CC protein has anti-atherogenic activity so is useful for treatment and
 CC prevention of cardiovascular diseases such as atherosclerosis,
 CC restenosis, myocardial infarct, angina, sudden death, stroke and cardiac
 CC decompensation, or more generally any condition involving genetic or
 CC metabolic deficit of apoA-1.
 CC Note: this sequence is not given in the specification but is generated
 CC from the wild type apoA-1 gene disclosed in the specification and has
 CC the appropriate amino acid changed.

SQ Sequence 267 AA;

Query Match 99.1%; Score 877; DB 18; Length 267;
 Best Local Similarity 99.4%; Pred. No. 1.7e-65;
 Matches 169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEPPSPMDRVKDLATVYVDVLDKSGRDVYSQFEGSALGKQLNKLDMDSVSTFSKL 60
 DB 25 deppspmdrvkdlatvyvdvldksgrdvysqfegsalsgqlnklldmwsvtfskl 84
 QY 61 RRLGPGVYQEFMDNLEKETEGRLRQEMSKDLEEVKAKVQPYLDFOKKQEMELYRQKVE 120
 DB 85 rrlgpgvyrqefmdnleketegrlrqemskdleevkakvpylddfqkkqemelyrqkve 144
 QY 121 PLRAELQEGARQKLHELOEKLSPGSEMRDRAHVAALRTHLAPYSDEL 170
 DB 145 plraelqegarqklhelqeklsplgeemrdrarahvalrthlapysdel 194

RESULT 13

AAU28184 standard; Protein; 244 AA.

XX AAU28184;

DT 18-DEC-2001 (first entry)

XX Novel human secretory protein, Seq ID No 353.

XX Human: secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; Rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.

XX Homo sapiens.
 OS WO200166689-A2.

PD 13-SEP-2001.
 PP HSE-2001. 2001WO-US04942.
 XX 05-MAR-2001. 2001WO-US04942.
 XX 07-MAR-2000. 2000US-0519705.
 PR 19-MAY-2000. 2000US-0574454.
 PR 17-JUN-2000. 2000US-0596193.
 PR 14-JUL-2000. 2000US-0616847.
 PR 19-SEP-2000. 2000US-0665363.
 PR 20-OCT-2000. 2000US-0693267.
 XX (HSE-) HXSEQ INC.
 PA Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P,
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX WPI: 2001-589934/66.
 DR N-PSDB; AAS45084.
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 PS
 XX Example 5: SEQ ID NO 353; 107pp; English.
 XX The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the *in vivo* activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC anabolic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention.
 CC
 XX
 XX Sequence 244 AA:
 Query Match 83.6%; Score 739.5; DB 22; Length 244;
 Best Local Similarity 85.9%; Pred. No. 4.6e-54;
 Matches 146; Conservative 1; Mismatches 0; Indels 23; Gaps 1
 QY 1 DEPOS:PD:DRYK:DIATYVVDYKSGRGYVSGFBSALGRQLNKLDMNDVSTPFSKL 60
 Db 25 deppspmdrykdiatyyvvdylksggk-----dsvststskl 61
 QY 61 RGLQAPVVOEPMNDLKEKTEGLRDEMSSKDLFEVAKVQVYLDLDFOKKWOEMELRYCKVE 120

Db	62	reg19vltgcfwlnlaketeg1lrgemskoleevkavp1ddfgkhwgemelyrqvke	121
Oy	121	PLRAELQEGAROKLHLEQLSPLGEMRDRAHVDALRTHLAAYSDQL	170
Db	122	plraelqegargklhnelqklspjgeemdrararahlrhlapydel	171
RESULT	14		
ID	AAO02278		
XX	AAO02278 standard; Protein; 151 AA.		
AC	AAO02278:		
XX			
DT	06-NOV-2001 (first entry)		
XX			
DE	Human polypeptide SEQ ID NO 16170.		
XX			
XX	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
KM	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;		
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;		
KM	nervous system disorders; arthritis; inflammation.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200164835-A2.		
XX			
PD	07-SEP-2001.		
XX			
PF	26-FEB-2001; 2001WO-US04927.		
XX			
PR	28-FEB-2000; 2000US-0515126.		
PR	18-MAY-2000; 2000US-0577409.		
XX			
PA	(HYSE-) HYSEQ INC.		
XX			
PI	Tang YF, Liu C, Dermanac RT;		
XX			
DR	WPI: 2001-514838/56.		
XX	N-PSDB; AA182209.		
PT	Isolated nucleic acids and polypeptides, useful for preventing		
XX	diagnosing and treating e.g. leukaemia, inflammation and immune		
PT	disorders -		
XX			
PS	Claim 20; SEQ ID NO 16170; 1399pp + Sequence Listing; English.		
XX			
CC	The invention relates to human polynucleotides (AA179941-AA193841) and		
CC	the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to		
CC	cytokine, cell proliferation or cell differentiation or which may induce		
CC	production of other cytokines in other cell populations. The		
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or		
CC	peptide therapy. The polypeptides have various cytokine-like activities,		
CC	e.g. stem cell growth factor activity, haematopoiesis regulating		
CC	activity, tissue growth factor activity, immunomodulatory activity and		
CC	activity/inhibit activity and may be useful in the diagnosis and/or		
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and		
CC	inflammation.		
CC	Note: The sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences.		
XX			
SQ	Sequence 151 AA:		
Query Match	82.1%; Score 727; DB 22; Length 151;		
Best Local Similarity	94.0%; Pred. No. 2,8e-53;		
Matches 140; Conservative	4; Mismatches 5; Indels	0; Gaps	0;
Oy	22 LKDSGRDYVSQFBSAGKOLNKLDDNWSYVSTSKLREQLGVPYTOEFMDLKEKTEG	81	
Db	1 Lkdsgrdyvsqfegcalqgknikllldnwdsstsklreq19vltgcfwlnlaketeg	60	
Oy	82 LRQMSMDLEEVKAKVOPYLDDFQKRWQEMEMELYRQKVEPLRAELQEGAROKLHLEQL	141	

RESULT	15
AAU29835	
ID	AAU29835 standard; Protein; 221 AA
xx	

Novel human secreted protein #326

Homo sapiens.
XXXXXX
immune suppression; immune stimulation; anti-inflammatory; leukaemia treatment; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration

MO200179449-A2.

25-OCT-2001.

95980U-OMT007; ZOOI; 2007

26-JAN-2001; 2001ITS-0770160

(HYSE-) HYSEQ INC.

rang RT, Liu C, Drmanac RT;

WFL; 2001-611725/70.

...a range of human polypeptides, useful in genetic vaccination, testing and therapy -

claim 20; page 199; 765pp; English.

CC polypeptides and/or antibodies to novel human secreted polypeptides. The
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptides. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AA029510-AA03304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX
XX Sequence 221 AA;

Query Match	80.5%	Score 712;	DB 22;	Length 221;
Best Local Similarity	83.6%;	Pred. No. 8.1e-52;		
Matches 143;	Conservative 2;	Mismatches 3;		

QY	1	DEPQSPADRVKDLATYYDVVL-KDSGRYYVQSEFGSALGKLNKLDMNDSTYFESK	59
D0	38	deppqspwadrvkdlatyvdgltedsgk-----dsvltstsk	74

QY 60 LREGLGVTVOEPMNDLNEKETBESLOEWSKULDEYKAVQVYLDDEFORKWOEMELYSROKV 119
Db 75 Lxrlqpvqcbefwldlaketeglqgmskdldeevkxavqpylddfrqkxqgemelyleyrgkv 134
QY 120 EPURALIOGCAQORALHEIOEKSTSPIGGEMDBRAVHVDLFTHLAPYSDEL 170
Db 135 eplraeiqegargqlheiqeklspjlgemdrararavhdllthlspysdel 185

Search completed: September 22, 2002, 12:05:15
Job time: 290 sec

Sun Sep 22 12:10:27 2002

us-09-803-918a-2_copy_25_194.rag

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:06:30 ; Search time 66.91 Seconds
(without alignments)
56,008 Million cell updates/sec

Title: US-09-803-918a-2_COPY_75_113

Perfect score: 201

Sequence: 1 DSVSTFSKLRQLPGVQGFMDNLEKETEGLRQMSKD 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR-71:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201	100.0	267	1	LPHUA1
2	194	96.5	267	1	A26529
3	194	96.5	267	2	JS0079
4	180	89.6	241	2	A24998
5	179	89.1	264	2	S31394
6	179	89.1	265	2	A46018
7	177	88.1	265	1	LPRB1B
8	177	88.1	266	1	LPRB1Z
9	175	87.1	231	2	JU0672
10	173	86.1	265	2	JU0672
11	173	86.1	266	1	LPDGA1
12	164	81.6	265	2	A56858
13	143	71.1	259	2	A24700
14	142	70.6	262	2	UC1237
15	142	70.6	262	2	S22420
16	142	70.6	264	1	LPCHA1
17	73	37.3	264	1	JCS456
18	72	35.8	246	2	A61448
19	63	31.3	396	1	LPHUA4
20	63	31.3	401	1	A47141
21	63	31.3	429	2	S29565
22	60	29.9	172	2	JU0391
23	59	29.4	317	2	S33450
24	58	28.9	180	2	C70428
25	57	28.4	210	2	S64376
26	57	28.4	312	1	LPRTT
27	57	28.4	312	1	LPRTT
28	56.5	28.1	309	2	D71559
29	56.5	28.1	677	2	F88456
					S73798

30	56.5	28.1	1025	2	H81751	exodeoxyribonuclea
31	56	27.9	311	2	JU0036	apolipoprotein E p
32	56	27.9	365	2	B81713	ref. protein, prob
33	56	27.9	986	2	T10754	cis-60kD matrix p
34	56	27.9	1091	2	T34107	hypothetical prote
35	55.5	27.6	194	2	S76087	hypothetical prote
36	55.5	27.6	579	2	JH0820	160K golgi antigen
37	55	27.4	317	2	A28792	apolipoprotein E p
38	55	27.4	317	2	S03185	apolipoprotein E p
39	55	27.4	906	2	T45158	pre-mRNA splicing
40	55	27.4	1410	1	A57013	early endosome ant
41	54.5	27.1	377	2	D72317	hypothetical prote
42	54.5	27.1	701	2	JN0674	ubiquitin-like fus
43	54	26.9	163	2	E69133	conserved hypothet
44	54	26.9	207	2	S56209	probable membrane
45	54	26.9	2514	2	T37320	ataxia telangiecta

ALIGNMENTS

RESULT 1

LPHUA1

apolipoprotein A-I precursor [validated] - human

N:Alternate names: apoA-I-2; apoA-I-4; preproapoA-I; prostacyclin stabilizing factor

C:Species: Homo sapiens (man)

C>Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 08-Dec-2000

C:Accession: A90947; B90947; S02373; A93465; A21147; A93519; B93519; A93472; A94010; 6197

R:Seilhamer, J.J.; Protter, A.A.; Frossard, P.; Levy-Wilson, B.

DNA 3, 309-317, 1984

A>Title: Isolation and DNA sequence of full-length cDNA and of the entire gene for hu

A:Reference number: A90947; MUID:85026665

A:Accession: A90947

A:Molecule type: DNA

A:Residues: 1-267 <SEI>

A:Cross-references: GB:X01038; NID:q28769; PIDN:CAA25519.1; PID:q296635

A:Accession: B90947

A:Molecule type: mRNA

A:Residues: 1-267 <SE2>

A:Cross-references: GB:X01038; NID:q28769; PIDN:CAA25519.1; PID:q296635

R:Makrides, S.C.; Ruiz-Opazo, N.; Hayden, M.; Nussbaum, A.L.; Breslow, J.L.; Zannis, Eur. J. Biochem. 173, 465-471, 1988

A>Title: Sequence and expression of Tangier apoA-I gene.

A:Reference number: S02373; MUID:88196137

A:Accession: S02373

A:Molecule type: DNA

A:Residues: 1-267 <MAK>

A:Cross-references: EMBL:X07496; NID:q28774; PIDN:CAA30377.1; PID:q296729

R:Shoulders, C.C.; Kornblith, A.R.; Munro, B.S.; Baralle, F.E.

Nucleic Acids Res. 11, 2827-2837, 1983

A>Title: Gene structure of human apolipoprotein A1.

A:Reference number: A93465; MUID:83220822

A:Accession: A93465

A:Molecule type: DNA

A:Residues: 1-267 <SHO>

A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; R:Karathanasis, S.K.; Zannis, V.I.; Breslow, J.L.

Proc. Natl. Acad. Sci. U.S.A. 80, 6147-6151, 1983

A>Title: Isolation and characterization of the human apolipoprotein A-I gene.

A:Reference number: A21147; MUID:84016011

A:Accession: A21147

A:Molecule type: DNA

A:Residues: 1-267 <KAR>

A:Cross-references: GB:J00098; GB:J03222; NID:q178765; PIDN:AA59519.1; PID:q178768

R:Sharpe, C.R.; Sidoli, A.; Shelley, C.S.; Lucero, M.A.; Shoulders, C.C.; Baralle, F.

Nucleic Acids Res. 12, 3917-3932, 1984

A>Title: Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA abundan

A:Reference number: A93519; MUID:84221405

A:Accession: A93519

A:Molecule type: mRNA

A:Residues: 1-267 <SHA>

A:Cross-references: GB:X00566; NID:q28765; PIDN:CAA25232.1; PID:q732753

A:Accession: B93519
 A:Molecule type: DNA
 A:Residues: 1-24 <SH2>
 R:Cheng, P.; Chan, L.
 Nucleic Acids Res. 11, 3703-3715, 1983
 A:Title: Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.
 A:Reference number: A93472; MUID:83220772
 A:Accession: A93472
 A:Molecule type: mRNA
 A:Residues: 1-267 <CHE>
 A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GR:Law, S.W.; Brewer Jr., H.B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 66-70, 1984
 A:Title: Nucleotide sequence and the encoded amino acids of human apolipoprotein A-I mRNA
 A:Reference number: A94010; MUID:84119464
 A:Accession: A94010
 A:Molecule type: mRNA
 A:Residues: 1-267 <LAW>
 A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GR:Law, S.W.; Brewer Jr., H.B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 66-70, 1984
 A:Title: Intracellular and extracellular processing of human apolipoprotein A-I: secreted
 A:Reference number: A21118; MUID:83195100
 A:Accession: A21118
 A:Molecule type: mRNA
 A:Residues: 1-24 <ZAN>
 R:Brewer Jr., H.B.; Fairwell, T.; Kay, L.; Meng, M.; Ronan, R.; Law, S.; Light, J.A.
 Biochem. Biophys. Res. Commun. 113, 626-632, 1983
 A:Title: Human plasma proapo-A-I: isolation and amino-terminal sequence.
 A:Reference number: A90112; MUID:83256553
 A:Accession: A90112
 A:Molecule type: protein
 A:Residues: 19-27 <BRE>
 R:Brewer Jr., H.B.; Fairwell, T.; LaRue, A.; Ronan, R.; Houser, A.; Bronzert, T.J.
 Biochem. Biophys. Res. Commun. 80, 623-630, 1978
 A:Title: The amino acid sequence of human ApoA-I, an apolipoprotein isolated from high density lipoproteins
 A:Reference number: A90209; MUID:78123731
 A:Accession: A90209
 A:Molecule type: protein
 A:Residues: 25-57, 'Q', '59-169, 'QQ', '172-267 <BR2>
 R:Yui, Y.; Aoyama, T.; Morishita, H.; Takahashi, M.; Takatsu, Y.; Kawai, C.
 J. Clin. Invest. 82, 803-807, 1988
 A:Title: Serum prostacyclin stabilizing factor is identical to apolipoprotein A-I (Apo A-I).
 A:Reference number: A30516; MUID:88331387
 A:Accession: A30516
 A:Molecule type: protein
 A:Residues: 25-56 <YUI>
 R:Nichols, W.C.; Dwalet, F.E.; Liepnieks, J.; Benson, M.D.
 Biochem. Biophys. Res. Commun. 156, 762-768, 1988
 A:Title: Variant apolipoprotein AI as a major constituent of a human hereditary amyloid.
 A:Reference number: A31582; MUID:89050104
 A:Accession: A31582
 A:Molecule type: protein
 A:Residues: 25-49, 'R', '51-85, 'D', '87-107 <NIT>
 A:Note: Variant sequence from patient with familial amyloidotic polyneuropathy type III
 R:Manjunath, P.; Marcel, Y.L.; Uma, J.; Seidah, N.G.; Chretien, M.; Chappelaine, A.
 J. Biol. Chem. 264, 16853-16857, 1989
 A:Title: Apolipoprotein A-I binds to a family of bovine seminal plasma proteins.
 A:Reference number: A34409; MUID:89380318
 A:Accession: A34409
 A:Molecule type: protein
 A:Residues: 25-48 <MAN>
 R:Stoffel, W.; Binczek, E.
 Biol. Chem. Hoppe-Seyler 369, 1055-1063, 1988
 A:Title: Structural requirements of human preproapolipoprotein AI for translocation and
 A:Reference number: S02737; MUID:89149957
 A:Accession: S02737
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-6, 'AV', '9, 'LV', '12-29 <STO>
 A:Note: part of this sequence, including the amino end of the mature protein, was confirmed
 R:Stoffel, W.; Binczek, E.
 Biol. Chem. Hoppe-Seyler 372, 481-488, 1991

A:Title: Transient expression of wild type and mutant human apolipoprotein AI in COS
 A:Reference number: S16197; MUID:92029676
 A:Contents: annotation; extension of studies in reference S02737
 R:Stoffel, W.; Krüger, E.; Deutzmann, R.
 Hoppe-Seyler's Z. Physiol. Chem. 364, 227-237, 1983
 A:Title: Cell-free translation of human liver apolipoprotein AI and AII mRNA processed
 A:Reference number: A19913; MUID:83236195
 A:Accession: B19913
 A:Molecule type: protein
 A:Residues: 1-6, 'X', '8-13, 'XXX', '17-18, 'XX', '21, 'X', '23-25, 'X', '27-29 <ST2>
 R:Edholm, C.; Bozas, S.E.; Tenkkanen, H.; Kirsbaum, L.; Metsu, J.; Murphy, B.; Walke
 Biochim. Biophys. Acta 1086, 255-260, 1991
 A:Title: The apolipoprotein A-I binding protein of placenta and the SP-40,40 protein
 A:Reference number: A56815; MUID:92075698
 A:Accession: A56815
 A:Molecule type: protein
 A:Residues: 25-31, 'P', '33 <EHN>
 A:Experimental source: serum
 A:Note: sequence extracted from NCBI backbone (NCBIP:69759)
 A:Note: 32-Trip was also found
 R:Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
 Biochemistry 33, 1988-1993, 1994
 A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipoproteins
 A:Reference number: A54223; MUID:94162201
 A:Accession: A54223
 A:Molecule type: protein
 A:Residues: 25-39 <RUN>
 R:Moguljevsky, N.; Roobol, C.; Loriau, R.; Guillaume, J.P.; Jacobs, P.; Cravador, A.;
 DNA 8, 429-436, 1989
 A:Title: Production of human recombinant proapolipoprotein A-I in Escherichia coli: p
 A:Reference number: I39476; MUID:89377481
 A:Accession: I39476
 A:Molecule type: protein
 A:Residues: 19-267 <RES>
 A:Cross-references: GB:M29068; NID:9178774; PIDN:AAA51746.1; PID:9178775
 R:Higuchi, K.; Law, S.W.; Hoeg, J.M.; Schumacher, U.R.; Meglin, N.; Brewer, H.B.
 J. Biol. Chem. 263, 18530-18536, 1988
 A:Title: Tissue-specific expression of apolipoprotein A-I (ApoA-I) is regulated by th
 A:Reference number: I39475; MUID:89054040
 A:Accession: I39475
 A:Molecule type: DNA
 A:Residues: 1-14 <RE2>
 A:Cross-references: GB:J04066; NID:9178763; PIDN:AAA51746.1; PID:9553183
 R:Breslow, J.L.
 Annu. Rev. Biochem. 54, 699-727, 1985
 A:Title: Human apolipoprotein molecular biology and genetic variation.
 A:Reference number: A90042; MUID:85278004
 A:Contents: annotation; review of sequences, variants and gene location
 R:Hoeg, J.M.; Meng, M.S.; Ronan, R.; Fairwell, T.; Brewer Jr., H.B.
 J. Biol. Chem. 261, 3911-3914, 1986
 A:Title: Human apolipoprotein A-I. Post-translational modification by fatty acid acyl
 A:Reference number: A92577; MUID:86140194
 A:Contents: annotation; acylation with palmitate
 A:Note: an underdetermined serine or threonine is acylated by fatty acid: the acylating
 R:Law, S.W.; Brewer, H.B.
 J. Biol. Chem. 260, 12810-12814, 1985
 A:Title: Tangier disease: The complete mRNA sequence encoding for preproapo-A-I.
 A:Reference number: I55336; MUID:86008382
 A:Accession: I55336
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-143, 'D', '145-267 <RE3>
 A:Cross-references: GB:M11791; NID:9178776; PIDN:AAA5545.1; PID:9178777
 C:Comment: Apolipoprotein A-I precursor is synthesized in the liver and small intestine
 (HDL) in plasma.
 C:Genes: GDB:APOAI
 A:Cross-references: GDB:119684; OMIM:107680
 A:Map position: 11q23.3-11q23.3
 A:Introns: 15/1; 67/2
 C:Function:
 A:Description: participates in the reverse transport of cholesterol from tissues to t
 sterol acyltransferase (LCAT); noncovalently binds and stabilizes prostacyclin (PGI-2)

C:Superfamily: apolipoprotein A-I
 C:Keywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid binding; lipid
 F:1-18/Domain: signal sequence #status experimental <SIG>
 F:19-24/Domain: propeptide #status experimental <PRO>
 F:25-267/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 100.0%; Score 201; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3.2e-17;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVSTFSKRLRDLGPTVQTFWMDLKEKTEGLRQEMSKD 39
 |||||
 Db 75 DSVSTFSKRLRDLGPTVQTFWMDLKEKTEGLRQEMSKD 113

RESULT 2

A26529

apolipoprotein A-I precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 30-Sep-1989 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999

C:Accession: A26529; A26627; S3135; A57766
 R:Polites, H.G.; Melchior, G.W.; Castle, C.K.; Marotti, K.R.

Gene 49, 103-110, 1986
 A:Title: The primary structure of cynomolgus monkey apolipoprotein A-I deduced from the

A:Reference number: A26529; MUID:87191989
 A:Accession: A26529

A:Molecule type: mRNA
 A:Residues: 1-267 <POL>

A:Cross-references: GB:M15411; NID:g342074; PIDN:AAA36834.1; PID:g342075
 R:Herbert, P.N.; Bauserman, L.L.; Lynch, K.M.; Saritelli, A.L.; Kantor, M.A.; Nicolosi,

Biochemistry 26, 1457-1463, 1987
 A:Title: Homologues of the human C and A apolipoproteins in the Macaca fascicularis (cyt

A:Reference number: A26627; MUID:87185451
 A:Accession: A26627

A:Molecule type: protein
 A:Residues: 25-48 <HER>

R:Murray, R.W.; Marotti, K.R.
 Biochim. Biophys. Acta 1131, 207-210, 1992

A:Title: Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene and corres
 A:Reference number: S3135; MUID:92305062

A:Accession: S3135
 A:Molecule type: DNA

A:Residues: 1-12, '1', '14-267 <MUR>
 A:Cross-references: GB:M83242; NID:g342070; PIDN:AAA36832.1; PID:g342071

R:Sorci-Thomas, M.; Kearns, M.W., 1991
 J. Biol. Chem. 266, 18045-18050, 1991

A:Title: Transcriptional regulation of the apolipoprotein A-I gene.
 A:Reference number: A57766; MUID:92011532

A:Accession: A57766
 A:Molecule type: DNA

A:Residues: 1-10 <RES>
 A:Cross-references: GB:M69223; NID:g342066; PIDN:AAA36831.1; PID:g553820

C:Comment: The precursor is synthesized in the liver and small intestine. The propeptide
 C:Comment: ApoA-I makes up about 70% of the protein of the high density lipoproteins (HDL)

promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin
 C:Genetics:

A:Introns: 15/1; 67/2
 C:Superfamily: apolipoprotein A-I

C:Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem repe
 F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-24/Domain: propeptide #status predicted <PRO>
 F:25-267/Product: apolipoprotein A-I #status predicted <MAT>

Query Match 96.5%; Score 194; DB 1; Length 267;
 Best Local Similarity 97.4%; Pred. No. 2.3e-16;
 Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSVSTFSKRLRDLGPTVQTFWMDLKEKTEGLRQEMSKD 39
 |||||
 Db 75 DSVSTFSKRLRDLGPTVQTFWMDLKEKTEGLRQEMSKD 113

RESULT 3

JS0079

apolipoprotein A-I precursor - baboon
 C:Species: Papio sp. (baboon)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Jun-1997

C:Accession: JS0079
 R:Hixon, J.E.; Borenstein, S.; Cox, L.A.; Rainwater, D.L.; Vandenberg, J.L.

Gene 74, 483-490, 1988
 A:Title: The baboon gene for apolipoprotein A-I: characterization of a cDNA clone and

A:Reference number: JS0079; MUID:89232739
 A:Accession: JS0079

A:Molecule type: mRNA
 A:Residues: 1-267 <HIX>

A:Experimental source: liver
 C:Comment: This protein is the principal protein component of high density lipoprotein

C:Comment: This protein serves as a cofactor for lecithin cholesterol acyltransferase
 C:Comment: This protein contains a region of repeated amino acids which form amphipat

C:Genetics:
 A:Gene: apoA1

C:Superfamily: apolipoprotein A-I
 C:Keywords: HDL; lipid binding; lipoprotein

F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-267/Product: apolipoprotein A-I #status predicted <LAT>

F:123-144,145-166,167-188,189-210,211-232,233-254/Region: tandem repeats

Query Match 96.5%; Score 194; DB 2; Length 267;
 Best Local Similarity 97.4%; Pred. No. 2.3e-16;
 Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSVSTFSKRLRDLGPTVQTFWMDLKEKTEGLRQEMSKD 39
 |||||
 Db 75 DSVSTFSKRLRDLGPTVQTFWMDLKEKTEGLRQEMSKD 113

RESULT 4

A24998

apolipoprotein A-I - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-1993

C:Accession: A24998
 R:Yang, C.; Yang, T.; Pownall, H.J.; Gotto Jr., A.M.

Eur. J. Biochem. 160, 427-431, 1986
 A:Title: The primary structure of apolipoprotein A-I from rabbit high-density lipopro

A:Reference number: A24998; MUID:87030294
 A:Accession: A24998

A:Molecule type: protein
 A:Residues: 1-241 <YAN>

C:Superfamily: apolipoprotein A-I
 C:Keywords: HDL; lipid binding; lipoprotein

Query Match 89.6%; Score 180; DB 2; Length 241;
 Best Local Similarity 87.2%; Pred. No. 1.1e-14;
 Matches 34; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSVSTFSKRLRDLGPTVQTFWMDLKEKTEGLRQEMSKD 39
 |||||
 Db 49 DSVSTFSKRLRDLGPTVQTFWMDLKEKTEGLRQEMSKD 87

RESULT 5

S31394

apolipoprotein A-I - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999

C:Accession: S31394
 R:Meckel, B.; Flach, R.; Weiss, B.; Weller-Guetli, H.; Frey, A.; Zinke, H.; Gassen

submitted to the EMBL Data Library, November 1992
 A:Description: Genomic organization of the porcine apolipoprotein AI gene and study o

A:Reference number: S31394
 A:Accession: S31394

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-264 <MOE>
A:Cross-references: EMBL:X69477; NID:g1889; PIDN:CAA9234.1; PID:g1890
C:Superfamily: apolipoprotein A-I

Query Match 89.1%; Score 179; DB 2; Length 264;
Best Local Similarity 87.2%; Pred. No. 1.6e-14;
Matches 34; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRLEQGLGPTQGFMDNLEKETEGRLROEMSKD 39
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 74 DLSGSTFTKVRBQLGPTQGFMDNLEKETEGRLROEMSKD 112

RESULT 6
A46018
apolipoprotein AI - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C:Accession: A46018
R:Birchbauer, A.; Knipping, G.; Juritsch, B.; Aschauer, H.; Zechner, R.
Genomics 15, 643-652, 1993
A:Title: Characterization of the apolipoprotein AI and CIII genes in the domestic pig.
A:Reference number: A46018; MUID:93224154
A:Accession: A46018
A:Status: preliminary
A:Molecule type: DNA; Protein
A:Residues: 1-265 <Bir>
A:Cross-references: GB:L00626; NID:g164358; PIDN:AAA30992.1; PID:g164359
A:Note: sequence extracted from NCBI backbone (NCBIN:129509, NCBIPI:129511)
C:Superfamily: apolipoprotein A-I

Query Match 89.1%; Score 179; DB 2; Length 265;
Best Local Similarity 87.2%; Pred. No. 1.6e-14;
Matches 34; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DSVTSTFSKLRLEQGLGPTQGFMDNLEKETEGRLROEMSKD 39
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 74 DLSGSTFTKVRBQLGPTQGFMDNLEKETEGRLROEMSKD 112

RESULT 7
LPRB1B
apolipoprotein A-I precursor (clone PRBA-502) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999
C:Accession: S00230; S20557
R:Pan, T.C.; Hao, Q.L.; Yamin, T.T.; Dai, P.H.; Chen, B.S.; Chen, S.L.; Kroon, P.A.; Cha
Eur. J. Biochem. 170, 99-104, 1987
A:Title: Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit apolipoprotein A-
A:Reference number: S00230; MUID:88082866
A:Accession: S00230
A:Molecule type: mRNA
A:Residues: 1-265 <PAN>
A:Cross-references: EMBL:X06658; NID:g1461; PIDN:CAA29857.1; PID:g1462
A:Note: the authors translated the codon AGC for residue 174 as Arg
A:Accession: S20557
A:Molecule type: DNA
A:Residues: 1-17, 'R', 19-44, 'T', 46-122, 'Y', 124-146, 'V', 148-265 <PAN2>
A:Cross-references: EMBL:X06659; NID:g1459; PIDN:CAA29858.1; PID:g1460
C:Comment: This protein is synthesized in the small intestine.
C:Comment: This protein is a major component of the high density lipoproteins in plasma.
C:Genetics:
A:Introns: 15/1; 66/2
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem repe
E:1-18/Domain: signal sequence #status predicted <SIG>
F:19-24/Domain: propeptide #status predicted <PRO>
F:25-265/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 88.1%; Score 177; DB 1; Length 265;
Best Local Similarity 84.6%; Pred. No. 2.8e-14;
Matches 33; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRLEQGLGPTQGFMDNLEKETEGRLROEMSKD 39
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 74 DLSSTVSKLRLEQGLGPTQGFMDNLEKETEGRLROEMSKD 112

RESULT 8
LPRB1Z
apolipoprotein A-I precursor (clone 22ap AI) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999
C:Accession: S06064
R:Parakevopoulou, T.B.; Kritis, A.; Zannis, V.
submitted to the EMBL Data Library, July 1989
A:Reference number: S06064
A:Accession: S06064
A:Molecule type: mRNA
A:Residues: 1-266 <PAR>
A:Cross-references: EMBL:X15908; NID:g1457; PIDN:CAA34024.1; PID:g1458
C:Comment: This protein is synthesized in the small intestine.
C:Comment: This protein is a major component of the high density lipoproteins in plas
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem r
E:1-18/Domain: signal sequence #status predicted <SIG>
F:19-24/Domain: propeptide #status predicted <PRO>
F:25-266/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 88.1%; Score 177; DB 1; Length 266;
Best Local Similarity 84.6%; Pred. No. 2.8e-14;
Matches 33; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 DSVTSTFSKLRLEQGLGPTQGFMDNLEKETEGRLROEMSKD 39
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 74 DLSSTVSKLRLEQGLGPTQGFMDNLEKETEGRLROEMSKD 112

RESULT 9
J00704
apolipoprotein A-I - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 28-Oct-1994
C:Accession: J00704
R:Weller-Guttler, H.; Sommerfeldt, M.; Papandrikopoulou, A.; Mischek, U.; Bonitz, D.
J. Neurochem. 54, 444-450, 1990
A:Title: Synthesis of apolipoprotein A-I in pig brain microvascular endothelial cells
A:Reference number: J00704; MUID:90132667
A:Accession: J00704
A:Molecule type: mRNA
A:Residues: 1-231 <WEI>
A:Note: the authors translated the codon CAG for residue 124 as His and GAC for resid
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; lipid binding; lipid transport; lipoprotein;

Query Match 87.1%; Score 175; DB 2; Length 231;
Best Local Similarity 84.6%; Pred. No. 4.1e-14;
Matches 33; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRLEQGLGPTQGFMDNLEKETEGRLROEMSKD 39
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 41 DLSGSTFTKVRBQLGPTQGFMDNLEKETEGRLROEMSKD 79

RESULT 10
J00672
apolipoprotein A-I - pig
N:Alternate names: apo-A-I
C:Species: Sus scrofa domestica (domestic pig)

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C-Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_Change 11-May-2000
C-Accession: J00672; P00471; A05311
R:Rieu V.N.; Patel, B.; Zhan, R.; Black, D.D.
Gene 134, 267-270, 1993
A>Title: Sequence of the porcine apoA-I gene.
A:Reference number: J00672; MUID:94085789
A:Accession: J00672
A:Molecule type: DNA
A:Residues: 1-265 <TR>
A:Cross-references: EMBL:Z1124; NID:91893
A>Note: this translation is not annotated in GenBank entry SSA0AIG, release 111.0; the
R:Rieu, V.N.; Hasler-Rapacz, J.; Rapacz, J.; Black, D.D.
Gene 123, 173-179, 1993
A>Title: Sequences and expression of the porcine apolipoprotein A-I and C-III mRNAs.
A:Reference number: P00471; MUID:93154581
A:Accession: P00471
A:Molecule type: mRNA
A:Residues: 105-265 <TR>
A:Experimental source: Liver
R:Malley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.
Biochemistry 15, 1928-1933, 1976
A>Title: Characterization of the plasma lipoproteins and apoproteins of the Erythrocyte
A:Reference number: A90395; MUID:76104721
A:Accession: A05311
A:Molecule type: Protein
A:Residues: 25-34 <MA>
C:Comment: This protein is the major apolipoprotein of high-density lipoprotein and ser
C:Genetics:
A:Gene: apoA-I
A:Introns: 15/1; 66/2
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid metabolism; lip
F:99/Region: ochre stop codon

Query Match      86.1%  Score 173; DB 2; Length 265;
Best Local Similarity 84.6%  Pred No 8,5e-14;
Matches 33; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 DSVTSFESKIREQLGVTOEFMDNLEKETEGILROESKSD 39
      11:||||:||||||||||||||||| 1111111111
Db      74 DSGSTFTYVREQLGPVTOEFMDNLEKETEGALROESKSD 112

RESULT 11
LIPDGI
apolipoprotein A-I precursor - dog
C:Species: Canis lupus familiaris (dog)
C-Date: 17-Dec-1982 #sequence_revision 14-Jul-1994 #text_Change 07-May-1999
C-Accession: A60940; A03092; A61418
R:Luo, C.C.; Li, W.H.; Chan, L.
R:Luo, C.C.; Li, W.H.; Chan, L.
A>Title: Structure and expression of dog apolipoprotein A-I, E, and C-I mRNAs: implicati
A:Reference number: A60940; MUID:90132271
A:Accession: A60940
A:Molecule type: mRNA
A:Residues: 1-266 <LU>
R:Chung, H.; Randolp, A.; Reardon, I.; Helmrksen, R.L.
J. Biol. Chem. 257, 2961-2967, 1982
A>Title: The covalent structure of apolipoprotein A-I from canine high density lipoprote
A:Reference number: A03092; MUID:82142425
A:Accession: A03092
A:Molecule type: Protein
A:Residues: 25-167; 'G',169-201, 'Q',203-234, 'Q',236-266 <CHU>
R:Nakai, T.; Whayne, T.F.; Tang, J.
FEBS Lett. 64, 409-411, 1976
A>Title: The amino- and carboxyl-terminal sequences of canine apolipoprotein A-I.
A:Reference number: A61418; MUID:76210910
A:Accession: A61418
A:Molecule type: Protein
A:Residues: 25-56; 'Z',261-262, 'A' <NAK>
C:Superfamily: apolipoprotein A-I
C:Keywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid transport; lip

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F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-24/Domain: propeptide #status predicted <PRO>
F:25-266/Product: apolipoprotein A-I #status experimental <MAT>

Query Match          86.1%; Score 173; DB 1; Length 266;
Best Local Similarity 84.6%; Pred. No. 8.6e-14;
Matches 33; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 DSVSTFSKRLRQLGPVTOEFMDLKEKETGLRQEMSKD 39
Db 74 DLSSTVTKLRQLRQIGPVTOEFMDLKEKETGLRQEMSKD 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
|:::|:|:::|:|:::|:|:::|:|:::|:|:::|:|:::|:|

RESULT 12
A56858
apolipoprotein A-I precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 05-Jan-1996 #sequence, revision 23-Aug-1997 #text_change 13-Aug-1999
C:Accession: I45853; A:56853; A34649
R:O'Huigin, C.; Chan, L.; Li, W.
Mol. Biol. Evol. 7, 327-339, 1990
A:Title: Cloning and sequencing of bovine apolipoprotein A-I cDNA and molecular evolution
A:Reference number: I45853; MUID:90348478
A:Accession: I45853
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-265 <ONX>
A:Cross-references: GB:M3870; NID:g162677; PID:NAA30381.1; PID:g162678
R:Sparrow, D.A.; Lee, B.R.; Laplaud, P.M.; Auboliron, S.; Bauchart, D.; Chapman, M.J.;
Biochim. Biophys. Acta 1123, 145-150, 1992
A:Title: Plasma lipid transport in the prenatant calf, Bos spp: primary structure o
A:Reference number: A56858; MUID:92153895
A:Accession: A56858
A:Status: preliminary
A:Molecule type: protein
A:Residues: 19-184, 'QL', 187-265 <SPA>
A:Experimental source: Friesian-Holstein male calves aged 2-4 weeks
A:Note: sequence extracted from NCBI backbone (NCBI:P:83520)
R:Auboliron, S.; Sparrow, D.A.; Beaubatie, L.; Bauchart, D.; Sparrow, J.T.; Laplaud, P
Biochem. Biophys. Res. Commun. 166, 833-839, 1990
A:Title: Characterization and amino-terminal sequence of apolipoprotein AI from plasma
A:Reference number: A34649; MUID:90147795
A:Accession: A34649
A:Molecule type: protein
A:Residues: 25-70 <AUB>
A:Experimental source: Friesian-Holstein male calves aged 2-4 weeks
C:Superfamily: apolipoprotein A-I
C:Keywords: lipid binding; lipoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-265/Product: apolipoprotein A-I #status experimental <MAT>

Query Match          81.6%; Score 164; DB 2; Length 265;
Best Local Similarity 79.5%; Pred. No. 1.1e-12;
Matches 31; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 DSVSTFSKRLRQLGPVTOEFMDLKEKETGLRQEMSKD 39
Db 74 DLSSTVTKLRQLRQIGPVTOEFMDLKEKETGLRQEMSKD 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
|:::|:|:::|:|:::|:|:::|:|:::|:|:::|:|:::|:|

RESULT 13
A24700
apolipoprotein A-I precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence, revision 30-Jun-1988 #text_change 13-Aug-1999
C:Accession: A24700; S00298; A05314
R:Haddad, I.A.; Ordovas, J.M.; Fitzpatrick, T.; Karathanasis, S.K.
J. Biol. Chem. 261, 13268-13277, 1986
A:Title: Linage, evolution, and expression of the rat apolipoprotein A-I, C-III, and
A:Reference number: A92558; MUID:87008540

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A:Molecule type: DNA
 A:Residues: 1-259 <HMD>
 A:Cross-references: EMBL:J02597; NID:g202935; PIDN:AAA0745.1; PID:g202939
 R:Poncin, J.E.; Martial, J.A.; Gielem, J.E.
 Eur. J. Biochem. 140, 493-498, 1984
 A:Title: Cloning and structure analysis of the rat apolipoprotein A-I cDNA.
 A:Reference number: S00298; MUID:84207987
 A:Accession: S00298
 A:Molecule type: mRNA
 A:Residues: 1-259 <PON>
 A:Cross-references: GB:M00001; EMBL:X00558; NID:g202944; PIDN:AAA0749.1; PID:g202945
 R:Corcoran, J.I.; Smith, D.P.; Andy, R.; Alpers, D.H.; Schonfeld, G.; Strauss, A.W.
 J. Biol. Chem. 257, 971-978, 1982
 A:Title: The primary translation product of rat intestinal apolipoprotein A-I mRNA is an
 A:Reference number: A05314; MUID:82098162
 A:Accession: A05314
 A:Molecule type: protein
 A:Residues: 1-18, 'X', 20-21, 'X', 23-28, 'X', 30-38, 'X', 40-41, 'X', 43-45 <GOR>
 C:Comment: This protein is synthesized in the liver and small intestine. The propeptide
 C:Comment: This protein is a major component of the high density lipoproteins in plasma.
 C:Genetics:
 A:Introns: 15/1; 66/2
 C:Superfamily: apolipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipop
 F:1-18/Domain: signal sequence #status experimental <SIG>
 F:19-24/Domain: propeptide #status experimental <PRO>
 F:25-259/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 71.1%; Score 143; DB 2; Length 259;
 Best Local Similarity 69.2%; Pred. No. 4e-10;
 Matches 27; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 1 DSVTSTFKRLRQGLGVPTQEFMDNLEKETEGLRQEMSKD 39
 Db 74 DTIGSTVSRLOEQLGPVTOEFMDNLEKETEGLRQEMSKD 112
 RESULT 14
 JCI237
 apolipoprotein A-I precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-1993
 C:Accession: JCI237
 R:Boyle, T.P.; Marotli, K.R.
 Gene 117, 243-247, 1992
 A:Title: Structure of the murine gene encoding apolipoprotein A-I.
 A:Reference number: JCI237; MUID:92347700
 A:Accession: JCI237
 A:Molecule type: DNA
 A:Residues: 1-262 <BO>
 A:Cross-references: GB:M77801
 C:Genetics:
 A:Gene: ApoA-I
 A:Introns: 15/1; 66/2
 C:Superfamily: apolipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipop
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-262/Product: apolipoprotein A-I #status predicted <MAT>

Query Match 70.6%; Score 142; DB 2; Length 262;
 Best Local Similarity 64.1%; Pred. No. 5.3e-10;
 Matches 25; Conservative 11; Mismatches 3; Indels 0; Gaps 0;

QY 1 DSVTSTFKRLRQGLGVPTQEFMDNLEKETEGLRQEMSKD 39
 Db 74 DTIGSTVSRLOEQLGPVTOEFMDNLEKETEGLRQEMSKD 112

RESULT 15
 S22420
 apolipoprotein A-I precursor - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
 C:Accession: S22420; S22421; A44364
 R:Stoffel, W.; Mueller, R.; Blinczek, E.; Hofmann, K.
 Biol. Chem. Hoppe-Seyler 373, 187-193, 1992
 A:Title: Mouse apolipoprotein AI. cDNA-derived primary structure, gene organisation a
 A:Reference number: S22420; MUID:92281682
 A:Accession: S22420
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-264 <STO>
 A:Cross-references: EMBL:X64262; NID:g50014; PIDN:CAA45560.1; PID:g50015
 A:Accession: S22421
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-264 <STO>
 A:Cross-references: EMBL:X64263; NID:g50020; PIDN:CAA45561.1; PID:g50021
 R:Januzzi, J.L.; Azrolan, N.; O'Connell, A.; Aalto-Setälä, K.; Breslow, J.L.
 Genomics 14, 1081-1088, 1992
 A:Title: Characterization of the mouse apolipoprotein ApoA-1/Apoc-3 gene locus: genom
 A:Reference number: A44364; MUID:93122774
 A:Accession: A44364
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-264 <JAN>
 A:Note: sequence extracted from NCBI backbone (NCBIN:122400, NCBI:P.122407)
 C:Genetics:
 A:Introns: 15/1; 66/2
 C:Superfamily: apolipoprotein A-I

Query Match 70.6%; Score 142; DB 2; Length 264;
 Best Local Similarity 64.1%; Pred. No. 5.4e-10;
 Matches 25; Conservative 11; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DSVTSTFKRLRQGLGVPTQEFMDNLEKETEGLRQEMSKD 39
 Db 74 DTIGSTVSRLOEQLGPVTOEFMDNLEKETEGLRQEMSKD 112

Search completed: September 22, 2002, 12:06:31
 Job time: 326 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:22:19 ; Search time 35.02 seconds
(without alignments)
43.120 Million cell updates/sec

Title: US-09-803-918a-2_COPY_75_113
Perfect score: 201
Sequence: 1 DSVSTSTFKRLRQLGPTVQEFWDNLEKREGLRQEMSKD 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	100.0	267	1 APAL_HUMAN	P02647 homo sapien
2	194	96.5	267	1 APAL_MACFA	P15568 macaca fasc
3	179	89.1	265	1 APAL_PIG	P18648 sus scrofa
4	177	88.1	266	1 APAL_RABIT	P09809 oryctolagus
5	173	86.1	266	1 APAL_CANFA	P02648 canis famil
6	164	81.6	265	1 APAL_BOVIN	P15497 bos taurus
7	143	71.1	259	1 APAL_RAT	P04639 ratius norv
8	142	70.6	264	1 APAL_MOUSE	P00623 mus musculu
9	137	68.2	265	1 APAL_TUPGB	O18759 tupala glis
10	75	37.3	264	1 APAL_CHICK	P08250 gallus gall
11	73	36.3	264	1 APAL_CONJA	P32918 coturnix co
12	72	35.8	264	1 APAL_ANAPL	O42286 anas platyr
13	63	31.3	366	1 APAL_HUMAN	P06727 homo sapien
14	63	31.3	401	1 APAL_PAPAN	Q28758 papio anubi
15	63	31.3	429	1 APAL_PAPAN	P33621 macaca fasc
16	60	29.9	172	1 MBEB_ECOLI	P13659 escherichia
17	59	29.4	317	1 APE_PIG	O67453 sus scrofa
18	58	28.9	180	1 YEF6_AQUAE	O67453 aquifex aeo
19	58	28.9	707	1 HS88_NEUCR	O74225 neuropept
20	57	28.4	210	1 YG21_YEAST	P53251 saccharomyc
21	57	28.4	312	1 APE_RAT	P02650 ratius norv
22	57	28.4	365	1 RECF_CHLTR	O84077 chlamydia t
23	56.5	28.1	677	1 YD64_MYCPN	P75417 mycoplasma
24	56	27.9	311	1 APE_MOUSE	P08226 mus musculu
25	56	27.9	365	1 RECF_CHLMU	Q9PWX5 chlamydia m
26	56	27.9	986	1 GM13_RAT	O62839 ratius norv
27	56	27.9	2035	1 EYPL_MOUSE	O9d952 mus musculu
28	55.5	27.6	579	1 G160_HUMAN	O08378 homo sapien
29	55	27.4	107	1 APE_MACMU	Q28502 macaca mula
30	55	27.4	107	1 APE_SAISC	Q28995 salmifil sci
31	55	27.4	317	1 APE_MACFA	P10517 macaca fasc
32	55	27.4	317	1 APE_PAPAN	P05770 papio anubi
33	55	27.4	906	1 PR01_SCHPO	Q12381 schizosacch

34	54.5	27.1	475	1	FA01_HUMAN	O75844 homo sapien
35	54	26.9	207	1	YEP6_YEAST	P43557 saccharomyc
36	54	26.9	382	1	APFA_PIG	O46409 sus scrofa
37	53.5	26.6	565	1	HEMA_TATKO	P16060 influenza a
38	53	26.4	317	1	APB_HUMAN	P02649 homo sapien
39	53	26.4	367	1	MREC_ECOLI	P16926 escherichia
40	53	26.4	391	1	APFA_RAT	P02651 ratius norv
41	53	26.4	550	1	G6P1_SCHPO	P78917 schizosacch
42	53	26.4	5327	1	ACF7_MOUSE	O9qxx0 mus musculu
43	52.5	26.1	564	1	HEMA_TAMAP	P87506 influenza a
44	52.5	26.1	565	1	HEMA_TAWIL	P03454 influenza a
45	52.5	26.1	629	1	GIDA_PASMO	P57945 pasteurella

ALIGNMENTS

RESULT ID	APAL_HUMAN	STANDARD	PRT	267 AA.
AC	P02647			
DT	21-JUL-1986 (rel. 01, Created)			
DT	21-JUL-1986 (rel. 01, Last sequence update)			
DT	16-OCT-2001 (rel. 40, Last annotation update)			
DE	Apolipoprotein A-I precursor (Apo-AI).			
GN	APOA1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84221405; PubMed=6328445;			
RA	Sharpe C.R., Sidoti A., Shelley C.S., Lucero M.A., Shoulders C.C.,			
RA	Baralle F.E.;			
RT	"Human apolipoproteins AI, AII, CII and CIIL. CDNA sequences and mRNA			
RL	abundance.";			
RL	Nucleic Acids Res. 12:3917-3932(1984).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8502665; PubMed=6207999;			
RA	Seilhamer J.J., Protter A.A., Frossard P., Levy-Wilson B.;			
RT	"Isolation and DNA sequence of full-length cDNA and of the entire			
RT	gene for human apolipoprotein AI -- discovery of a new genetic			
RT	polymorphism in the apo AI gene.";			
RL	DNA 3:309-317(1984).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83220822; PubMed=6406984;			
RA	Shoulders C.C., Kornblith A.R., Munro B.S., Baralle F.E.;			
RT	"Gene structure of human apolipoprotein AI.";			
RL	Nucleic Acids Res. 11:2827-2837(1983).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83220772; PubMed=6304641;			
RA	Cheung P., Chan L.;			
RT	"Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.";			
RL	Nucleic Acids Res. 11:3703-3715(1983).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84119464; PubMed=6198645;			
RA	Law S.W., Brewer H.B. Jr.;			
RT	"Nucleotide sequence and the encoded amino acids of human			
RT	apolipoprotein A-I mRNA.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 81:66-70(1984).			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86008382; PubMed=2995392;			
RA	Law S.W., Brewer H.B. Jr.;			
RT	"Tanger disease. The complete mRNA sequence encoding for			
RT	preproapo-A-I.";			
RL	J. Biol. Chem. 260:12810-12814(1985).			
RN	[7]			

RP SEQUENCE FROM N.A.
 RX MEDLINE=84016011; PubMed=6413973;
 RA Karathanasis S.K., Zannis V.I., Breslow J.L.;
 RT "Isolation and characterization of the human apolipoprotein A-I
 gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:6147-6151(1983).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89377481; PubMed=2673706;
 RA Mogulievsky N., Roobol C., Loriau R., Guillaume J.P., Jacobs P.,
 RA Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,
 RA Holmquist L., Carlson L.A., Bollen A.;
 RT "Production of human recombinant proapolipoprotein A-I in *Escherichia*
 coli: purification and biochemical characterization.";
 RL DNA 8:429-436(1989).
 RN [9]
 RP SEQUENCE FROM N.A. (VARIANT TANGIER).
 RX MEDLINE=88196137; PubMed=3129297;
 RA Makrides S.C., Ruiz-Opazo N., Hayden M., Nussbaum A.L., Breslow J.L.,
 RA Zannis V.I.;
 RT "Sequence and expression of Tangier apoA-I gene.";
 RL Eur. J. Biochem. 173:465-471(1988).
 RN [10]
 RP SEQUENCE OF 118-267 FROM N.A.
 RX MEDLINE=83091059; PubMed=6294659;
 RA Breslow J.L., Ross D., McPherson J., Williams H.W., Kurnit D.,
 RA Nussbaum A.L., Karathanasis S.K., Zannis V.I.;
 RT "Isolation and characterization of cDNA clones for human
 apolipoprotein A-I.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6861-6865(1982).
 RN [11]
 RP SEQUENCE OF 19-27.
 RX MEDLINE=83256553; PubMed=6409108;
 RA Brewer H.B. Jr., Fairwell T., Kay L., Meng M., Roman R., Law S.,
 RA Light J.A.;
 RT "Human plasma proapoA-I: isolation and amino-terminal sequence.";
 RL Biochem. Biophys. Res. Commun. 113:626-632(1983).
 RN [12]
 RP SEQUENCE OF 25-267.
 RX MEDLINE=78123731; PubMed=204308;
 RA Brewer H.B. Jr., Fairwell T., Larue A., Roman R., Houser A.,
 RA Bronzert T.J.;
 RT "The amino acid sequence of human apoA-I, an apolipoprotein isolated
 from high density lipoproteins.";
 RL Biochem. Biophys. Res. Commun. 80:623-630(1978).
 RN [13]
 RP SEQUENCE OF 25-267.
 RX MEDLINE=75133493; PubMed=164450;
 RA Baker H.N., Goto A.M. Jr., Jackson R.L.;
 RT "The primary structure of human plasma high density apolipoprotein
 glutamine I (apoA-I). II. The amino acid sequence and alignment of
 cyanogen bromide fragments IV, III, and I.";
 RL J. Biol. Chem. 250:2725-2738(1975).
 RN [14]
 RP SEQUENCE OF 25-56.
 RX MEDLINE=88331387; PubMed=3047170;
 RA Yui Y., Aoyama T., Morishita H., Takahashi M., Takatsu Y., Kawai C.;
 RT "Serum prostaticin stabilizing factor is identical to apolipoprotein
 A-I (apo A-I). A novel function of Apo A-I.";
 RL J. Clin. Invest. 82:803-807(1988).
 RN [15]
 RP SEQUENCE OF 25-48.
 RX MEDLINE=89380318; PubMed=2506184;
 RA Manjunath P., Marcel Y.L., Uma J., Seidah N.G., Chretien M.,
 RA Chappelaine A.;
 RT "Apolipoprotein A-I binds to a family of bovine seminal plasma
 proteins.";
 RL J. Biol. Chem. 264:16853-16857(1989).
 RN [16]
 RP SEQUENCE OF 25-43.
 RX MEDLINE=88070603; PubMed=3120314;
 RA Prizzi R.P., Ordovas J.M., Rosenberg I., Schaeffer E.J.,
 RA Pereira M.E.A.;

RT "Similarity of cruzin, an inhibitor of Trypanosoma cruzi
 RT neuraminidase, to high-density lipoprotein.";
 RL Science 238:1417-1419(1987).
 RN [17]
 RP SEQUENCE OF 25-42.
 RC TISSUE=Heart;
 RX MEDLINE=95203287; PubMed=7895732;
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
 RT "The human myocardial two-dimensional gel protein database: update
 1994.";
 RL Electrophoresis 15:1459-1465(1994).
 RN [18]
 RP PALMITOYLATION.
 RX MEDLINE=86140194; PubMed=3005308;
 RA Hoeg J.M., Meng M.S., Roman R., Fairwell T., Brewer H.B. Jr.;
 RT "Human apolipoprotein A-I. Post-translational modification by fatty
 acid acylation.";
 RL J. Biol. Chem. 261:3911-3914(1986).
 RN [19]
 RP PROCESSING.
 RX MEDLINE=83195100; PubMed=6405383;
 RA Zannis V.I., Karathanasis S.K., Keutmann H.T., Goldberger G.,
 RA Breslow J.L.;
 RT "Intracellular and extracellular processing of human apolipoprotein
 A-I: secreted apolipoprotein A-I isoprotein 2 is a propeptide.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2574-2578(1983).
 RN [20]
 RP STRUCTURE BY NMR OF 190-209.
 RX MEDLINE=96270776; PubMed=8664326;
 RA Wang G., Trelaevan W.D., Cushman R.J.;
 RT "Conformation of human serum apolipoprotein A-I(166-185) in the
 presence of sodium dodecyl sulfate or dodecylphosphocholine by ¹H-NMR
 and CD. Evidence for specific peptide-SDS interactions.";
 RL Biochim. Biophys. Acta 1301:174-184(1996).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (4.0 ANGSTROMS) OF 67-267.
 RX MEDLINE=88024124; PubMed=9356442;
 RA Borhani D.W., Rogers D.P., Engler J.A., Brouillette C.G.;
 RT "Crystal structure of truncated human apolipoprotein A-I suggests a
 lipid-bound conformation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12291-12296(1997).
 RN [22]
 RP VARIANT MILANO.
 RX MEDLINE=83109095; PubMed=6401735;
 RA Weisgraber K.H., Rall S.C. Jr., Bersot T.P., Mahley R.W.,
 RA Franceschini G., Sirtori C.R.;
 RT "Apolipoprotein A-I-Milano. Detection of normal A-I in affected
 subjects and evidence for a cysteine for arginine substitution in the
 variant A-I.";
 RL J. Biol. Chem. 258:2508-2513(1983).
 RN [23]
 RP VARIANT TANGIER.
 RX MEDLINE=83300108; PubMed=6412234;
 RA Schmitz G., Assmann G., Rall S.C. Jr., Mahley R.W.;
 RT "Tangier disease: defective recombination of a specific Tangier
 apolipoprotein A-I isoform (pro-apo A-I) with high density
 lipoproteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:6081-6085(1983).
 RN [24]
 RP VARIANT NORWAY.
 RX MEDLINE=84289383; PubMed=6437779;
 RA Rall S.C. Jr., Weisgraber K.H., Mahley R.W., Ogawa Y., Fielding C.J.,
 RA Utermann G., Haas J., Steinmetz A., Menzel H.J., Assmann G.;
 RT "Abnormal lecithin:cholesterol acyltransferase activation by a human
 apolipoprotein A-I variant in which a single lysine residue is
 deleted.";
 RL J. Biol. Chem. 259:10063-10070(1984).
 RN [25]
 RP SEQUENCE OF 25-107 (VARIANT IOWA).
 RX MEDLINE=89050104; PubMed=3142462;
 RA Nichols W.C., Dwulet F.E., Liepnieks J., Benson M.D.;
 RT "Variant apolipoprotein AI as a major constituent of a human
 hereditary amyloid.";

Query Match 100.0%; Score 201; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1e-17;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 75 DSVSTFSKLRBQGLPGVTOEFWMDNLEKETEGLRQEMSKD 113

QY 1 DSVSTFSKLRBQGLPGVTOEFWMDNLEKETEGLRQEMSKD 39
 |||||

RESULT 2
 ID APAL_MACFA STANDARD; PRT; 267 AA.
 AC P15568; P17929;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NCBI_TaxID=9541, 9557;
 [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=87191989; PubMed=3106152;
 RA Pollitt H.G., Melchior G.W., Castle C.K., Marotti K.R.;
 RT "The primary structure of cynomolgus monkey apolipoprotein A-1
 deduced from the cDNA sequence: comparison to the human sequence.";
 RL Gene 49:103-110(1986).
 [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=92305062; PubMed=1610902;
 RA Murray R.W., Marotti K.R.;
 RT "Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene
 and corresponding flanking regions.";
 RL Biochim. Biophys. Acta 1131:207-210(1992).
 [3]
 RP SEQUENCE OF 25-48.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=87185451; PubMed=3105581;
 RA Herbert P.N., Bausserman L.L., Lynch K.M., Saritelli A.L.,
 RA Kantor M.A., Nicolosi R.J., Shuman R.S.;
 RT "Homologues of the human C and A apolipoproteins in the Macaca
 fascicularis (cynomolgus) monkey.";
 RL Biochemistry 26:1457-1463(1987).
 [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas; TISSUE=Liver;
 RX MEDLINE=89232739; PubMed=2907746;
 RA Hixson J.E., Boranstein S., Cox L.A., Rainwater D.L., Vandenberg J.L.;
 RT "The baboon gene for apolipoprotein A-I: characterization of a cDNA
 clone and identification of DNA polymorphisms for genetic studies of
 cholesterol metabolism.";
 RL Gene 74:483-490(1988).
 [5]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC SPECIES=M.fascicularis;
 RA Sorci-Thomas M.;
 RL Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.

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 CC -----

DR EMBL: M15411; AAA36834.1; -
 DR EMBL: M83242; AAA36832.1; -
 DR EMBL: M35634; AAA35380.1; -
 DR EMBL: M69223; AAA36831.1; -
 DR PIR: A26529; A26529.
 DR PIR: A26627; A26627.
 DR PIR: J50079; J50079.
 DR PIR: S23135; S23135.
 DR HSSP: P02647; 10DR.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 267
 FT DOMAIN 68 267
 FT REPEAT 68 89
 FT REPEAT 90 111
 FT REPEAT 112 122
 FT REPEAT 123 144
 FT REPEAT 145 166
 FT REPEAT 167 188
 FT REPEAT 189 210
 FT REPEAT 211 232
 FT REPEAT 233 243
 FT REPEAT 244 267
 FT CONFLICT 13 13 L->P (IN REF. 1).
 FT SEQUENCE 267 AA; 30735 MW; 869955C024088E21 CRC64;

QY 1 DSVSTFSKLRBQGLPGVTOEFWMDNLEKETEGLRQEMSKD 39
 |||||

DB 75 DSVSTFSKLRBQGLPGVTOEFWMDNLEKETEGLRQEMSKD 113

RESULT 3
 ID APAL_PIG STANDARD; PRT; 265 AA.
 AC P18648;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93224154; PubMed=8468059;
 RA Birchbauer A., Knipping G., Jurtisch B., Aschauer H., Zechner R.;
 RT "Characterization of the apolipoprotein AI and CIII genes in the
 domestic pig.";
 RL Genomics 15:643-652(1993).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver, and Brain;
 RX MEDLINE=94125128; PubMed=8294940;
 RA Moeckel B., Zinke H., Flach R., Weiss B., Weller-Guettler H.,
 RA Gassen H.;

```

FT REPEAT 188 209 7.
FT REPEAT 210 230 9 (HALF-LENGTH) .
FT REPEAT 231 241 10.
FT REPEAT 242 265 10.
FT REPEAT 268 268 E -> K (IN REF. 3) .
FT CONFLICT 143 143 MISSING (IN REF. 2 AND 3) .
FT CONFLICT 173 173 D -> S (IN REF. 4) .
FT CONFLICT 180 180 E -> A (IN REF. 2 AND 3) .
FT CONFLICT 185 186 HV -> QL (IN REF. 1 AND 5) .
FT CONFLICT 209 209 G -> D (IN REF. 2 AND 3) .
FT CONFLICT 224 224 A -> G (IN REF. 4) .
SQ SEQUENCE 265 AA; 30325 MW; 2C6E578318BCF69C CRC64;

Query Match 89.1%; Score 179; DB 1; Length 265;
Best Local Similarity 87.2%; Pred. No. 5e-15;
Matches 34; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DSVSTFSKRLKRGQAPVQGFMDNKEKTEGRGEMSD 39
Db 74 DSLGSTFKVREGLGAPVQGFMDNKEKTEALRQMSMD 112
||:||||:|||||||:|||||||:|||||||

RESULT 4
APAL_RABIT STANDARD; PRT; 266 AA.
ID APAL_RABIT
AC P09809;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI) .
GN APOA1.
OS Oryctolagus cuniculus (Rabbit) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=22AP AI; TISSUE=Small intestine;
RA Paraskevopoulou T.B., Kritis A., Zannis V.I.;
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
[2]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=88082866; PubMed=3123329;
RA Pan T.C., Hao Q.L., Yamini T.T., Dai P.H., Chen B.S., Chen S.L.,
RA Ktiron P.A., Chao Y.S.;
RT "Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit
RT apolipoprotein A-I is synthesized in the intestine but not in the
RT liver."
RL Eur. J. Biochem. 170:99-104(1987).
[3]
RN RP SEQUENCE OF 25-266.
RX MEDLINE=87030294; PubMed=3095115;
RA Yang C., Yang T., Pownall H.J., Gotto A.M. Jr.;
RT "The primary structure of apolipoprotein A-I from rabbit high-density
RT lipoprotein."
RL Eur. J. Biochem. 160:427-431(1986) .
[4]
RN RP FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
-i- CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT) .
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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CC EMBL: X15908; CAA34024.1; -
 DR EMBL: X06658; CAA29857.1; -
 DR EMBL: X06659; CAA29858.1; -
 DR PIR: S06064; LPRB12.
 DR PIR: S00230; LPRB1B.
 DR PIR: A24998; A24998.
 DR HSSP: P02647; 1AV1.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein: 1.
 KM Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 266
 FT DOMAIN 67 266
 FT REPEAT 67 88
 FT REPEAT 89 110
 FT REPEAT 111 121
 FT REPEAT 122 143
 FT REPEAT 144 165
 FT REPEAT 166 187
 FT REPEAT 188 209
 FT REPEAT 210 231
 FT REPEAT 232 242
 FT REPEAT 243 266
 FT CONFLICT 18 18
 FT CONFLICT 44 44
 FT CONFLICT 45 45
 FT CONFLICT 107 107
 FT CONFLICT 123 123
 FT CONFLICT 147 147
 FT CONFLICT 150 150
 FT CONFLICT 191 191
 FT CONFLICT 195 195
 FT CONFLICT 211 211
 FT CONFLICT 255 256
 FT CONFLICT 256 256
 FT SEQUENCE 266 AA; 30591 MW; 0FF6DB386497C7D2 CRC64;

Query Match 88.1%; Score 177; DB 1; Length 266;
 Best Local Similarity 84.6%; Pred. No. 8.9e-15;
 Matches 33; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 DSVSTFSKLRQIGPVTOEFWDNLEKTEGLROMSKD 39
 DB 74 DSLSTVSKLRQIGPVTOEFWDNLEKTEGLREEMKD 112

RESULT 5
 APAL_CANFA STANDARD; PRT; 266 AA.
 AC P02648; 21-JUL-1986 (Rel. 01, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Canis familiaris (dog).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedata; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=90132271; PubMed=2515239;
 RA Luo C.-C., Li W.-H., Chan L.;
 RT "Structure and expression of dog apolipoprotein A-I, E, and C-I

RT MRNAs: implications for the evolution and functional constraints of
 FT apolipoprotein structure.";
 RL J. Lipid Res. 30:1735-1746(1989).
 RN [2]
 RP SEQUENCE OF 25-266.
 RX MEDLINE=82142425; PubMed=6801039;
 RA Chung H., Randolph A., Reardon I., Heinrichson R.L.;
 RT "The covalent structure of apolipoprotein A-I from canine high
 density lipoproteins.";
 RL J. Biol. Chem. 257:2961-2967(1982).
 RN [3]
 RP SEQUENCE OF 25-57 AND 262-265.
 RX MEDLINE=76210910; PubMed=179887;
 RA Nakai T., Whayne T.F., Tang J.;
 RT "The amino- and carboxyl-terminal sequences of canine apolipoprotein
 A-I.";
 RL FEBS Lett. 64:409-411(1976).
 RN [4]
 RP SEQUENCE OF 25-37.
 RC TISSUE=Heart;
 RX MEDLINE=9816340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -1- FUNCTION: APOA-I PARTICIPATES IN THE REVERSE TRANSPORT OF
 CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CHYLOMICRONS. SYNTHESIZED IN THE LIVER AND SMALL INTESTINE.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 DR PIR: A03092; LDPGAL.
 DR HSSP: P02647; 1ODR.
 DR HSC-2DPAGE: P02648; DOG.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein: 1.
 KM Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 266
 FT DOMAIN 67 266
 FT REPEAT 67 88
 FT REPEAT 89 110
 FT REPEAT 111 121
 FT REPEAT 122 143
 FT REPEAT 144 165
 FT REPEAT 166 187
 FT REPEAT 188 209
 FT REPEAT 210 231
 FT REPEAT 232 242
 FT REPEAT 243 266
 FT CONFLICT 168 168
 FT CONFLICT 202 202
 FT CONFLICT 235 235
 FT CONFLICT 264 266
 FT SEQUENCE 266 AA; 30196 MW; A3202620C28A869D CRC64;

Query Match 86.1%; Score 173; DB 1; Length 266;
 Best Local Similarity 84.6%; Pred. No. 2.8e-14;
 Matches 33; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 DSVSTFSKLRQIGPVTOEFWDNLEKTEGLROMSKD 39
 DB 74 DSLSTVSKLRQIGPVTOEFWDNLEKTEGLREEMKD 112

RESULT 6
 APAL_BOVIN STANDARD; PRT; 265 AA.
 ID APAL_BOVIN
 AC P13497;

FT CHAIN 25 259 APOLOPROTEIN A-I.
 FT DOMAIN 67 259 10 X APPROXIMATE TANDEM REPEATS.
 FT REPEAT 67 88 1.
 FT REPEAT 89 110 2.
 FT REPEAT 111 121 3 (HALF-LENGTH).
 FT REPEAT 122 143 4.
 FT REPEAT 144 161 5 (INCOMPLETE).
 FT REPEAT 162 183 6.
 FT REPEAT 184 203 7 (INCOMPLETE).
 FT REPEAT 204 225 8.
 FT REPEAT 226 236 9 (HALF-LENGTH).
 FT REPEAT 237 259 10.
 FT CONFLICT 201 201 R -> K (IN REF. 2).
 FT CONFLICT 214 214 G -> S (IN REF. 2).
 FT CONFLICT 218 218 R -> K (IN REF. 2).
 SQ SEQUENCE 259 AA; 30088 MW; 2E8D5E845FEAE88 CRC64;

Query Match 71.1%; Score 143; DB 1; Length 259;
 Best Local Similarity 69.2%; Pred. No. 1.3e-10;
 Matches 27; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DSVTSTSKRLRQLGPTVQEFWDLNLEKEEGLEKROEMSKD 39
 Db 74 DTLGSTVGRLOGLPVTQEFWDLNLEKEEGLEKROEMSKD 112

RESULT 8
 APAL_MOUSE STANDARD; PRT; 264 AA.
 AC Q00623;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92281682; PubMed=1596360;
 RA Stoffel W., Mueller R., Blinczek E., Hofmann K.;
 RT "Mouse apolipoprotein AI. cDNA-derived primary structure, gene
 RL organisation and complete nucleotide sequence.";
 RL Biol. Chem. Hoppe-Seyler 373:187-193(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93122774; PubMed=1478650;
 RA Janusz J.L., Azrolan N., O'Connell A., Aalto-Setälä K., Breslow J.L.;
 RT "Characterization of the mouse apolipoprotein ApoA-1/Apoc-3 gene
 RT locus: genomic, mRNA, and protein sequences with comparisons to other
 RT species.";
 RL Genomics 14:1081-1088(1992).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL EFFLUX FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECTITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC EMBL; X64262; CAA45560.1; -.

DR EMBL; X64263; CAA45561.1; -.
 DR EMBL; L04149; -; NOT ANNOTATED_CDS.
 DR EMBL; L04151; -; NOT ANNOTATED_CDS.
 DR PIR; S22420; S22420.
 DR PIR; A44364; A44364.
 DR HSSP; P02647; IAV1.
 DR SWISS-2DPAGE; Q00623; MOUSE.
 DR MGI; 88049; APOA1.
 DR InterPro; IPR00074; Apolipoprotein.
 DR Pfam; PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEL 19 24 BY SIMILARITY.
 FT CHAIN 25 264 APOLOPROTEIN A-I.
 FT DOMAIN 67 264 10 X APPROXIMATE TANDEM REPEATS.
 FT REPEAT 67 88 1.
 FT REPEAT 89 110 2.
 FT REPEAT 111 121 3 (HALF-LENGTH).
 FT REPEAT 122 143 4.
 FT REPEAT 144 165 5.
 FT REPEAT 166 187 6.
 FT REPEAT 188 207 7 (INCOMPLETE).
 FT REPEAT 208 229 8.
 FT REPEAT 230 240 9 (HALF-LENGTH).
 FT REPEAT 241 264 10.
 SQ SEQUENCE 264 AA; 30587 MW; C453FE2019634AAC CRC64;

Query Match 70.6%; Score 142; DB 1; Length 264;
 Best Local Similarity 64.1%; Pred. No. 1.8e-10;
 Matches 25; Conservative 11; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DSVTSTSKRLRQLGPTVQEFWDLNLEKEEGLEKROEMSKD 39
 Db 74 DTLGSTVQLRQLGPTVQEFWDLNLEKEEGLEKROEMSKD 112

RESULT 9
 APAL_TUPGB STANDARD; PRT; 265 AA.
 AC Q18759;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Tupai glis belangeri (Common tree shrew).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiinae.
 CX NCBI_TaxID=9396;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Lu X., Chen B., Zhao Y., Wang K., Xue H., Zeng W.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL EFFLUX FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECTITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC EMBL; AF005638; AAB82326.1; -.

DR HSSP; P02647; 1AV1.
 DR InterPro; IPR000074; Apolipoprotein.
 DR Pfam; PF01442; Apolipoprotein; 1.
 KM Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT STGNL 1 18 BY SIMILARITY.
 FT PROPEP 19 24
 FT CHAIN 25 265
 FT DOMAIN 67 265
 FT REPEAT 67 88
 FT REPEAT 89 110
 FT REPEAT 111 121
 FT REPEAT 122 143
 FT REPEAT 144 165
 FT REPEAT 166 187
 FT REPEAT 188 209
 FT REPEAT 210 231
 FT REPEAT 232 242
 FT REPEAT 243 265
 SQ SEQUENCE 265 AA; 30332 MW; 60076BC39FEA165 CRC64;

Query Match 68.2%; Score 137; DB 1; Length 265;
 Best Local Similarity 64.1%; Pred. No. 7.4e-10;
 Matches 25; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 DSVTSPSKLREQLGPYQGFMDLKEKTEGLRQEMSKD 39
 ID APAL_CHICK STANDARD; PRT; 264 AA.
 AC P08250;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 OX 11)
 RN SEQUENCE FROM N.A.
 RP MEDLINE=80049703; PubMed=3118875;
 RX Byrnes L., Luo C.-C., Li W.-H., Yang C.-Y., Chan L.;
 RT "Chicken apolipoprotein A-I: cDNA sequence, tissue expression and
 evolution.";
 RL Biochem. Biophys. Res. Commun. 148:485-492(1987).
 RN SEQUENCE FROM N.A.
 RP MEDLINE=8152500; PubMed=3126099;
 RX Ferrari S., Tarugi P., Drusiani E., Calandra S., Fregni M.;
 RT "The complete sequence of chick apolipoprotein AI mRNA and its
 expression in the developing chick.";
 RL Gene 60:39-46(1987).
 RN SEQUENCE FROM N.A.
 RP MEDLINE=87222301; PubMed=3108248;
 RX Rajavashisth T.B., Dawson P.A., Williams D.L., Shackelford J.E.,
 RA Leberer H., Lusis A.J.;
 RT "Structure, evolution, and regulation of chicken apolipoprotein A-I.";
 RL J. Biol. Chem. 262:7058-7065(1987).
 RN SEQUENCE FROM N.A.
 RP MEDLINE=92381402; PubMed=1512510;
 RX Iamori Fava S., Sastri R., Rajavashisth T.B.,
 RA Lusis A.J., Karathanasis S.K.;
 RT "Evolutionary distinct mechanisms regulate apolipoprotein A-I gene
 expression: differences between avian and mammalian apoA-I gene
 transcription control regions.";

RL J. Lipid Res. 33:831-842(1992).
 RN SEQUENCE OF 25-44.
 RP MEDLINE=83213466; PubMed=6406496;
 RX Shackelford J.E., Leberer H.G.;
 RT "Synthesis and secretion of apolipoprotein AI by chick breast
 muscle.";
 RL J. Biol. Chem. 258:7175-7180(1983).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
 THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC -----
 DR EMBL; M17961; AAA48593.1; -;
 DR EMBL; M18746; AAA48594.1; -;
 DR EMBL; M25559; AAA48592.1; -;
 DR EMBL; M96012; AAA48597.1; -;
 DR PIR; S01453; LPCHA1.
 DR PIR; JH0471; JH0471.
 DR HSSP; P02647; 10DR.
 DR InterPro; IPR000074; Apolipoprotein.
 DR Pfam; PF01442; Apolipoprotein; 1.
 KM Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 264
 FT DOMAIN 67 264
 FT REPEAT 67 88
 FT REPEAT 89 110
 FT REPEAT 111 121
 FT REPEAT 122 143
 FT REPEAT 144 165
 FT REPEAT 166 187
 FT REPEAT 188 209
 FT REPEAT 210 231
 FT REPEAT 232 242
 FT REPEAT 243 264
 FT CONFLICT 16 16 T -> I (IN REF. 4).
 FT CONFLICT 16 16 E -> K (IN REF. 3).
 FT CONFLICT 148 148
 SQ SEQUENCE 264 AA; 30680 MW; 968370B81E2AC5C2 CRC64;

Query Match 37.3%; Score 75; DB 1; Length 264;
 Best Local Similarity 38.5%; Pred. No. 0.031;
 Matches 15; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 DSVTSPSKLREQLGPYQGFMDLKEKTEGLRQEMSKD 39
 DB 74 DTLSSAAAKLREDMAPPYKEVEMWLKDTALRAELTKD 112

RESULT 11
 ID APAL_COTJA STANDARD; PRT; 264 AA.
 AC P32918;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Coturnix coturnix japonica (Japanese quail).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Colurnix.
 OX NCBI_TaxID=93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=97212027; PubMed=9058967;
 RA Oku H., Toda T., Nagata J., Ishikawa M., Neyazaki K., Shinjo C.,
 RA Chinen I.;
 RT "Apolipoprotein A-I of Japanese quail: CDNA sequence and modulation of
 RT tissue expression by cholesterol feeding.";
 RL Biosci. Biotechnol. Blochem. 61:286-290(1997).
 RN [2]
 RP SEQUENCE OF 25-60.
 RA MEDLINE=93213845; PubMed=8461329;
 RX Oku H., Ishikawa M., Nagata J., Toda T., Chinen I.;
 RT "Lipoprotein and apoprotein profile of Japanese quail.";
 RL Blochim. Biophys. Acta 1167:22-28(1993).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF VLDL, HDL, LDL AND IN
 CC CHLROMICRONS. EXPRESSED IN A NUMBER OF TISSUES INCLUDING LIVER,
 CC SMALL INTESTINE, LUNG, KIDNEY, HEART AND MUSCLE WITH HIGHEST
 CC EXPRESSION IN LIVER AND SMALL INTESTINE.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOE FAMILY.
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 CC -----
 DR EMBL: D85133; BAI2729.1; -
 DR HSSP: P02647; IGW4.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 264
 FT DOMAIN 67 264
 FT REPEAT 67 88
 FT REPEAT 89 110
 FT REPEAT 111 121
 FT REPEAT 122 143
 FT REPEAT 144 165
 FT REPEAT 166 187
 FT REPEAT 188 209
 FT REPEAT 210 231
 FT REPEAT 232 242
 FT REPEAT 243 264
 SQ SEQUENCE 264 AA; 30753 MW; 8781DE213C3F863F CRC64;
 Query Match 36.3%; Score 73; DB 1; Length 264;
 Best Local Similarity 38.5%; Pred. No. 0.054;
 Matches 15; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
 OY 1 DSVSTFSKRLRGOLGPTQGFMDNLEKETEGRLQEMSKD 39
 ID DTLGAATAAKLRDMPTPYRREVMKLDTEALRAELTKD 112
 DB 74 DTLGAATAAKLRDMPTPYRREVMKLDTEALRAELTKD 112
 RESULT 12
 ID APAL ANAPL STANDARD; PRT; 264 AA.
 AC 042296;

DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Anas platyrhynchos (Domestic duck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=8839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEKIN BRED; TISSUE=Liver;
 RA Chen B., Lu X., Wang K., Xue H., Zeng W., Zhu D., Chi L.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DDA databases.
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC -----
 DR EMBL: U86131; AAB64381.1; -
 DR HSSP: P02647; 10DR.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 264
 FT DOMAIN 67 264
 FT REPEAT 67 88
 FT REPEAT 89 110
 FT REPEAT 111 121
 FT REPEAT 122 143
 FT REPEAT 144 165
 FT REPEAT 166 187
 FT REPEAT 188 209
 FT REPEAT 210 231
 FT REPEAT 232 242
 FT REPEAT 243 264
 SQ SEQUENCE 264 AA; 30659 MW; 7546F4BAF2846900 CRC64;
 Query Match 35.8%; Score 72; DB 1; Length 264;
 Best Local Similarity 38.5%; Pred. No. 0.072;
 Matches 15; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
 OY 1 DSVSTFSKRLRGOLGPTQGFMDNLEKETEGRLQEMSKD 39
 ID DTLGAATAAKLRDMPTPYRREVMKLDTEALRAELTKD 112
 DB 74 DTLGAATAAKLRDMPTPYRREVMKLDTEALRAELTKD 112
 RESULT 13
 ID APAA HUMAN STANDARD; PRT; 396 AA.
 AC P06727;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV).
 GN APOA4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=89194198; PubMed=2930771;
 RA Yang C., Gu Z.W., Xiong W., Rosseneu M., Yang H.X., Lee B.M.,
 Goto A.M. Jr., Chan L.;
 "The primary structure of human apolipoprotein A-IV.";
 RN Biochim. Biophys. Acta 1002:231-237(1989).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87041474; PubMed=3095836;
 RA Karathanasis S.K., Oetgen P., Haddad I.A., Antonarakis S.E.;
 RT "Structure, evolution, and polymorphisms of the human apolipoprotein
 A4 gene (APOA4).";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8457-8461(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86296629; PubMed=3755616;
 RA Karathanasis S.K., Yunis I.;
 RT "Structure, evolution, and tissue-specific synthesis of human
 apolipoprotein AIV.";
 RL Biochemistry 25:3962-3970(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87250378; PubMed=3036793;
 RA Elshoutdag N.A., Walker D.W., Boguski M.S., Freeman M.,
 Gordon J.I., Taylor J.M.;
 RT "Structure and expression of the human apolipoprotein A-IV gene.";
 RL J. Biol. Chem. 262:7973-7981(1987).
 RN [5]
 RP SEQUENCE OF 21-396 FROM N.A.
 RX MEDLINE=86111885; PubMed=3080432;
 RA Elshoutdag N.A., Walker D.W., Boguski M.S., Gordon J.I., Taylor J.M.;
 RT "The nucleotide and derived amino acid sequence of human
 apolipoprotein A-IV mRNA and the close linkage of its gene to the
 genes of apolipoproteins A-I and C-III.";
 RL J. Biol. Chem. 261:1998-2002(1986).
 RN [6]
 RP SIGNAL SEQUENCE CLEAVAGE SITE.
 RX MEDLINE=84161950; PubMed=6706947;
 RA Gordon J.I., Bisgaler C.L., Sims H.F., Sachdev O.P., Glickman R.M.,
 Strauss A.W.;
 RT "Biosynthesis of human preapolipoprotein A-IV.";
 RL J. Biol. Chem. 259:468-474(1984).
 RN [7]
 RP REVIEW ON POLYMORPHISM.
 RX Lohse P., Brewer H.B. Jr.;
 RT "Genetic polymorphism of apolipoprotein A-IV.";
 RL Curr. Opin. Lipidol. 2:90-95(1991).
 RN [8]
 RP VARIANT A-IV*2.
 RX MEDLINE=90277616; PubMed=2351649;
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
 RT "Genetic polymorphism of human plasma apolipoprotein A-IV is due to
 nucleotide substitutions in the apolipoprotein A-IV gene.";
 RL J. Biol. Chem. 265:10061-10064(1990).
 RN [9]
 RP VARIANTS A-IV*0 AND A-IV*3.
 RX MEDLINE=90324273; PubMed=1973689;
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
 RT "Human plasma apolipoproteins A-IV-0 and A-IV-3. Molecular basis for
 two rare variants of apolipoprotein A-IV-1.";
 RL J. Biol. Chem. 265:12734-12739(1990).
 RN [10]
 RP VARIANTS.
 RX MEDLINE=91310615; PubMed=1677358;
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
 RT "Three genetic variants of human plasma apolipoprotein A-IV: apoA-IV-
 1 (Thr-347-->Ser), apoA-IV-0 (Lys-167-->Glu, Gln-360-->His), and apoA-IV-
 3 (Glu-165-->Lys).";
 RL J. Biol. Chem. 266:13513-13518(1991).

RN [11]
 RP ERRATUM.
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
 RL J. Biol. Chem. 266:19866-19866(1991).
 RN [12]
 RP VARIANT MET-13.
 RX MEDLINE=92238494; PubMed=1349197;
 RA von Eckardstein A., Funke H., Schulte M., Eren M., Schulte H.,
 Assmann G.;
 RT "Nonsynonymous polymorphic sites in the apolipoprotein (apo) A-IV
 gene are associated with changes in the concentration of apo B- and
 apo A-I-containing lipoproteins in a normal population.";
 RL Am. J. Hum. Genet. 50:1115-1128(1992).
 RN [13]
 RP VARIANT SER-147.
 RX MEDLINE=92144647; PubMed=1737067;
 RA Tenkanen H., Koskinen P., Muto J., Baumann M., Lukka M.,
 Kauppinen-Makelin R., Kontula K., Taskinen M.R., Mantari M.,
 Manninen V., Ehnholm C.;
 RT "A novel polymorphism of apolipoprotein A-IV is the result of an
 asparagine to serine substitution at residue 127.";
 RL Biochim. Biophys. Acta 1138:27-33(1992).
 RN [14]
 RP VARIANT A-IV*5.
 RX MEDLINE=93138374; PubMed=1487136;
 RA Kamboh M.I., Williams E.R., Law J.C., Aston C.E., Bunker C.H.,
 Ferrell R.E., Pollitzer W.S.;
 RT "Molecular basis of a unique African variant (A-IV 5) of human
 apolipoprotein A-IV and its significance in lipid metabolism.";
 RL Genet. Epidemiol. 9:379-386(1992).
 RN [15]
 RP VARIANTS LYS-44 (BUDAPEST-2); CYS-305 AND SER-367 (BUDAPEST-1).
 RX MEDLINE=95245341; PubMed=7728150;
 RA Menzel H.J., Dieplinger H., Sandholzer C., Karadi I., Utermann G.,
 Caszaz A.;
 RT "Apolipoprotein A-IV polymorphism in the Hungarian population: gene
 frequencies, effect on lipid levels, and sequence of two new
 variants.";
 RL Hum. Mutat. 5:58-65(1995).
 RN [16]
 RP VARIANTS FCBL SEATTLE SER-161; LEU-178 AND GLN-264.
 RX MEDLINE=97114287; PubMed=8956036;
 RA Deeb S.S., Nevin D.N., Iwasaki L., Brunzell J.D.;
 RT "Two novel apolipoprotein A-IV variants in individuals with familial
 combined hyperlipidemia and diminished levels of lipoprotein lipase
 activity.";
 RL Hum. Mutat. 8:319-325(1996).
 CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
 CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
 LIPASE BY APOC-II. POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
 COMPONENT OF HDL AND CHYLOMICRONS.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE INTESTINE.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO. A AND B, RELATED 11-
 MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
 HELICAL, AND MANY OF THESE HELICES ARE PREDICTED TO BE HIGHLY ALPHA-
 THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECTININ:CHOLESTEROL
 ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
 CC -1- POLYMORPHISM: EIGHT ALLELES HAVE BEEN CHARACTERIZED (APOA-IV*0
 TO APOA-IV*7). APOA-IV*1 IS THE MAJOR ALLELE (90%). IV*2 IS ALSO
 COMMON (8%). THE OTHERS ARE RARE ALLELES.
 CC -1- DISEASE: DEFECTS IN APOA MAY CONTRIBUTE, ALONG WITH DEFECTS IN
 OTHER GENES OR ENVIRONMENTAL FACTORS, TO THE DEVELOPMENT OF
 FAMILIAL COMBINED HYPERLIPIDEMIA (FCHL).
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----
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CC EMBL; M14642; AAA51745.1; -
 CC EMBL; X13629; CAA31955.1; -
 DR EMBL; M14566; AAA51748.1; -
 DR EMBL; J02758; AAA96731.1; -
 DR EMBL; M13654; AAA51744.1; -
 DR PIR; A26481; LPH044.
 DR PIR; A24449; A24449.
 DR PIR; A29330; A29330.
 DR PIR; A26280; A26280.
 DR PIR; S02715; S02715.
 DR HSP; P02649; INFO.
 DR SWISS-2DPAGE; P06727; HUMAN.
 DR MIM; 107690; -
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal;
 KW Disease mutation; Polymorphism.
 FT SIGNAL 1 20
 FT CHAIN 21 396 APOLIPOPROTEIN A-IV.
 FT DOMAIN 33 330 13 X 22 AA APPROXIMATE TANDEM REPEATS.
 FT REPEAT 33 54 1.
 FT REPEAT 60 81 2.
 FT REPEAT 82 103 3.
 FT REPEAT 115 136 4.
 FT REPEAT 137 158 5.
 FT REPEAT 159 180 6.
 FT REPEAT 181 202 7.
 FT REPEAT 203 224 8.
 FT REPEAT 225 246 9.
 FT REPEAT 247 268 10.
 FT REPEAT 269 286 11.
 FT REPEAT 287 308 12.
 FT REPEAT 309 330 13.
 FT DOMAIN 372 389 GLU/GLN-RICH.
 FT VARIANT 13 13 V -> W (IN APOA-IV*1D).
 FT VARIANT 44 44 /FTID=VAR_000626.
 FT VARIANT 147 147 E -> K (IN BUDPEST-2).
 FT VARIANT 161 161 /FTID=VAR_000627.
 FT VARIANT 161 161 N -> S (IN APOA-IV*1B).
 FT VARIANT 161 161 /FTID=VAR_000628.
 FT VARIANT 161 161 A -> S (IN SEATTLE-3; IN FCHL).
 FT VARIANT 161 161 /FTID=VAR_000629.

Query Match 31.3%; Score 63; DB 1; Length 396;
 Best Local Similarity 27.8%; Pred. No. 1.5;
 Matches 10; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

OY 3 VTSTFSKLRDQGPVTOEFMDNLEKTEGLRQEMSK 38
 DB 256 ISASAEILRRLAPLAEDVRGNLKGNTGLQKSLAE 291
 ID APO4_PAPAN STANDARD; PRT; 401 AA.
 AC Q28758;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV) (Fragment).
 OS APOA4.
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OX NCBI_Taxid=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=93340170; PubMed=8101842;

RA Hixson J.E., Kammerer C.M., Mott G.E., Britten M.L., Birnbaum S.,
 RA Powers P.K., Vandenberg J.L.;
 RT "Baboon apolipoprotein A-IV. Identification of Lys-76-->Glu that
 RT distinguishes two common isoforms and detection of length
 RT polymorphisms at the carboxyl terminus."
 RL J. Biol. Chem. 268:15667-15673(1993).
 CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
 CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN AND
 CC LIPIASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
 CC COMPONENT OF HDL AND CHYLOMICRONS.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE INTESTINE.
 CC -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
 CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
 CC HELICAL, AND MANY OF THESE HELICES ARE PREDICTED TO BE HIGHLY ALPHA-
 CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL
 CC ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
 CC -1- POLYMORPHISM: THERE ARE TWO COMMON APOA-IV ISOFORMS, I (SHOWN
 CC HERE) AND E. THE I ISOFORM IS ASSOCIATED WITH HIGHER LEVELS OF
 CC HIGH DENSITY LIPOPROTEIN-C ON A HIGH CHOLESTEROL, SATURATED FAT
 CC DIET.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----
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DR EMBL; L13174; AAA35379.1; -
 DR HSP; P02649; INFO.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal;
 KW Polymorphism.
 FT SIGNAL 1 1
 FT CHAIN 5 4 POTENTIAL.
 FT DOMAIN 17 314 APOLIPOPROTEIN A-IV.
 FT REPEAT 17 38 13 X 22 AA APPROXIMATE TANDEM REPEATS.
 FT REPEAT 44 65 1.
 FT REPEAT 66 87 2.
 FT REPEAT 99 120 3.
 FT REPEAT 121 142 4.
 FT REPEAT 143 164 5.
 FT REPEAT 165 186 6.
 FT REPEAT 187 208 7.
 FT REPEAT 209 230 8.
 FT REPEAT 231 252 9.
 FT REPEAT 253 270 10.
 FT REPEAT 271 292 11.
 FT REPEAT 293 314 12.
 FT REPEAT 356 394 13.
 FT DOMAIN 356 394 GLU/GLN-RICH.
 FT VARIANT 80 80 K -> E (IN ISOFORM E).
 SO SEQUENCE 401 AA; 46538 MW; 0A76D1284AA937F CRC64;

Query Match 31.3%; Score 63; DB 1; Length 401;
 Best Local Similarity 27.8%; Pred. No. 1.5;
 Matches 10; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

OY 3 VTSTFSKLRDQGPVTOEFMDNLEKTEGLRQEMSK 38
 DB 240 ISASAEILRRLAPLAEDVRGNLKGNTGLQKSLAE 275
 ID APO4_MACFA STANDARD; PRT; 429 AA.
 AC Q28758;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV) (Fragment).
 OS APOA4.
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OX NCBI_Taxid=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=93340170; PubMed=8101842;

AC P33621; (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 13-DEC-1998 (Rel. 37, Last annotation update)
DE Apolipoprotein A-IV precursor (Apo-AIV).
GN APOA4.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
CX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=93192330; PubMed=8448212;
RA Ooseda J., Pocovi M., Nicolosi R.J., Schaefer E.J., Ordovas J.M.;
RT "Nucleotide sequences of the Macaca fascicularis apolipoprotein C-II
RL Biochim. Biophys. Acta 1172:335-339(1993).
CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
CC CARBOHYDRATE METABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
CC LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
CC COMPONENT OF HDL AND CHYLOMICRONS.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: SECRETED IN PLASMA.
CC -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
CC 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
CC MEMES) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL
CC ACTIVATORTRANSFERASE (LCAT) ACTIVATING ABILITIES.
CC -1- SIMILARITY: BELONGS TO THE APOAI / APOA4 / APOE FAMILY.
CC -----
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CC -----
CC DR EMBL; X68361; CAA48421.1; -.
DR PIR; S29565; S29565.
DR PIR; S30195; S30195.
DR HSSP; P02649; INFO.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein_1.
KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 429 APOLIPOPROTEIN A-IV.
FT DOMAIN 33 330 13 X 22 AA APPROXIMATE TANDEM REPEATS.
FT REPEAT 33 54 1.
FT REPEAT 60 81 2.
FT REPEAT 82 103 3.
FT REPEAT 115 136 4.
FT REPEAT 137 158 5.
FT REPEAT 159 180 6.
FT REPEAT 181 202 7.
FT REPEAT 203 224 8.
FT REPEAT 225 246 9.
FT REPEAT 247 268 10.
FT REPEAT 269 286 11.
FT REPEAT 287 308 12.
FT REPEAT 309 330 13.
FT DOMAIN 372 420 GLUT/GLN-RICH.
SQ SEQUENCE 429 AA; 49876 MW; 3D45B5F551DD0DB60C CRC64;

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Db      256 ISAAEELRQRLAPLAEDMRGNLRGNTGGLQKSLAE 291
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Search completed: September 22, 2002, 12:22:19
Job time: 1019 sec

Query Match	31.3%	Score 63;	DB 1;	Length 429;
Best Local Similarity	27.8%;	Pred. No. 1.6;		
Matches 10;	Conservative 15;	Mismatches 11;	Indels 0;	Gaps 0;

QY 3 VTST*SKLRQŁGPVTQEFWDNLEKETEGLRQEMSK 38

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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:21:39 ; Search time 111.17 seconds

(without alignments)
60.689 Million cell updates/sec

Title: US-09-803-918a-2_COPY_75_113

Perfect score: 1 DSVTSTFSKLRQDLPVTOEFMDNLEKTEGLROEMSKD 39

Sequence: 1 DSVTSTFSKLRQDLPVTOEFMDNLEKTEGLROEMSKD 39

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEL:19:*
2: SP_ARCHAEL:19:*
3: SP_FUNGI:19:*
4: SP_FUNGI:19:*
5: SP_MAMMAL:19:*
6: SP_MAMMAL:19:*
7: SP_MHC:19:*
8: SP_ORGANELLE:19:*
9: SP_ORGANELLE:19:*
10: SP_PLANT:19:*
11: SP_PLANT:19:*
12: SP_VIRUS:19:*
13: SP_VIRUS:19:*
14: SP_VIRUS:19:*
15: SP_VIRUS:19:*
16: SP_VIRUS:19:*
17: SP_VIRUS:19:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	167	83.1	56	6	002762 ovis aries
2	155	77.1	264	11	092214 mesocricetu
3	142	70.6	263	11	009042 mus musculu
4	142	70.6	263	11	008855 mus musculu
5	133	66.2	258	11	009054 mus musculu
6	133	66.2	258	11	008877 mus musculu
7	131	65.2	241	6	09T549 mus musculu
8	64.5	32.1	329	11	09D495 mus musculu
9	63	31.3	244	4	013784 homo sapien
10	60.5	30.1	562	12	067018 influenza a
11	59.5	29.6	259	13	098T61 macaca fasc
12	58	28.4	311	6	095K18 macaca fasc
13	57	28.4	90	2	09ICRO paenibacill
14	57	28.4	172	2	09P898 escherichia
15	57	28.4	172	2	069425 enterobacte
16	56.5	28.1	131	12	067047 influenza a

17	56.5	28.1	309	5	023138 caenorhabdi
18	56.5	28.1	562	12	067017 influenza a
19	56.5	28.1	562	12	067032 influenza a
20	56.5	28.1	562	12	067048 influenza a
21	56.5	28.1	565	12	067010 influenza a
22	56.5	28.1	1025	16	09P477 chlamydia m
23	56	27.9	444	11	09CV95 mus musculu
24	56	27.9	1091	5	018082 caenorhabdi
25	55.5	27.6	194	16	055564 synchocyst
26	55.5	27.6	348	16	098KPS rhizobium l
27	55.5	27.6	562	12	067016 influenza a
28	55.5	27.6	562	12	067326 influenza a
29	55.5	27.6	562	12	067325 influenza a
30	55.5	27.6	562	12	067327 influenza a
31	55.5	27.6	565	12	082544 influenza a
32	55.5	27.6	566	12	082751 influenza a
33	55.5	27.6	566	12	082545 influenza a
34	55.5	27.6	566	12	091808 influenza a
35	55.5	27.6	566	12	091807 influenza a
36	55.5	27.6	566	12	091806 influenza a
37	55.5	27.6	566	12	043241 homo sapien
38	55.5	27.6	1530	4	052254 salmonella
39	55	27.4	172	2	052254 salmonella
40	55	27.4	270	4	09H738 homo sapien
41	55	27.4	313	6	09G1C0 lupula galls
42	55	27.4	366	13	093601 gallus gall
43	55	27.4	487	5	09N3W4 caenorhabdi
44	55	27.4	1410	4	014221 homo sapien
45	55	27.4	1411	4	015075 homo sapien

ALIGNMENTS

RESULT 1	002762	PRELIMINARY;	PRT;	56 AA.
ID	002762			
AC	002762			
DT	01-JUL-1997 (TREMURel. 04, Created)			
DT	01-JUL-1997 (TREMURel. 04, Last sequence update)			
DT	01-DEC-2001 (TREMURel. 19, Last annotation update)			
DE	APOLIPOPROTEIN A1 (FRAGMENT).			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OX	Bovidae; Caprinae; Ovis.			
RN	NCBI_TaxID=9940.			
RP	[1]			
RA	SEQUENCE FROM N.A.			
RX	MEDLINE=99098454; PubMed=9883985;			
RT	Robertson J.A., Bhattacharya S., Ing N.H.;			
RT	"Tamoxifen up-regulates oestrogen receptor-alpha, c-fos and			
RT	glyceraldehyde 3-phosphate-dehydrogenase mRNAs in ovine endometrium.";			
RL	J. Steroid Biochem. Mol. Biol. 67:285-292(1998).			
DR	EMBL: U94720; AAB57840.1; -			
DR	HSSP: P02647; IAV1.			
KW	Lipoprotein.			
FT	NON_TER			
FT	NON_TER			
SO	SEQUENCE			
	56 AA;	6617 MW;	2AB3BE08F1E8F1BC CRC64;	

Query Match 83.1%; Score 167; DB 6; Length 56;
Best local similarity 82.1%; Pred. No. 1.9e-14;
Matches 32; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRQDLPVTOEFMDNLEKTEGLROEMSKD 39
Db 5 DSVTSTFSKLRQDLPVTOEFMDNLEKTEGLROEMSKD 43
RESULT 2
QY 2
Db 5
RESULT 2
QY 2
Db 5

ID 092214 PRELIMINARY: PRT: 264 AA.
 AC 092214;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE APOLIPROTEIN A-I.
 GN APOA1.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GOLDEN SYRIAN; TISSUE=INTESTINE;
 RX MEDLINE=99061559; PubMed=9843713;
 RA Wu J.Y., Reeves S.K., Wang Y.R., Wu Y., Lei P.P., Lei K.Y.;
 RT "Zinc deficiency decreases plasma level and hepatic mRNA abundance of
 apolipoprotein A-I in rats and hamsters."
 RL EMBL: AF046919; AAC98484.1; -.
 DR HSSP: P02647; IAV1.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 DR Lipoprotein.
 KW SEQUENCE 264 AA; 30739 MW; 280B22F4C0F0B129 CRC64;

Query Match 77.1%; Score 155; DB 11; Length 264;
 Best Local Similarity 74.4%; Pred. No. 3.8e-12;
 Matches 29; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DSVTSTFSKLRQOLGPVTOEFWMDLKEKTEGLROEMSKD 39
 Db 74 DTLGSTVGRLOELGPVTOEFWMDLKEKTEGLRREMNKD 112

RESULT 3
 ID 009042 PRELIMINARY: PRT: 263 AA.
 AC 009042;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE APOLIPROTEIN A-I.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR AND BALB/C, AND C3H; TISSUE=SPLEEN;
 RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U79575; AAB58427.1; -.
 DR EMBL: U79572; AAB58424.1; -.
 DR EMBL: U79573; AAB58425.1; -.
 DR HSSP: P02647; IAV1.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 DR Lipoprotein.
 KW SEQUENCE 263 AA; 30516 MW; E245DF7483A5A0DD CRC64;

Query Match 70.6%; Score 142; DB 11; Length 263;
 Best Local Similarity 64.1%; Pred. No. 1.8e-10;
 Matches 25; Conservative 11; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DSVTSTFSKLRQOLGPVTOEFWMDLKEKTEGLROEMSKD 39
 Db 74 DTLGSTVGRLOELGPVTOEFWMDLKEKTEGLRREMNKD 112

RESULT 4
 ID 008855 PRELIMINARY: PRT: 263 AA.
 AC 008855;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE APOLIPROTEIN A-I.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=SPLEEN;
 RX MEDLINE=98077648; PubMed=9415807;
 RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
 RT "Repetitive elements in the third intron of murine apolipoprotein A-I
 gene."
 RL Biochem. Mol. Biol. Int. 43:989-996(1997).
 DR EMBL: U79574; AAB58426.1; -.
 DR HSSP: P02647; IAV1.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 DR Lipoprotein.
 KW SEQUENCE 263 AA; 30544 MW; 7825DF7483A5B24A CRC64;

Query Match 70.6%; Score 142; DB 11; Length 263;
 Best Local Similarity 64.1%; Pred. No. 1.8e-10;
 Matches 25; Conservative 11; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DSVTSTFSKLRQOLGPVTOEFWMDLKEKTEGLROEMSKD 39
 Db 74 DTLGSTVGRLOELGPVTOEFWMDLKEKTEGLRREMNKD 112

RESULT 5
 ID 009054 PRELIMINARY: PRT: 258 AA.
 AC 009054;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE APOLIPROTEIN A-I.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WKY, AND SHRSP; TISSUE=SPLEEN;
 RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U79578; AAB58430.1; -.
 DR EMBL: U79577; AAB58429.1; -.
 DR HSSP: P02647; IAV1.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 DR Lipoprotein.
 KW SEQUENCE 258 AA; 29918 MW; 093B6EF2E629CDC8 CRC64;

Query Match 66.2%; Score 133; DB 11; Length 258;
 Best Local Similarity 64.1%; Pred. No. 2.6e-09;
 Matches 25; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DSVTSTFSKLRQOLGPVTOEFWMDLKEKTEGLROEMSKD 39
 Db 73 DTLGSTVGRLOELGPVTOEFWMDLKEKTEGLRREMNKD 111

RESULT 6

	Query Match	66.28;	Score 133;	DB 11;	Length 258;
	Best Local Similarity	64.18;	Pred. No.	2.6e-09;	
Matches	25; Conservative	7;	Mismatches	7;	Gaps 0;
DQ	1 DSVSTFSEKRRGCGVYGFNDNLAKETEGTGRDMSKD	39			
Dc	:: :: :: ::				
	73 DTGGTVGRQLDGFLVDPMANKEKTIDPFRRENMDD	111			

Query Match	65.2%	Score 131	DB 6	Length 241
Best Local Similarity	61.5%	Pred. No. 4.3e+09		
Matches 24; Conservative	6;	Mismatches 9;	Indels 0;	Gaps 0;
QY	1	DSVTSFSEKRLRQIGVYQDEFNDINERKTEGIRQMSKD	39	
		::: ::: ::: ::: ::: ::: :::		
Db	50	DFVSSALLKRRQMKPIAEFGNGNKEKTEGIRQVSKD	88	

ID	Q9D495	PRELIMINARY	PRT:	329 AA.
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DE	4933406J07RIK PROTEIN.			
GN	4933406J07RIK			
OS	Mus musculus (mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID=10090;				
NP	SEQUENCE FROM N.A.			
RP	SPRAIN-C57BL/6J; TISSUE=TESTIS;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shihagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,			
RA	Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,			
RA	Kodota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., Kling B., Kochwa H.,			
RA	Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsi G.,			
RA	Blake J., Boilelli D., Bojunga N., Carrinci P., de Bonardo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Guistincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,			
RA	Lyons P., Marchionni I., Mashima M., Mazzarelli S., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,			
RA	Hayashizaki Y.;			
RT	*Functional annotation of a full-length mouse cDNA collection.*;			
RL	Nature 409:665-690(2001).			
DR	EMBL: AK016594; BAB30383.1; -;			
DR	MGI: 1921325; 4933406J07RIK.			
SQ	SEQUENCE 329 AA; 36205 MW; E843B245DEDAIC029 CRC64;			
Qy	1 DSVSTSKRLREQLPVYQEFNDLKEKEGRQE 35			
Db	63 NEVQDAKKKASEELGE-AQTVMNDLQKRELDLREE 96			
Query Match	32.1%;	Score 64.5;	DB 11;	Length 329;
Best Local Similarity	42.9%;	Pred. No. 2.4;		
Matches 15;	Conservative 5;	Mismatches 14;	Indels 1;	Gaps 1;
RESULT 9				
ID 013784	PRELIMINARY;	PRT;	244 AA.	
AC 013784;				
DT 01-NOV-1996 (TREMBLrel. 01, Created)				
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE APOA4 PROTEIN (FRAGMENT).				
DE APOA4.				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
NCBI_TaxID=9606;				
NP	SEQUENCE FROM N.A.			
RP	TISSUE=LIVER;			
RX	MEDLINE=86016704; PubMed=3931073;			
RA	Karathanasis S.K.;			
RT	*Apolipoprotein multigene family: tandem organization of human			
RT	apolipoprotein AI, CIII, and AIV genes.*;			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:6374-6378(1985).			
DR	EMBL: M10373; AAB59516.1; -;			
DR	HSP: P02649; IEB24.			
InterPro: IPR000074; Apolipoprotein				

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RESULT 11
Q98TGI PRELIMINARY; PRT; 259 AA.
ID Q98TGI
AC Q98TGI;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE 28KDA-1E APOLIPROTEIN.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae
OC Anguillidae; Anguilla.
NC NC_000000000
NC TaxID=7937;

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RESULT 13
Q9LCRO PRELIMINARY; PRT; 90 AA.
ID Q9LCRO
AC Q9LCRO
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE OREX.
GN OREX.
OS Paenibacillus polymyxa (Bacillus polymyxa).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Paenibacillus.
OX NCBI_TaxID=1406;
RN [1]

```

RP SEQUENCE FROM N.A.
 RX MEDLINE=20092478; PubMed=10628856;
 RA Ishikawa S., Kawahara S., Sekiguchi J.;
 RT "Cloning and expression of two autolysin genes, cwiU and cwiV, which
 RT are tandemly arranged on the chromosome of Bacillus polymyxa var.
 RL colistinus";
 RM Mol. Gen. Genet. 262:738-748(1999).
 DR EMBL: AB003153; BAA90652.1; -
 SQ SEQUENCE 90 AA; 10260 MW; 510D4E5DC0253C52 CRC64;

Query Match 28.4%; Score 57; DB 2; Length 90;
 Best Local Similarity 45.5%; Pred. No. 5.3;
 Matches 15; Conservative 5; Mismatches 11; Indels 2; Gaps 1;

QY 7 FSKLRQLGPTVQEFWDLNLEKETEGLRQEMSKD 39
 DB 14 FSDIFEOI--VTTEFAENERELEGITVSHSGD 44

RESULT 14
 ID 09F898 PRELIMINARY; PRT; 172 AA.
 AC 09F898;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE MOBB.
 GN MOBB.
 OS Escherichia coli.
 OC Plasmid pLG13.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LG74;
 RA Zakharova M.V.;
 RT Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF251289; AAG18129.1; -
 KW Plasmid.
 SQ SEQUENCE 172 AA; 19527 MW; AD1C52C782860B55 CRC64;

Query Match 28.4%; Score 57; DB 2; Length 172;
 Best Local Similarity 33.3%; Pred. No. 11;
 Matches 12; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRQLGPTVQEFWDLNLEKETEGLRQEM 36
 DB 39 EAVTSNETKIRDAIALFTASTEKSLKRGVKEAM 74

RESULT 15
 ID 069425 PRELIMINARY; PRT; 172 AA.
 AC 069425;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MBEB.
 GN MBEB.
 OS Enterobacter cloacae.
 OC Plasmid pECU18.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 OX NCBI_TaxID=550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-18K;
 RA Solomon A.S.;
 RL Submitted (Nov-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: Y16897; CAA76524.1; -
 KW Plasmid.
 SQ SEQUENCE 172 AA; 19518 MW; AD1C52D94DBA8655 CRC64;

Query Match 28.4%; Score 57; DB 2; Length 172;
 Best Local Similarity 33.3%; Pred. No. 11;
 Matches 12; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRQLGPTVQEFWDLNLEKETEGLRQEM 36
 DB 39 EAVTSNETKIRDAIALFTASTEKSLKRGVKEAM 74

Search completed: September 22, 2002, 12:21:39
 Job time: 1119 sec

Sun Sep 22 12:10:39 2002

us-09-803-918a-2_copy_75_113.rsp

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: September 22, 2002, 12:05:16 : Search time 139.03 Seconds
(without alignments)
31.158 Million cell updates/sec

Title: US-09-803-918a-2_COPY_75_113

Perfect score: 201

Sequence: 1 DSVSTFFSKLRQLGPFVQEFWDLNLEKETEGLRQMSKD 39

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	100.0	119	AAU30468	Novel human secret
2	201	100.0	120	AAU30467	Novel human secret
3	201	100.0	120	AAU30466	Novel human secret
4	201	100.0	166	AAU28372	Novel human secret
5	201	100.0	243	AAU28372	Novel human secret
6	201	100.0	244	AAU28184	Sequence of mature
7	201	100.0	264	AAU28184	Novel human secret
8	201	100.0	264	AAU28184	Novel human secret
9	201	100.0	267	AAU28184	Novel human secret
10	201	100.0	267	AAU28184	Novel human secret
11	201	100.0	267	AAU28184	Novel human secret

Result No.	Score	Query Match	Length	ID	Description
12	201	100.0	267	AAU28184	Novel human secret
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15	201	100.0	267	AAU28184	Novel human secret
16	201	100.0	267	AAU28184	Novel human secret
17	201	100.0	267	AAU28184	Novel human secret
18	201	100.0	267	AAU28184	Novel human secret
19	201	100.0	267	AAU28184	Novel human secret
20	201	100.0	267	AAU28184	Novel human secret
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25	201	100.0	267	AAU28184	Novel human secret
26	201	100.0	267	AAU28184	Novel human secret
27	201	100.0	267	AAU28184	Novel human secret
28	201	100.0	267	AAU28184	Novel human secret
29	201	100.0	267	AAU28184	Novel human secret
30	201	100.0	267	AAU28184	Novel human secret
31	201	100.0	267	AAU28184	Novel human secret
32	201	100.0	267	AAU28184	Novel human secret
33	201	100.0	267	AAU28184	Novel human secret
34	201	100.0	267	AAU28184	Novel human secret
35	201	100.0	267	AAU28184	Novel human secret
36	201	100.0	267	AAU28184	Novel human secret
37	201	100.0	267	AAU28184	Novel human secret
38	201	100.0	267	AAU28184	Novel human secret
39	201	100.0	267	AAU28184	Novel human secret
40	201	100.0	267	AAU28184	Novel human secret
41	201	100.0	267	AAU28184	Novel human secret
42	201	100.0	267	AAU28184	Novel human secret
43	201	100.0	267	AAU28184	Novel human secret
44	201	100.0	267	AAU28184	Novel human secret
45	201	100.0	267	AAU28184	Novel human secret

ALIGNMENTS

RESULT 1

ID: AAU30468 standard; Protein; 119 AA.

XX AAU30468;

XX 18-DEC-2001 (first entry)

XX Novel human secreted protein #959.

XX Human: vaccination; gene therapy; nutritional supplement;

XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;

XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX Homo sapiens.

XX WO200179449-A2.

XX 25-OCT-2001.

XX 16-APR-2001: 2001WO-US08656.

XX 18-APR-2000: 2000US-0552929.

XX 26-JAN-2001: 2001US-0770160.

XX (HYSE-) HYSE INC.

XX Tang YT, Liu C, Dormanac RT;

XX WPI; 2001-611725/70.

XX Nucleic acids encoding a range of human polypeptides, useful in genetic

XX vaccination, testing and therapy -

PS Claim 20; Page 297; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for

CC determining the presence of or predisposition to a disease associated

CC with altered levels of polypeptide. The polypeptides are also useful for

CC identifying agents (agonists and antagonists) that bind to them. Cells

CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or

CC physiological interactions of the polypeptide. Vectors comprising

CC the nucleic acids encoding the polypeptides and cells genetically

CC engineered to express them are also useful for producing the proteins.

CC The proteins are useful in genetic vaccination, testing and

CC therapy, and can be used as nutritional supplements. They may be used to

CC increase stem cell proliferation; to regulate haematopoiesis; and in

CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;

CC immune suppression and/or stimulation; as anti-inflammatory agents; and

CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid

CC sequences of novel human secreted proteins of the invention.

XX

SO Sequence 119 AA;

Query Match 100.0%; Score 201; DB 22; Length 119;

Best Local Similarity 100.0%; Pred. No. 1.4e-18;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSVTSPFKRLREOLGPIVTOEFMDNLKETEGSLROEMSKD 39

DB 10 dsvtstfslkrlreqlgpyvtgfwdnlekeleglrqemskd 48

RESULT 2

AAU30267

ID AAU30267 standard; Protein; 120 AA.

XX

AC AAU30267;

XX

DT 18-DEC-2001 (first entry)

XX

DE Novel human secreted protein #758.

XX

KW Human; vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

XX

PN WO200179449-A2.

XX

PD 25-OCT-2001.

XX

PF 16-APR-2001; 2001WO-US08656.

XX

PR 18-APR-2000; 2000US-0552929.

XX

PR 26-JAN-2001; 2001US-0770160.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-611725/70.

XX

PT Nucleic acids encoding a range of human polypeptides, useful in genetic

XX vaccination, testing and therapy -

XX

PS Claim 20; Page 270; 765pp; English.

XX

CC The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for

CC determining the presence of or predisposition to a disease associated

CC with altered levels of polypeptide. The polypeptides are also useful for

CC identifying agents (agonists and antagonists) that bind to them. Cells

CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or

CC physiological interactions of the polypeptide. Vectors comprising

CC the nucleic acids encoding the polypeptides and cells genetically

CC engineered to express them are also useful for producing the proteins.

CC The proteins are useful in genetic vaccination, testing and

CC therapy, and can be used as nutritional supplements. They may be used to

CC increase stem cell proliferation; to regulate haematopoiesis; and in

CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;

CC immune suppression and/or stimulation; as anti-inflammatory agents; and

CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid

CC sequences of novel human secreted proteins of the invention.

XX

SO Sequence 120 AA;

Query Match 100.0%; Score 201; DB 22; Length 120;

Best Local Similarity 100.0%; Pred. No. 1.4e-18;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSVTSPFKRLREOLGPIVTOEFMDNLKETEGSLROEMSKD 39

DB 52 dsvtstfslkrlreqlgpyvtgfwdnlekeleglrqemskd 90

RESULT 3

AAU30469

ID AAU30469 standard; Protein; 120 AA.

XX

AC AAU30469;

XX

DT 18-DEC-2001 (first entry)

XX

DE Novel human secreted protein #960.

XX

KW Human; vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

XX

PN WO200179449-A2.

XX

PD 25-OCT-2001.

XX

PF 16-APR-2001; 2001WO-US08656.

XX

PR 18-APR-2000; 2000US-0552929.

XX

PR 26-JAN-2001; 2001US-0770160.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-611725/70.

XX

PT Nucleic acids encoding a range of human polypeptides, useful in genetic

XX vaccination, testing and therapy -

XX

PS Claim 20; Page 297; 765pp; English.

XX

CC The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for

CC determining the presence of or predisposition to a disease associated

CC with altered levels of polypeptide. The polypeptides are also useful for

CC identifying agents (agonists and antagonists) that bind to them. Cells

CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or

CC physiological interactions of the polypeptide. Vectors comprising

CC the nucleic acids encoding the polypeptides and cells genetically

CC engineered to express them are also useful for producing the proteins.

CC The proteins are useful in genetic vaccination, testing and

CC therapy, and can be used as nutritional supplements. They may be used to

CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX
SQ Sequence 120 AA;

Query Match 100.0%; Score 201; DB 22; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.4e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSVSTFSKLRQLGPTQGFMDNLEKETEGLRQEMSKD 39
Db 52 dsvstfsklrqlgptqgfmdnleketeglrqemskd 90
|||||
RESULT 4
AAU28372 standard; Protein; 166 AA.
XX
AC AAU28372;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secretory protein, Seq ID No 729.
XX
XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
KW angiotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
KW gut protection; lung; liver fibrosis; immune deficiency; infection;
KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
KW fertility; analgesic; pain; antigen.
XX
OS Homo sapiens.
XX
PN WO20016689-A2.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-US04942.
XX
PR 07-MAR-2000; 2000US-0519705.
PR 19-MAY-2000; 2000US-0574454.
PR 17-JUN-2000; 2000US-0596193.
PR 14-JUL-2000; 2000US-0616847.
PR 19-SEP-2000; 2000US-065363.
PR 20-OCT-2000; 2000US-0693267.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
XX
DR N-PSDB; AAS45272.
XX
XX WPI: 2001-589934/66.
XX
XX Novel polypeptides and nucleic acids obtained from cDNA libraries
XX prepared from various human tissues, for diagnosis and treatment of
XX cancer, neurological, inflammatory, and autoimmune disorders -
XX
PS Example 2; SEQ ID No 729; 107pp; English.
XX
XX The invention relates to novel isolated human secreted polypeptides (I)
XX and polynucleotides (II). (I) and (II) are useful for treating
XX inflammatory conditions such as arthritis, nephritis, Crohn's disease,
XX ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
XX involved in increasing haematopoiesis, stem cell survival, bone growth
XX and remodeling. (I), (II) and modulators of (II) are useful for

CC prophylaxis or treatment of one or more cancers. (II) is also useful for
CC creating transgenic animals useful for studying the in vivo activities of
CC the polypeptide as well as for studying modulators of the polypeptides.
CC (I) induces the proliferation of neural cells and regeneration of nerve
CC and brain tissue and is useful for the treatment of central and
CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
CC activity, regulation of haematopoiesis and is useful for treating myeloid
CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
CC tissue growth, and in tissue repair, healing of burns, incisions,
CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
CC disorders, or periodontal disease. Furthermore, (I) is also useful for
CC gut protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, various immune deficiencies and
CC disorders including severe combined immunodeficiency (SCID), bacterial or
CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
CC reactions and conditions, such as asthma or other respiratory problems.
CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
CC fertility, metabolism, catabolism, anabolism, storage or elimination of
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
CC analgesic effects or other pain reducing effects, immunoglobulin like
CC activity and can act as an antigen in a vaccine composition to raise an
CC immune response. AAU28020-AAU28395 represent novel human secreted protein
XX amino acid sequences of the invention.
XX
SQ Sequence 166 AA;

Query Match 100.0%; Score 201; DB 22; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSVSTFSKLRQLGPTQGFMDNLEKETEGLRQEMSKD 39
Db 61 dsvstfsklrqlgptqgfmdnleketeglrqemskd 99
|||||
RESULT 5
AAP81082
ID AAP81082 standard; protein; 243 AA.
XX
AC AAP81082;
XX
DT 14-JAN-1991 (first entry)
XX
DE Sequence of mature human apolipoprotein AI (apoAI).
XX
KW Atherosclerosis; therapy; cardiovascular disease.
XX
OS Homo sapiens.
XX
PN WO8803166-A.
XX
PD 05-MAY-1988.
XX
PF 21-OCT-1987; 87WO-EP00621.
XX
PR 23-OCT-1986; 86GB-0025435.
XX
XX (FARM) FARMITALIA C ERBA SPA.
XX
PI Lorenzetti R, Monaco L, Soria M, Palomba R, Isacchi A, Sarmientos P;
XX
DR WPI: 1988-133240/19.
XX
DR N-PSDB; AAN80243.
XX
XX Recombinant human apo:lipoprotein AI -
XX used to lower plasma cholesterol and/or tri glyceride levels and
XX to combat atherosclerosis and cardiovascular diseases

PS Disclosure: Fig 1; 51pp; English.

XX The protein comprising apo AI genetic variants may be used to lower

CC plasma cholesterol and/or triglyceride levels. They may also be used to

CC combat atherosclerosis and cardiovascular diseases such as coronary

CC heart disease. Pref'd. proteins are Met-apo AI, Met-apo AI-T6, Met-apo

CC AI-MI and Met-apo AI-T6/MI.

XX

SQ Sequence 243 AA;

Query Match 100.0%; Score 201; DB 9; Length 243;

Best Local Similarity 100.0%; Pred. No. 3.3e-18;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSVTSTFSKLRQGLPVTQEPFMDNLEKETEGLRQEMSKD 39

DB 51 dsvstfslkrlreqlpgvtqefwmdnleketeglrqemskd 89

RESULT 6

AAU28184

ID AAU28184 standard; Protein; 244 AA.

XX

AC AAU28184;

XX

DT 18-DEC-2001 (first entry)

XX

DE Novel human secretory protein, Seq ID No 353.

XX

XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;

KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;

KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;

KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;

KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;

KW gut protection; lung; liver fibrosis; immune deficiency; infection;

KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;

KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;

KW fertility; analgesic; pain; antigen.

OS Homo sapiens.

XX

XX WO20016689-A2.

PN

XX

PD 13-SEP-2001.

XX

XX

PF 05-MAR-2001; 2001WO-US04942.

XX

XX 07-MAR-2000; 2000US-0519705.

PR 19-MAY-2000; 2000US-0574454.

PR 17-JUN-2000; 2000US-0596193.

PR 14-JUL-2000; 2000US-0616847.

PR 19-SEP-2000; 2000US-065363.

PR 20-OCT-2000; 2000US-0693267.

XX

XX (HYSEQ-) HYSEQ INC.

PA

XX

XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

XX

DR WPI; 2001-589934/66.

XX

DR N-PSDB; AAS45084.

XX

XX Novel polypeptides and nucleic acids obtained from cDNA libraries

PT prepared from various human tissues, for diagnosis and treatment of

XX cancer, neurological, inflammatory, and autoimmune disorders -

XX

XX Example 5; SEQ ID No 353; 107pp; English.

XX

CC The invention relates to novel isolated human secreted polypeptides (I)

CC and polynucleotides (II). (I) and (II) are useful for treating

CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,

CC ischaemia, reperfusion injury, shock, sepsis, immune responses, and is

CC involved in increasing haematopoiesis, stem cell survival, bone growth

CC and remodeling. (I), (II) and modulators of (II) are useful for

CC prophylaxis or treatment of one or more cancers. (II) is also useful for

CC creating transgenic animals useful for studying the in vivo activities of

CC the polypeptide as well as for studying modulators of the polypeptides.

CC (I) induces the proliferation of neural cells and regeneration of nerve

CC and brain tissue and is useful for the treatment of central and

CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,

CC Parkinson's disease, Huntington's disease, and amyotrophic lateral

CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic

CC activity, regulation of haematopoiesis and is useful for treating myeloid

CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia

CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve

CC tissue growth, and in tissue repair, healing of burns, incisions,

CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative

CC disorders, or periodontal disease. Furthermore, (I) is also useful for

CC gut protection or regeneration and treatment of lung or liver fibrosis,

CC reperfusion injury in various tissues, various immune deficiencies and

CC disorders including severe combined immunodeficiency (SCID), bacterial or

CC fungal infections, autoimmune disorders e.g. multiple sclerosis,

CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic

CC reactions and conditions, such as asthma or other respiratory problems.

CC In addition, (I) affects biorythms or circadian cycles of rhythms,

CC fertility, metabolism, catabolism, anabolism, storage or elimination of

CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides

CC analgesic effects or other pain reducing effects, immunoglobulin like

CC activity and can act as an antigen in a vaccine composition to raise an

CC immune response. AAU28020-AAU28395 represent novel human secreted protein

CC amino acid sequences of the invention.

XX

SQ Sequence 244 AA;

Query Match 100.0%; Score 201; DB 22; Length 244;

Best Local Similarity 100.0%; Pred. No. 3.3e-18;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DSVTSTFSKLRQGLPVTQEPFMDNLEKETEGLRQEMSKD 39

DB 52 dsvstfslkrlreqlpgvtqefwmdnleketeglrqemskd 90

RESULT 7

AAR56863

ID AAR56863 standard; Protein; 264 AA.

XX

XX AAR56863;

AC

XX

DT 26-JAN-1995 (first entry)

XX

XX Apo-1ipoprotein AI-M.

DE

XX

XX Apo-1ipoprotein AI-M; Apo AI-M; Escherichia coli; plasmid pKF683;

KW vector; atherosclerosis; cardiovascular disease.

KW

XX

OS Homo sapiens.

XX

XX WO9413819-A.

PN

XX

XX 23-JUN-1994.

PD

XX

XX 09-DEC-1993; 93WO-SE01061.

PF

XX

XX 11-DEC-1992; 92SE-0003753.

PR

XX

XX (KABI) KABI PHARMACIA AB.

PA

XX

XX Abrahmsen L, Holmgren E, Kalderen C, Lake M, Mikaelsson A;

PI Sejlitz T;

XX

XX WPI; 1994-217892/26.

DR

XX

DR N-PSDB; AAO68357.

XX

PT Expression vector for extracellular prodn of apo-lipoprotein AI-M
PT in E. coli - includes inducible promoter and signal peptide
PT sequences providing improved yield, useful in treating
PT atherosclerosis and cardiovascular disease.
XX
PS Disclosure; Fig. 3; 33pp; English.
XX
CC Plasmid pKP683 encodes human apo-lipoprotein AI-M in E. coli. The
CC NotI-HindIII segment of pKP683 and the deduced amino acid sequence
CC of the translated Apo AI-M protein were determined. The plasmid
CC provides high yields of extracellular Apo AI-M.
XX
SQ Sequence 264 AA;

Query Match 100.0%; Score 201; DB 15; Length 264;
Best Local Similarity 100.0%; Pred. No. 3,6e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRQLGPTQEFMDNLEKETEGLRQEMSKD 39
Db 72 dsvtstfsklrqlgptvqetfwdnleketeglrqemskd 110

RESULT 8

AAR56864
ID AAR56864 standard; Protein; 264 AA.

XX AAR56864;

XX 26-JAN-1995 (first entry)

DE Apo-lipoprotein AI-M.

KM Apo-lipoprotein AI-M; Apo AI-M; Escherichia coli; plasmid pKP764;
KM vector; atherosclerosis; cardiovascular disease.

OS Homo sapiens.

XX W09413819-A.

XX 23-JUN-1994.

XX 09-DEC-1993; 93WO-SE01061.

XX 11-DEC-1992; 92SE-0003753.

XX (KABI) KABI PHARMACIA AB.

PI Abrahmsen L, Holmgren E, Kalderen C, Lake M, Mikaelsson A;
PI Sejlitz T;

DR WPI; 1994-217892/26.
DR N-PSDB; AAQ68358.

XX Expression vector for extracellular prodn of apo-lipoprotein AI-M
PT in E. coli - includes inducible promoter and signal peptide
PT sequences providing improved yield, useful in treating
PT atherosclerosis and cardiovascular disease.

XX Disclosure; Fig. 4; 33pp; English.

XX Plasmid pKP764 encodes human apo-lipoprotein AI-M in E. coli. The
CC NotI-HindIII segment of pKP764 and the deduced amino acid sequence
CC of the translated Apo AI-M protein were determined. The plasmid
CC provides high yields of extracellular Apo AI-M.

XX Sequence 264 AA;

Query Match 100.0%; Score 201; DB 15; Length 264;
Best Local Similarity 100.0%; Pred. No. 3,6e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRQLGPTQEFMDNLEKETEGLRQEMSKD 39
Db 72 dsvtstfsklrqlgptvqetfwdnleketeglrqemskd 110

RESULT 9

AAP61079
ID AAP61079 standard; Protein; 267 AA.

XX AAP61079;

XX 07-OCT-1991 (first entry)

DE Assumed human apolipoprotein A-1 derivative gene product.

XX Hyperlipaemia; arteriosclerosis.

OS Homo sapiens.

XX JP61096998-A.

XX 15-MAY-1986.

XX 16-OCT-1984; 84JP-0216988.

XX 16-OCT-1984; 84JP-0216988.

XX (MITU) MITSUBISHI CHEM IND KK.

XX WPI; 1986-165025/26.

XX N-PSDB; AAN60886.

PT Human apo-lipoprotein A-1 (deriv.) prepn. - by providing DNA
PT fragment in cloning site downstream of expression vector promoter
PT and introducing into host microorganism.

XX Disclosure; Fig 2; 9pp; Japanese.

XX The human apolipoprotein may be produced by a suitable transformed
CC host, it is effective in treating hyperlipaemia and arteriosclerosis.

SQ Sequence 267 AA;

Query Match 100.0%; Score 201; DB 7; Length 267;
Best Local Similarity 100.0%; Pred. No. 3,6e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRQLGPTQEFMDNLEKETEGLRQEMSKD 39
Db 75 dsvtstfsklrqlgptvqetfwdnleketeglrqemskd 113

RESULT 10

AAP82128
ID AAP82128 standard; protein; 267 AA.

XX AAP82128;

XX 24-OCT-1990 (first entry)

DE Entire human preproapoprotein AI.

XX human preproapoprotein AI; high density lipoprotein deficiency; ss.

XX synthetic.

XX Key Location/Qualifiers

FT Peptide 1..18

FT Peptide 19..24

FT Peptide /label=propeptide

FT Protein 25.267
 XX /label=mature apoprotein
 XX EP293357-A.
 XX 30-NOV-1988.
 PD 24-MAY-1988; 88EP-0870095.
 XX 28-MAY-1987; 87GB-0012540.
 XX (UNIO) UCB SA.
 PA Bollen A, Gobert J, Wulfert E;
 PI WPI; 1988-339891/48.
 XX N-PSDB; AAN82064.
 DR N-PSDB; AAN82064.
 XX
 PT New DNA encoding human preproapoprotein A1 -
 PT modified to eliminate hairpin structures
 XX
 PS Disclosure; ; P; French.
 XX
 CC The cDNA 878bp fragment encoding preproapoprotein A1 was detected
 CC in clone pUBI609 derived from human liver cells.
 CC See also AAN81258.
 CC
 XX Sequence 267 AA;
 SQ

Query Match 100.0%; Score 201; DB 9; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3.6e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRQLGPVTOEFMDLKEKTEGLRQMSKD 39
 DB 75 dsvstfskrlreqlgpyvtqetfwdnleketeglrqmskd 113

RESULT 11
 AAR34032
 ID AAR34032 standard; Protein; 267 AA.
 XX
 AC AAR34032;
 XX
 DT 13-AUG-1993 (first entry)
 XX
 DE Sequence of apo A1.
 XX
 KW Lipoprotein; apoprotein; B-100; A-I; LDL; HDL; assay.
 XX
 OS Homo sapiens.
 XX
 PN W09307165-A.
 PD 15-APR-1993.
 XX
 PF 09-OCT-1992; 92WO-US08634.
 XX
 PR 09-OCT-1991; 91US-0774633.
 PR 08-OCT-1992; 92US-0555555.
 PR 28-JUN-1992; 92US-0901706.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Curtiss LK, Koduri KR, Smith RS, Witztum JL, Young SG;
 XX
 DR WPI; 1993-134378/16.
 DR N-PSDB; AAQ40030.
 XX
 PT Polypeptide mimic of native apo B-100 and native apo A-I - useful
 PT in assays for LDL and HDL in plasma samples
 XX

PS Claim 19; Pages 105-106; 137pp; English.
 XX
 CC The inventors claim a portion of the polypeptide contg. apo B-100
 CC that immunoreacts with antibodies secreted by the hybridoma MB47
 CC having ATCC Accession No. 8746. Polypeptides specifically claimed
 CC include residues 217-297, 216-310, 216-331, 216-352, 216-377, 1-377,
 CC 205-297, 173-297, 140-297. DNA sequences encoding the polypeptides
 CC are also claimed. Also claimed are a fusion polypeptide that
 CC contains: (a) a first amino acid residue sequence up to 250 residues
 CC in length that includes residues 120-135 of apo A-I. (b) a second
 CC amino acid residue sequence up to 375 residues in length that
 CC includes residues 217-297 of apo B-100 and DNA encoding it.
 CC
 XX Sequence 267 AA;
 SQ

Query Match 100.0%; Score 201; DB 14; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3.6e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRQLGPVTOEFMDLKEKTEGLRQMSKD 39
 DB 75 dsvstfskrlreqlgpyvtqetfwdnleketeglrqmskd 113

RESULT 12
 AAR72705
 ID AAR72705 standard; Protein; 267 AA.
 XX
 AC AAR72705;
 XX
 DT 31-OCT-1995 (first entry)
 XX
 DE Human apo A-I including signal and propeptide sequences.
 XX
 KW Apo A-I; LDL cholesterol; low density lipoprotein; lipid.
 XX
 OS Homo sapiens.
 XX

Key	Location/Qualifiers
FT Peptide	1..18
FT Peptide	/label= presignal
FT Peptide	19..24
FT Peptide	/label= propeptide
FT Peptide	120..135
FT Peptide	/label= claimed
FT Peptide	/note= "as part of fusion polypeptide"
FT Peptide	19..240
FT Peptide	/label= claimed
FT Peptide	/note= "as part of fusion polypeptide"

US5408038-A.
 18-APR-1995.
 PD 09-OCT-1991; 91US-0774633.
 XX
 PR 09-OCT-1991; 91US-0774633.
 PR 18-JUN-1992; 92US-0901706.
 PR 08-OCT-1992; 92US-0959946.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Curtiss LK, Koduri KR, Smith RS, Witztum JL, Young SG;
 XX
 DR WPI; 1995-161146/21.
 DR N-PSDB; AAQ89634.
 XX
 PT New apo:lipoprotein B-100 peptide(s) and fusion peptide(s) - used
 PT in assay systems for detecting LDL and HDL cholesterol levels in
 PT body fluids.
 XX
 PS Claim 10; Fig 2; 41pp; English.

XX
+
CC AAB89634 and AAR72705 depict the AA sequence of human apo A-I and its
CC corresp. cDNA, including prestigial residues and propeptide
CC residues, according to Sellhammer et al., DNA 3(4):309 (1984).
CC A dispersible apo A-I/B-100 fusion polypeptide is claimed which
CC contains a first AA sequence of apo A-I and that includes at
CC least AA sequence positions 120-135 (see AAR72606) and which reacts
CC with pan anti-apo AI antibodies such as: AI-4 ATCC HB8744; AI-7
CC ATCC HB 8745; AI-9 ATCC HB 8741; AI-10 ATCC HB 9200; AI-11 ATCC
CC HB 9201; AI-12 ATCC HB 9202; AI-13 ATCC HB 9203; AI-14 ATCC HB
CC 9204; AI-18 ATCC HB 9507.
XX
SQ Sequence 267 AA;

Query Match	100.0%	Score 201	DB 16	Length 267
Best Local Similarity	100.0%	Pred. No. 3	6e-18	
Matches 39	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	DATSTSPFKIREGLGAVTQEFMDNLKETEKGIRQMSKD	39	
Db	75	dsvltsfiskireglgvvtqeiwdnleketeqlrsmxsd	113	

RESULT	13
AAW08602	
ID	AAW08602 standard; Protein; 267 AA

AC AAW08602;

DT 04-SEP-1997 (first entry)

Human apolipoprotein A-1 variant "Paris" protein sequence.

KM Human; apolipoprotein A-1; variant; mutation; serum lipid; cholesterol;
KM high density lipoprotein; triglyceride; symptom; cardiovascular disease
KM atherosclerosis; restenosis; myocardial infarct; angina; death; stroke;
KM cardiac decompensation; metabolic deficit.

OS Homo sapiens.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
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62	62	62
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73	73	73
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85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

FT	/note= "prepro peptide"
FT	172..178
Region	

FT	/note=	"this sequence which contains the mutated amino acid residue is claimed - claim 2"
FT		
FT	Misc-difference	175
FT	/note=	"changed from Arg residue in wild type protein, due to a C to T transition mutation"
FT		

PN WO9637608-A1.

PD 28-NOV-1996

20-MAY-1996; 96WO-FR00747.

22-MAY-1995; 95FR-0006061.

PA (INSP) INST PASTEUR LILLE.

(UNIV CURIE PARIS VI P & M.)

PI Benoit P, Bruckert E, Denefle P, Duverger N, Fruchart J,
Two C

XX
DB WBT: 1987-021218 /03

DK N-PSDB; AAT43691.
YY

PT New variant of human apoA-1 with Cys at position 151 - has
PT anti-atherogenic activity for treatment and prevention of
PT cardiovascular disease

PS Claim 2; Page -; 58pp; French.
vz

CC This is the amino acid sequence of a human apolipoprotein A-1 variant
CC designated the "Paris" variant which has a Cys replacing the Arg residue
CC at position 151. The substitution is generated by a mutation of
CC the C nucleotide at position 523 in the wild type gene to a T residue,
CC changing the encoded residue from an Arg to a Cys. The gene was isolated
CC from a patient with an unusual pattern of serum lipids i.e. low levels of
CC apoA-1 and high density lipoprotein (HDL)-cholesterol and high
CC triglycerides, but showing symptoms of atherosclerosis. The new variant
CC protein has anti-atherogenic activity so is useful for treatment and
CC prevention of cardiovascular diseases such as atherosclerosis,
CC restenosis, myocardial infarct, angina, sudden death, stroke and cardiac
CC decompensation, or more generally any condition involving genetic or
CC metabolic deficit of apoA-1.
CC Note: this sequence is not given in the specification but is generated
CC from the wild type apoA-1 gene disclosed in the specification and has
CC the appropriate amino acid changed.

SQ Sequence 267 AA;

	Query March	100.0%;	Score 201;	DB 18;	Length 267;
	Best Local Similarity	100.0%;	Pred. No. 3	6e-18;	
	Matches 39;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1 DSVYSTFSKLRDQLGPTVDENMDLKEETGLRQMSKD	39			
Db	75 dsvytsfkskrrqglgptvtefdwnlekeetglrqsmskd	113			

RESULT 14

ID	AA	Y18675	standard; protein; 267 AA.
1	MA	1	MA
2	MA	2	MA
3	MA	3	MA
4	MA	4	MA
5	MA	5	MA
6	MA	6	MA
7	MA	7	MA
8	MA	8	MA
9	MA	9	MA
10	MA	10	MA
11	MA	11	MA
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17	MA	17	MA
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101	MA	101	MA
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103	MA	103	MA
104	MA	104	MA
105	MA	105	MA
106	MA	106	MA
107	MA	107	MA
108	MA	108	MA
109	MA	109	MA

AC AAY18675;

DT 09-JUL-1999 (first entry)

Human apolipoprotein AI protein sequence.

KM Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder;
KM ApoA-I; cardiovascular disease; atherosclerosis; restenosis; LCAT;
KM hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase
vz

OS Homo sapiens

PN W09916409-A2

PD 08-APR-1999.

PF 28-SEP-1998; 98WO-US20329.

PR 29-SEP-1997; 97US-0940136.

PA (BUTT/) BUTTNER K.

PA (DASS/) DASSEUX J.

PA (METZ/) METZ G.

XX	Buttner K	Corr
PT		

Pl Sekul R,
xy

DR WP1: 1999-254921/21
DR N-PCNP: AY55071

XX
PT

Nucleic acid conc

XX Example; Fig 1, 232pp; English.

CC The present invention describes a nucleic acid (A) encoding an

CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,
 CC which forms an amphipathic alpha-helix in presence of lipids. (A),
 CC optionally as a complex with lipids, and host cells that contain (A),
 CC are useful for gene therapy, or prevention, of diseases associated with
 CC dyslipidemia, specifically hypercholesterolemia, cardiovascular disease,
 CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I
 CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat
 CC endotoxemia (septic shock). Host cells containing (A) can be used
 CC to study the role of apoA-I in lipid metabolism; (B) can be used
 CC diagnostically, e.g., to measure serum HDL (particularly its
 CC subpopulation involved in retrograde cholesterol transport) and for
 CC imaging the circulatory system or HDL accumulations at fatty streaks.
 CC The present sequence represents human apoA-I.
 CC
 CC Sequence 267 AA:
 SO

Query Match 100.0%; Score 201; DB 20; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3.6e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRQLGPVTOEFMDNLEKRTGLRQMSKD 39
 ||||||||||||||||||||||||||||||||||||
 Db 75 dsvstfsklrqlgpvtqetwlnleketglrqmskd 113

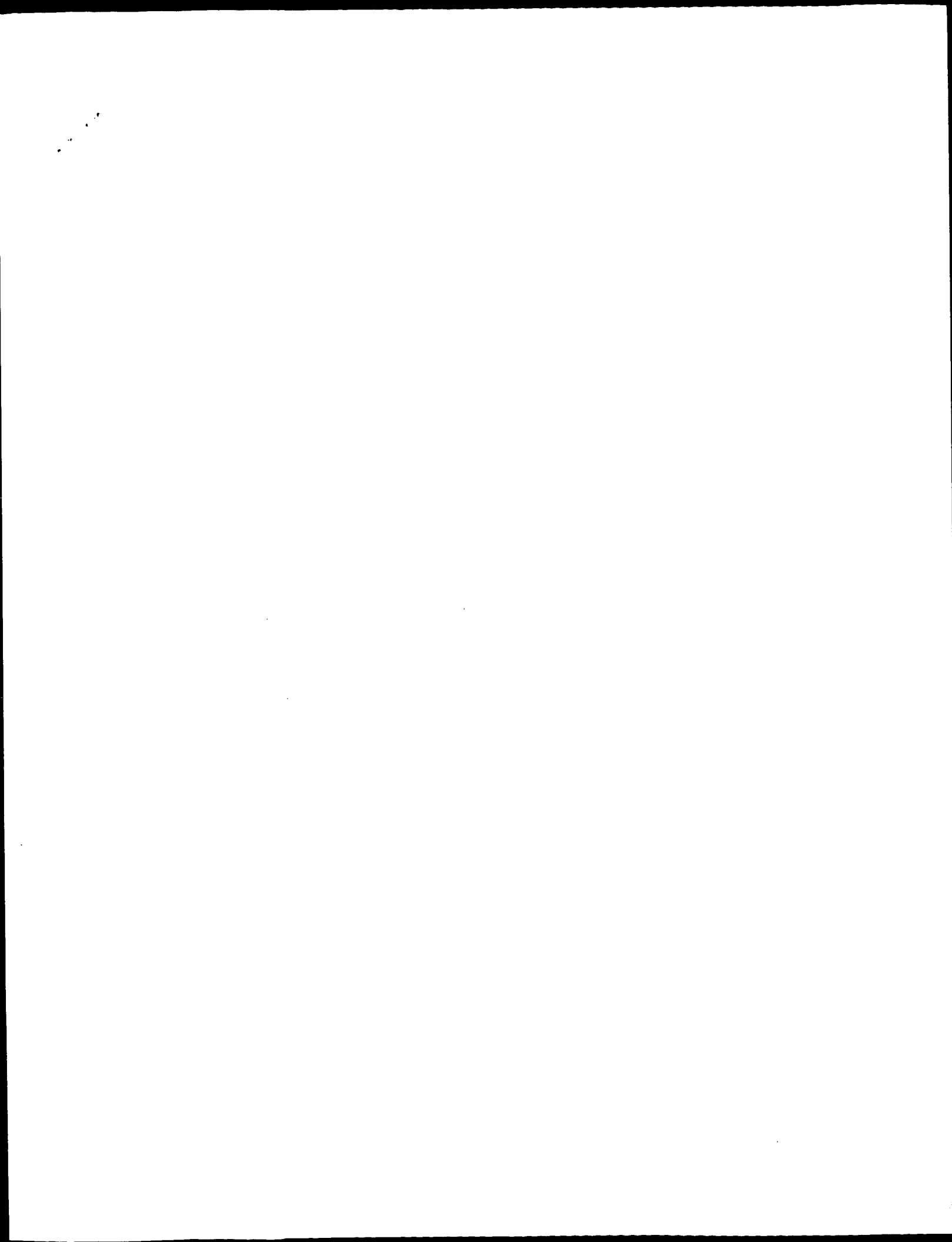
RESULT 15
 AAB47620
 ID AAB47620 standard; Protein: 267 AA.
 XX
 AC AAB47620;
 XX
 DT 21-JAN-2002 (first entry)
 XX
 DE Full length Apo-A1.
 XX
 XX Apolipoprotein; Apo-A1; Apo-A-I fragment T-cell activation inhibitor;
 KW AFTI; monocyte; IL-1; interleukin 1; TNF; tumor necrosis factor;
 KW acute pancreatitis; Alzheimer's disease; asthma; cancer; fever;
 KW inflammatory bowel disease; ischemia; multiple sclerosis; osteoporosis;
 KW Parkinson's disease; psoriasis; probe.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Binding-site 44..65
 FT /label= Helical lipid binding domain
 FT Binding-site 220..241
 FT /label= Helical lipid binding domain
 FT Domain 74..111
 FT /note= "Involved in lipoprotein-mediated cholesterol
 FT efflux from monocytes"
 FT Binding-site 149..219
 FT /label= Receptor binding domain
 FT Domain 99..120
 FT /label= Major antigenic epitope domain
 FT Domain 99..143
 FT /label= Hinged domain
 FT Domain 66..120
 FT /label= phylogenetically conserved domain
 FT Domain 90..111
 FT /note= "Involved in lectin-cholesterol acyltransferase
 FT activity"
 FT Domain 44..65
 FT /label= Amphipathic helix
 FT Domain 66..98
 FT /label= Amphipathic helix
 FT Domain 99..120
 FT /label= Amphipathic helix
 FT Domain 121..142
 FT /label= Amphipathic helix
 FT Domain 143..164
 FT /label= Amphipathic helix

FT Domain 165..208
 FT /label= Amphipathic helix
 FT Domain 209..219
 FT /label= Amphipathic helix
 FT Domain 220..241
 FT /label= Amphipathic helix
 FT Peptide 25..194
 FT /label= AFTI
 FT /note= "18 KD N-terminal fragment"
 FT Peptide 25..144
 FT /label= AFTI
 FT /note= "13 KD N-terminal fragment"
 FT Peptide 156..267
 FT /label= AFTI
 FT /note= "13 KD C-terminal fragment"
 XX
 PN WO200168852-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 13-MAR-2001; 2001WO-US07826.
 XX
 PR 13-MAR-2000; 2000US-189008P.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Edwards CK, Burger D, Dayer J, Kohno T;
 XX
 DR WPI: 2001-596908/67.
 DR N-PSTDB; AAH43623.
 XX
 XX Apo-A-I fragment T-cell activation inhibitor (AFTI) polynucleotides,
 PT useful for treating, diagnosing, ameliorating diseases associated with
 PT IL-1 and/or TNF activity, e.g. acute pancreatitis, Alzheimer's disease
 PT and asthma -
 XX
 PS Claim 1; Fig 1A; 132pp; English.
 XX
 CC This sequence shows full length apolipoprotein (Apo-A1). Fragments
 CC of Apo-A1 may be used as Apo-A-I fragment T-cell activation inhibitors
 CC (AFTI). These fragments are selected from an 18 KD N-terminal fragment
 CC (amino acids 25-194), a 13 KD N-terminal fragment (amino acids 25-144)
 CC and a 13 KD C-terminal fragment (amino acids 156-267). The AFTI
 CC polypeptides and polynucleotides are useful for regulating T-cell
 CC mediated activation of monocytes and for treating, diagnosing,
 CC ameliorating diseases associated with IL-1 and/or TNF activity.
 CC The diseases are acute pancreatitis, Alzheimer's disease, asthma,
 CC cancer, fever, inflammatory bowel disease, ischemia, multiple
 CC sclerosis, osteoporosis, Parkinson's disease or psoriasis. Numerous
 CC examples of other diseases are given in the specification.
 CC The AFTI nucleic acids are useful as hybridization probes in diagnostic
 CC assays to test for the presence of an AFTI or Apo-A-I DNA in mammalian
 CC tissue or bodily fluid samples.
 CC
 XX
 SO Sequence 267 AA:

Query Match 100.0%; Score 201; DB 22; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3.6e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRQLGPVTOEFMDNLEKRTGLRQMSKD 39
 ||||||||||||||||||||||||||||||||||||
 Db 75 dsvstfsklrqlgpvtqetwlnleketglrqmskd 113

Search completed: September 22, 2002, 12:05:16
 Job time: 291 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2002, 12:02:53 ; Search time 51.49 seconds
(without alignments)
18.501 Million cell updates/sec

Title: US-09-803-918a-2_COPY_75_113

Perfect score: 201
Sequence: 1 DSVTSFSLRRLQPGVQEWDLKEKTEGLRQEMSKD 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/2/1aa/5a_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5b_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6a_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6b_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201	100.0	200	4	US-08-952-796-15
2	201	100.0	264	1	US-08-448-606-6
3	201	100.0	267	1	US-07-959-946-3
4	201	100.0	267	1	US-08-333-577-3
5	201	100.0	267	4	US-08-952-796-2
6	201	100.0	267	5	PCT-US92-08634-3
7	59	29.4	317	4	US-08-949-155-6
8	56	27.9	22	3	US-08-940-095-73
9	56	27.9	22	3	US-08-940-093-73
10	56	27.9	22	3	US-08-940-096-73
11	56	27.9	22	4	US-09-465-719-73
12	56	27.9	22	4	US-09-453-605-73
13	54.5	27.1	348	1	US-08-229-781-50
14	54.5	27.1	348	1	US-08-630-918-50
15	54.5	27.1	348	4	US-09-004-422-50
16	54.5	27.1	474	3	US-09-022-699-2
17	51.5	25.6	593	1	US-08-018-129-5
18	51.5	25.6	593	2	US-08-448-250-5
19	51.5	25.6	593	2	US-08-448-250-5
20	51	25.4	22	1	US-07-928-930A-8
21	51	25.4	22	1	US-08-288-568-8
22	51	25.4	22	1	US-08-487-461-8
23	51	25.4	22	1	US-08-432-691-8
24	51	25.4	22	1	US-08-487-459-8
25	51	25.4	110	1	US-07-849-389-7
26	51	25.4	220	1	US-08-726-306A-29
27	51	25.4	317	1	US-07-709-949-2

28	50.5	25.1	713	1	US-08-190-802A-63	Sequence 63, Appl
29	50.5	25.1	713	4	US-08-477-346-63	Sequence 63, Appl
30	50.5	25.1	713	4	US-08-473-089-63	Sequence 63, Appl
31	49.5	24.6	366	1	US-08-004-492-8	Sequence 8, Appl
32	49	24.4	191	4	US-08-842-306B-6	Sequence 6, Appl
33	49	24.4	191	4	US-08-838-973B-6	Sequence 6, Appl
34	49	24.4	599	2	US-08-846-526-11	Sequence 11, Appl
35	49	24.4	599	4	US-09-172-339-2	Sequence 2, Appl
36	48	23.9	22	3	US-08-940-095-75	Sequence 75, Appl
37	48	23.9	22	3	US-08-940-093-75	Sequence 75, Appl
38	48	23.9	22	3	US-08-940-096-75	Sequence 75, Appl
39	48	23.9	22	4	US-09-465-719-75	Sequence 75, Appl
40	48	23.9	22	4	US-09-453-605-75	Sequence 75, Appl
41	48	23.9	120	2	US-08-917-456-4	Sequence 4, Appl
42	48	23.9	120	4	US-09-229-804-2	Sequence 2, Appl
43	48	23.9	158	2	US-08-917-456-2	Sequence 2, Appl
44	48	23.9	158	4	US-09-229-804-2	Sequence 2, Appl
45	48	23.9	203	1	US-08-216-593-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-952-796-15
Sequence 15, Application US/08952796
Patent No. 6258596
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: BRUCKERT, Eric
APPLICANT: DENEPIE, Patricia
APPLICANT: DUBERGER, Nicolas
APPLICANT: FRUCHART, Jean-Charles
APPLICANT: LUC, Gerard
APPLICANT: TURPIN, Gerard
APPLICANT: ASSMANN, Gerald
APPLICANT: FONKE, Harald
TITLE OF INVENTION: NOVEL VARIANTS OF APOLOPROTEIN A-1
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcoia Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,796
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/06061
FILING DATE: 22-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/00747
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fehner Esq., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: ST95031-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-952-796-15

Query Match 100.0%; Score 201; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.4e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRQLGPGVTOEFMDNLEKETEGLRQEMSKD 39
|||||
DB 8 DSVTSTFSKLRQLGPGVTOEFMDNLEKETEGLRQEMSKD 46

RESULT 2

US-08-448-606-6
Sequence 6, Application US/08448606
Patent No. 5721114
GENERAL INFORMATION:
APPLICANT: Abrahams n, Lars
APPLICANT: Holmgren, Erik
APPLICANT: Kalder n, Christina
APPLICANT: Lake, Mats
APPLICANT: Mikaelsson, sa
APPLICANT: Sejlitz, Torsten
TITLE OF INVENTION: Expression System For Producing
TITLE OF INVENTION: Apolipoprotein AI-M
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pollock, Vande Sande & Priddy
STREET: 1990 W Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,606
FILING DATE: 25-AUG-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE93/01061
FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9203753-0
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Amerinick, Burton A.
REGISTRATION NUMBER: 24,852
REFERENCE/DOCKET NUMBER: 0151/00121
TELEPHONE: (202) 331-7111
TELEFAX: (202) 293-6229
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-448-606-6

Query Match 100.0%; Score 201; DB 1; Length 264;
Best Local Similarity 100.0%; Pred. No. 2e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRQLGPGVTOEFMDNLEKETEGLRQEMSKD 39
|||||
DB 72 DSVTSTFSKLRQLGPGVTOEFMDNLEKETEGLRQEMSKD 110

RESULT 3
US-07-959-946-3
Sequence 3, Application US/07959946
Patent No. 5408038
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Witzlum, Joseph U.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
ADDRESSEE: Milnamow, Ltd.
STREET: 180 No. 5408038th Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,946
FILING DATE: 19921008
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELEPHONE: (312) 616-5400
TELEFAX: (312) 616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-959-946-3

Query Match 100.0%; Score 201; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 2e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRQLGPGVTOEFMDNLEKETEGLRQEMSKD 39
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DB 75 DSVTSTFSKLRQLGPGVTOEFMDNLEKETEGLRQEMSKD 113

RESULT 4
US-08-333-577-3
Sequence 3, Application US/08333577
Patent No. 5786206
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Witzlum, Joseph U.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:

ADDRESS: Dressler, Goldsmith, Shore, Sutker &
ADDRESSEE: Milanow, Ltd.
STREET: 180 No. 5786206th Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,577
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: SCRF 234.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-333-577-3

Query Match 100.0%; Score 201; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 2e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRQLGPTQGFMDNLEKETEGSLRQEMSKD 39
DB 75 DSVTSTFSKLRQLGPTQGFMDNLEKETEGSLRQEMSKD 113

RESULT 5
US-08-952-796-2
Sequence 2, Application US/08952796
Patent No. 6258596
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: BRUCKERT, Eric
APPLICANT: DENEPIE, Patrice
APPLICANT: DUBERGER, Nicolas
APPLICANT: FRUCHART, Jean-Charles
APPLICANT: LOC, Gerold
APPLICANT: TURPIN, Gerold
APPLICANT: ASSMANN, Gerold
APPLICANT: FUNKE, Harald
TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPOPROTEIN A-I
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,796
FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/06061
FILING DATE: 22-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/00747
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fehner Esq., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: ST95031-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-952-796-2

Query Match 100.0%; Score 201; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 2e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFSKLRQLGPTQGFMDNLEKETEGSLRQEMSKD 39
DB 75 DSVTSTFSKLRQLGPTQGFMDNLEKETEGSLRQEMSKD 113

RESULT 6
PCT-US92-08634-3
Sequence 3, Application PC/TUS9208634
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Wiltz, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
ADDRESSEE: Milanow, Ltd.
STREET: 180 North Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08634
FILING DATE: 19921009
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids

TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-08634-3

Query Match 100.0%; Score 201; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 2e-19;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTSTFKRLQGLPVTOEFMDNLEKETEGRLROEMSKD 39
Db 75 DSVTSTFKRLQGLPVTOEFMDNLEKETEGRLROEMSKD 113

RESULT 7
US-08-949-155-6
Sequence 6, Application US/08949155
Patent No. 6271436
GENERAL INFORMATION:
APPLICANT: Piedrahita, Jorge A
APPLICANT: Bazer, Fuller W
TITLE OF INVENTION: Compositions and Methods for the
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE AND DURKEE
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,155
FILING DATE: Concurrently Herewith
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,338
FILING DATE: 11-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,094
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-949-155-6

Query Match 29.4%; Score 59; DB 4; Length 317;
Best Local Similarity 41.9%; Pred. No. 2.1;
Matches 13; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 9 KLRQLGPNVTOEFMDNLEKETEGRLROEMSKD 39
Db 94 ELERQLGPNVTOEFMDNLEKETEGRLROEMSKD 124

RESULT 8

US-08-940-095-73
Sequence 73, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther

TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-4935
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6004925e
FEATURE:
NAME/KEY: other
LOCATION: 13
OTHER INFORMATION: Xaa = Alb

US-08-940-095-73

Query Match 27.9%; Score 56; DB 3; Length 22;
Best Local Similarity 42.9%; Pred. No. 0.26;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 16 PVTOEFMDNLEKETEGRLROEM 36
Db 1 PVTOEFMDNLEKETEGRLROEM 21

RESULT 9
US-08-940-093-73
Sequence 73, Application US/08940093
Patent No. 6037323
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther

US-08-940-093-73

```

; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6037323e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
; OTHER INFORMATION: Xaa = Alb
;
US-08-940-093-73

Query Match 27.9%; Score 56; DB 3; Length 22;
Best Local Similarity 42.9%; Pred. No. 0.26;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 16 PVTQEFWDNLEKETEGRLQEM 36
DB 1 PVLDFEWEKINEXLEALKOKL 21

RESULT 10
US-08-940-096-73
; Sequence 73, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811

```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046166e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 13
; OTHER INFORMATION: Xaa = Alb
;
US-08-940-096-73

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Query Match 27.9%; Score 56; DB 3; Length 22;
Best Local Similarity 42.9%; Pred. No. 0.26;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 16 PVTQEFWDNLEKETEGRLQEM 36
DB 1 PVLDFEWEKINEXLEALKOKL 21

RESULT 11
US-09-465-719-73
; Sequence 73, Application US/09465719
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/465,719
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

```


INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-229-781-50

Query Match 27.1%; Score 54.5; DB 1; Length 348;
Best Local Similarity 38.9%; Pred. No. 9.4;
Matches 14; Conservative 5; Mismatches 16; Indels 1; Gaps 1;
QY 1 DSVTSTFSLKRLQGLPYTOEFMDNLEKETEGLRQEM 36
DB 176 NKVNSVIEKINTQPEAVGKEF-GNLEKRLNLNKKM 210

RESULT 14
US-08-630-918-50
Sequence 50, Application US/08630918
Patent No. 5631350
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,918
FILING DATE: April 5, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-630-918-50

Query Match 27.1%; Score 54.5; DB 1; Length 348;
Best Local Similarity 38.9%; Pred. No. 9.4;
Matches 14; Conservative 5; Mismatches 16; Indels 1; Gaps 1;
QY 1 DSVTSTFSLKRLQGLPYTOEFMDNLEKETEGLRQEM 36
DB 176 NKVNSVIEKINTQPEAVGKEF-GNLEKRLNLNKKM 210

RESULT 15
US-09-004-422-50
Sequence 50, Application US/09004422
Patent No. 6337070
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,422
FILING DATE: January 8, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-09-004-422-50

Query Match 27.1%, Score 54.5; DB 4; Length 348;
Best Local Similarity 38.9%, Pred. No. 9.4;
Matches 14; Conservative 5; Mismatches 16; Indels 1; Gaps 1;
QY 1 DSVTSTFSKLRQGLGPTVQGFMDNLKETEGLRQEM 36
: | | : | | : | | | | | | | : : :
Db 176 NKVNSVIEKINTQFEAVGKEF-GNLEKRLNLINKM 210

Search completed: September 22, 2002, 12:02:54
Job time: 254 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:06:29 ; Search time 66.91 Seconds

(without alignments)
160.843 Million cell updates/sec

Title: US-09-803-918a-2_COPY_156_267

Perfect score: 556

Sequence: 1 QKHLQGLKSLPGLGEMRDR.....SRKVSFLSALBEYTKKLNTQ 112

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR-71:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	100.0	267	1	apoliipoprotein A-I
2	538	96.8	267	1	apoliipoprotein A-I
3	538	96.8	267	2	apoliipoprotein A-I
4	449	80.8	266	1	apoliipoprotein A-I
5	430	77.3	266	1	apoliipoprotein A-I
6	425	76.4	241	2	apoliipoprotein A-I
7	418.5	75.3	265	1	apoliipoprotein A-I
8	414.5	74.6	265	2	apoliipoprotein A-I
9	408.5	73.5	265	2	apoliipoprotein A-I
10	403.5	72.6	265	2	apoliipoprotein A-I
11	400.5	72.0	164	2	apoliipoprotein A-I
12	400.5	72.0	231	2	apoliipoprotein A-I
13	400.5	72.0	264	2	apoliipoprotein A-I
14	296	53.2	264	2	apoliipoprotein A-I
15	290	52.2	262	2	apoliipoprotein A-I
16	273	49.1	259	2	apoliipoprotein A-I
17	272	48.9	246	2	apoliipoprotein A-I
18	255	45.9	264	1	apoliipoprotein A-I
19	237	42.6	264	1	apoliipoprotein A-I
20	125	22.5	396	1	apoliipoprotein A-I
21	119.5	21.5	429	1	apoliipoprotein A-I
22	113.5	20.4	401	2	apoliipoprotein A-I
23	111	20.0	391	1	apoliipoprotein A-I
24	111	20.0	1547	2	apoliipoprotein A-I
25	109.5	19.7	258	2	apoliipoprotein A-I
26	102.5	18.4	391	2	apoliipoprotein A-I
27	102.5	18.4	395	2	apoliipoprotein A-I
28	102.5	18.4	399	2	apoliipoprotein A-I
29	100.5	18.1	394	2	apoliipoprotein A-I

ALIGNMENTS

RESULT 1

LEPHDAI

apoliipoprotein A-I precursor [validated] - human

N:Alternate names: apoA-I-2; apoA-I-4; preproapoA-I; prostacyclin stabilizing factor

C:Species: Homo sapiens (man)

C>Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 08-Dec-2000

C:Accession: A90947; B90947; S02373; A93465; A21147; A93519; B93519; A93472; A94010; 6197

R:Seilhamer, J.J.; Protter, A.A.; Frossard, P.; Levy-Wilson, B.

DNA 3, 309-317, 1984

A:Title: Isolation and DNA sequence of full-length cDNA and of the entire gene for hu

A:Reference number: A90947; MUID:85026655

A:Accession: A90947

A:Molecule type: DNA

A:Residues: 1-267 <SEI>

A:Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635

A:Accession: B90947

A:Molecule type: mRNA

A:Residues: 1-267 <SE2>

A:Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635

R:Married, S.C.; Ruiz-Opazo, N.; Hayden, M.; Nussbaum, A.L.; Breslow, J.L.; Zannis, Eur. J. Biochem. 173, 465-471, 1988

A:Title: Sequence and expression of Tangier apoA-I gene.

A:Reference number: S02373; MUID:88196137

A:Accession: S02373

A:Molecule type: DNA

A:Residues: 1-267 <MAK>

A:Cross-references: EMBL:X07496; NID:g28774; PIDN:CAA30377.1; PID:g296729

R:Shoulters, C.C.; Kornblith, A.R.; Munro, B.S.; Baralle, F.E.

Nucleic Acids Res. 11, 2827-2837, 1983

A:Title: Gene structure of human apoliipoprotein A-I.

A:Reference number: A93465; MUID:83220822

A:Accession: A93465

A:Molecule type: DNA

A:Residues: 1-267 <SHO>

A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; R:Karathasis, S.K.; Zannis, V.I.; Breslow, J.L.

Proc. Natl. Acad. Sci. U.S.A. 80, 6147-6151, 1983

A:Title: Isolation and characterization of the human apoliipoprotein A-I gene.

A:Reference number: A21147; MUID:84016011

A:Accession: A21147

A:Molecule type: DNA

A:Residues: 1-267 <KAR>

A:Cross-references: GB:J00098; GB:J03222; NID:g178765; PIDN:AAB59514.1; PID:g178768

R:Sharpe, C.R.; Sidoli, A.; Shelley, C.S.; Lucero, M.A.; Shoulters, C.C.; Baralle, F.

Nucleic Acids Res. 12, 3917-3932, 1984

A:Title: Human apoliipoproteins A-I, A-II, CII and CIII. cDNA sequences and mRNA abundance

A:Accession: A93519

A:Molecule type: mRNA

A:Residues: 1-267 <SHA>

A:Cross-references: GB:X00566; NID:g28765; PIDN:CAA25232.1; PID:g732753

A:Accession: B93519
 A:Molecule type: DNA
 A:Residues: 1-24 <SH2>
 R:Cheung, P., Chan, L.
 Nucleic Acids Res. 11, 3703-3715, 1983
 A:Title: Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.
 A:Reference number: A93472; MUID:83220772
 A:Accession: A93472
 A:Molecule type: mRNA
 A:Residues: 1-267 <CH2>
 A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GB:K01519; GB:K01520
 R:Law, S.W.; Brewer, J., H.B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 66-70, 1984
 A:Title: Nucleotide sequence and the encoded amino acids of human apolipoprotein A-I mRNA
 A:Reference number: A94010; MUID:84119464
 A:Accession: A94010
 A:Molecule type: mRNA
 A:Residues: 1-267 <LAN>
 A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GB:K01519; GB:K01520
 R:Zannis, V.I.; Karathanasis, S.K.; Keutmann, H.T.; Goldberger, G.; Breslow, J.L.
 Proc. Natl. Acad. Sci. U.S.A. 80, 2574-2578, 1983
 A:Title: Intracellular and extracellular processing of human apolipoprotein A-I: secreted
 A:Reference number: A21118; MUID:83195100
 A:Accession: A21118
 A:Molecule type: mRNA
 A:Residues: 1-24 <LAN>
 R:Brewer, J., H.B.; Fairwell, T.; Kay, L.; Meng, M.; Roman, R.; Law, S.; Light, J.A.
 Biochem. Biophys. Res. Commun. 113, 626-632, 1983
 A:Title: Human plasma proapo-A-I: isolation and amino-terminal sequence.
 A:Reference number: A90112; MUID:83256553
 A:Accession: A90112
 A:Molecule type: protein
 A:Residues: 19-27 <BR2>
 R:Brewer, J., H.B.; Fairwell, T.; Kay, L.; Meng, M.; Roman, R.; Houser, A.; Bronzert, T.J.
 Biochem. Biophys. Res. Commun. 80, 623-630, 1978
 A:Title: The amino acid sequence of human APOA-I, an apolipoprotein isolated from high density lipoprotein
 A:Reference number: A90209; MUID:78123731
 A:Accession: A90209
 A:Molecule type: protein
 A:Residues: 25-57, 'O', '59-169, 'OO', '172-267 <BR2>
 R:Yui, Y.; Aoyama, T.; Morishita, H.; Takahashi, M.; Takatsu, Y.; Kawai, C.
 J. Clin. Invest. 82, 803-807, 1988
 A:Title: Serum prostacyclin stabilizing factor is identical to apolipoprotein A-I (Apo A-I)
 A:Reference number: A30516; MUID:88331387
 A:Accession: A30516
 A:Molecule type: protein
 A:Residues: 25-56 <YUI>
 R:Nichols, W.C.; Dwyer, F.E.; Liepnieks, J.; Benson, M.D.
 Biochem. Biophys. Res. Commun. 156, 762-768, 1988
 A:Title: Variant apolipoprotein AI as a major constituent of a human hereditary amyloid.
 A:Reference number: A31582; MUID:89050104
 A:Accession: A31582
 A:Molecule type: protein
 A:Residues: 25-49, 'R', '51-85, 'D', '87-107 <NIC>
 R:Manjunath, P.; Marcel, Y.L.; Uma, J.; Seidah, N.G.; Chretien, M.; Chappelaine, A.
 J. Biol. Chem. 264, 16853-16857, 1989
 A:Title: Apolipoprotein A-I binds to a family of bovine seminal plasma proteins.
 A:Reference number: A34409; MUID:89380318
 A:Accession: A34409
 A:Molecule type: protein
 A:Residues: 25-48 <MAN>
 R:Stoffel, W.; Binczek, E.
 Biol. Chem. Hoppe-Seyler 369, 1055-1063, 1988
 A:Title: Structural requirements of human preproapolipoprotein AI for translocation and
 A:Reference number: S02737; MUID:89149957
 A:Accession: S02737
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-6, 'AV', '9', 'LV', '12-29 <STO>
 A:Note: part of this sequence, including the amino end of the mature protein, was confirmed by Stoffel, W.; Binczek, E.
 Biol. Chem. Hoppe-Seyler 372, 481-488, 1991

A:Title: Transient expression of wild type and mutant human apolipoprotein AI in COS
 A:Reference number: S16197; MUID:92029676
 A:Contents: annotation; extension of studies in reference S02737
 R:Stoffel, W.; Kruger, E.; Deutzmann, R.
 Hoppe-Seyler's Z. Physiol. Chem. 364, 227-237, 1983
 A:Title: Cell-free translation of human liver apolipoprotein AI and AII mRNA processed
 A:Reference number: A19913; MUID:83236195
 A:Accession: B19913
 A:Molecule type: protein
 A:Residues: 1-6, 'X', '8-13, 'XXX', '17-18, 'XX', '21, 'X', '23-25, 'X', '27-29 <ST2>
 R:Enholm, C.; Bozas, S.E.; Tenkkanen, H.; Kirsbaum, L.; Metsu, J.; Murphy, B.; Walke
 Biochem. Biophys. Acta 1086, 255-260, 1991
 A:Title: The apolipoprotein A-I binding protein of placenta and the SP-40/40 protein
 A:Reference number: A56815; MUID:92075698
 A:Accession: A56815
 A:Molecule type: protein
 A:Residues: 25-31, 'P', '33 <EHN>
 A:Experimental source: serum
 A:Note: sequence extracted from NCBI backbone (NCBIP:69759)
 A:Note: 32-Tyr was also found
 R:Kuntake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
 Biochemistry 33, 1988-1993, 1994
 A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipoproteins
 A:Reference number: A54223; MUID:94162201
 A:Accession: A54223
 A:Molecule type: protein
 A:Residues: 25-39 <KUN>
 R:Mogullevsky, N.; Roobol, C.; Loriau, R.; Guillaume, J.P.; Jacobs, P.; Cravador, A.;
 DNA 8, 429-436, 1989
 A:Title: Production of human recombinant proapolipoprotein A-I in Escherichia coli: P
 A:Reference number: I39476; MUID:89377481
 A:Accession: I39476
 A:Molecule type: mRNA
 A:Residues: 19-267 <RES>
 A:Cross-references: GB:M29066; NID:9178774; PIDN:AAA51747.1; PID:9178775
 R:Higuchi, K.; Law, S.W.; Hoeg, J.M.; Schumacher, U.K.; Meglin, N.; Brewer, H.B.
 J. Biol. Chem. 263, 18530-18536, 1988
 A:Title: Tissue-specific expression of apolipoprotein A-I (ApoA-I) is regulated by the
 A:Reference number: I39475; MUID:89054040
 A:Accession: I39475
 A:Molecule type: DNA
 A:Residues: 1-14 <KR2>
 A:Cross-references: GB:J04066; NID:9178763; PIDN:AAA51746.1; PID:9553183
 R:Breslow, J.L.
 Annu. Rev. Biochem. 54, 699-727, 1985
 A:Title: Human apolipoprotein molecular biology and genetic variation.
 A:Reference number: A90042; MUID:85278004
 A:Contents: annotation; review of sequences, variants and gene location
 R:Hoeg, J.M.; Meng, M.S.; Roman, R.; Fairwell, T.; Brewer, J., H.B.
 J. Biol. Chem. 261, 3911-3914, 1986
 A:Title: Human apolipoprotein A-I. Post-translational modification by fatty acid acyl
 A:Reference number: A92577; MUID:86140194
 A:Contents: annotation; acylation with palmitate
 A:Note: an undetermined serine or threonine is acylated by fatty acid; the acylating
 R:Law, S.W.; Brewer, J., H.B.
 J. Biol. Chem. 260, 12810-12814, 1985
 A:Title: Tangier disease: The complete mRNA sequence encoding for preproapo-A-I.
 A:Reference number: I55236; MUID:86008382
 A:Accession: I55236
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-143, 'D', '145-267 <RE3>
 A:Cross-references: GB:M11191; NID:9178776; PIDN:AAA5545.1; PID:9178777
 A:Comment: Apolipoprotein A-I precursor is synthesized in the liver and small intestine
 C:Genetics: GDB:AP0A1
 A:Cross-references: GDB:119684; OMIM:107680
 A:Map position: 11q23.3-11q23.3
 A:Introns: 15/1; 67/2
 A:Function: participates in the reverse transport of cholesterol from tissues to the liver
 A:Description: participates in the reverse transport of cholesterol from tissues to the liver and stabilizes prostacyclin (per-2
 sterol acyltransferase (LCAT); noncovalently binds and stabilizes prostacyclin (per-2

C:Superfamily: apolipoprotein A-I
C:Keywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid binding; lipoprotein
F:1-18/Domain: signal sequence #status experimental <StG>
F:19-24/Domain: propeptide #status experimental <Pro>
F:25-267/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 100.0%; Score 556; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 4e-38;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OKLHELOEKLSPLGEEMDRARAHVDALRTHLAPYSDELROQLARLEALKENGARLAE 60
Db 156 OKLHELOEKLSPLGEEMDRARAHVDALRTHLAPYSDELROQLARLEALKENGARLAE 215
Qy 61 YHAKATEHLSTLSEKAKPALEDLROGLLPVLESFVSFLSALEEYTKKLTQ 112
Db 216 YHAKATEHLSTLSEKAKPALEDLROGLLPVLESFVSFLSALEEYTKKLTQ 267

RESULT 2

A26529
apolipoprotein A-I precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 30-Sep-1989 #sequence revision 19-Oct-1995 #text_change 22-Jun-1999
A:Accession: A26529; S23135; A57766
R:Polites, H.G.; Melchior, G.W.; Castle, C.K.; Marotti, K.R.
Gene 49, 103-110, 1986
A:Title: The primary structure of cynomolgus monkey apolipoprotein A-I deduced from the
A:Reference number: A26529; MUID:87191989
A:Accession: A26529

A:Residues: 1-267 <POL>
A:Cross-references: GB:M15411; NID:g342074; PIDN:AAA36834.1; PID:g342075
R:Herbert, P.N.; Bausserman, L.L.; Lynch, K.M.; Santelli, A.L.; Kantor, M.A.; Nicolosi,
Biochemistry 26, 1457-1463, 1987
A:Title: Homologues of the human C and A apolipoproteins in the Macaca fascicularis (cyt
A:Reference number: A26627; MUID:87185451
A:Accession: A26627

A:Molecule type: protein
A:Residues: 25-48 <HER>
R:Murray, R.W.; Marotti, K.R.
Biochim. Biophys. Acta 1131, 207-210, 1992
A:Title: Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene and corres
A:Reference number: S23135; MUID:92305062
A:Accession: S23135

A:Molecule type: DNA
A:Residues: 1-12, 'L', 14-267 <MUR>
A:Cross-references: GB:M83242; NID:g342070; PIDN:AAA36832.1; PID:g342071
R:Sorci-Thomas, M.; Kearns, M.W.
J. Biol. Chem. 266, 18045-18050, 1991
A:Title: Transcriptional regulation of the apolipoprotein A-I gene.
A:Reference number: A57766; MUID:92011532
A:Accession: A57766

A:Molecule type: DNA
A:Residues: 1-10 <RES>
A:Cross-references: GB:M69223; NID:g342066; PIDN:AAA36831.1; PID:g553820
C:Comment: The precursor is synthesized in the liver and small intestine. The propeptide
C:Comment: ApoA-I makes up about 70% of the protein of the high density lipoproteins (HDL)
y promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin
C:Genetics:
A:Introns: 15/1; 67/2

C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem repeat
F:1-18/Domain: signal sequence #status predicted <StG>
F:19-24/Domain: propeptide #status predicted <Pro>
F:25-267/Product: apolipoprotein A-I #status predicted <MAT>

Query Match 96.8%; Score 538; DB 1; Length 267;
Best Local Similarity 96.4%; Pred. No. 1.2e-36;
Matches 108; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OKLHELOEKLSPLGEEMDRARAHVDALRTHLAPYSDELROQLARLEALKENGARLAE 60
Db 156 OKLHELOEKLSPLGEEMDRARAHVDALRTHLAPYSDELROQLARLEALKENGARLAE 215
Qy 61 YHAKATEHLSTLSEKAKPALEDLROGLLPVLESFVSFLSALEEYTKKLTQ 112
Db 216 YHAKATEHLSTLSEKAKPALEDLROGLLPVLESFVSFLSALEEYTKKLTQ 267

RESULT 3

J50079
apolipoprotein A-I precursor - baboon
C:Species: Papio sp. (baboon)
C:Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 13-Jun-1997
A:Accession: J50079
R:Hixon, J.E.; Borenstein, S.; Cox, L.A.; Rainwater, D.L.; Vandenberg, J.L.
Gene 74, 483-490, 1988
A:Title: The baboon gene for apolipoprotein A-I: characterization of a cDNA clone and
A:Reference number: J50079; MUID:89232739
A:Accession: J50079

A:Molecule type: mRNA
A:Residues: 1-267 <HTX>
A:Experimental source: liver
A:Comment: This protein serves as a cofactor for lecithin cholesterol acyltransferase
C:Comment: This protein serves as a cofactor for lecithin cholesterol acyltransferase
C:Genetics:
A:Gene: APOA1
C:Superfamily: apolipoprotein A-I
C:Keywords: HDL; lipid binding; lipoprotein
F:1-18/Domain: signal sequence #status predicted <StG>
F:19-267/Product: apolipoprotein A-I #status predicted <Pro>
F:123-144, 145-166, 167-188, 189-210, 211-232, 233-254/Region: tandem repeats

Query Match 96.8%; Score 538; DB 2; Length 267;
Best Local Similarity 96.4%; Pred. No. 1.2e-36;
Matches 108; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OKLHELOEKLSPLGEEMDRARAHVDALRTHLAPYSDELROQLARLEALKENGARLAE 60
Db 156 OKLHELOEKLSPLGEEMDRARAHVDALRTHLAPYSDELROQLARLEALKENGARLAE 215
Qy 61 YHAKATEHLSTLSEKAKPALEDLROGLLPVLESFVSFLSALEEYTKKLTQ 112
Db 216 YHAKATEHLSTLSEKAKPALEDLROGLLPVLESFVSFLSALEEYTKKLTQ 267

RESULT 4

LPOGAI
apolipoprotein A-I precursor - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 17-Dec-1982 #sequence revision 14-Jul-1994 #text_change 07-May-1999
A:Accession: A60940; A03092; A61418
R: Luo, C.C.; Li, W.H.; Chan, L.
J. Lipid Res. 30, 1735-1746, 1989
A:Title: Structure and expression of dog apolipoprotein A-I, E, and C-I mRNAs: implic
A:Reference number: A60940; MUID:90132271
A:Accession: A60940

A:Molecule type: protein
A:Residues: 25-167, 'G', 169-201, 'O', 203-234, 'O', 236-266 <CHD>
R:Nakai, T.; Whayne, T.F.; Tang, J.
FEBS Lett. 64, 409-411, 1976
A:Title: The amino- and carboxyl-terminal sequences of canine apolipoprotein A-I.
A:Reference number: A61418; MUID:76210910
A:Accession: A61418

A:Molecule type: protein
 A:Residues: 25-56, 'Z', 261-262, 'A' <NAK>
 C:Superfamily: apolipoprotein A-I
 C:Keywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid transport; 14
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PRO>
 F:25-266/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 80.8%; Score 449; DB 1; Length 266;
 Best Local Similarity 80.4%; Pred. No. 1.9e-29;
 Matches 90; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 OKLHELOEKLSPLGEMDRARAHVDALRTHLAPYSDELQRRLARLEALKEGSGARLAE 60
 DB 155 OKLHELOEKLSPLAEELRDSARTHTVDTLRTKLAPYSDELQRRLARLEALKEGSGARLAE 214
 QY 61 YHAKATEHLSLSEKAKPALEDLRQGLLPVLESEFKVSFLSALEYTKKLNQ 112
 DB 215 YQAKAREHLSVLSSEKARPALEDLRQGLLPVLESEFKVSFLSALEYTKKLNQ 266

RESULT 5

apolipoprotein A-I precursor (clone 22ap A1) - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999
 C:Accession: S06064
 R:Paraskovopoulou, T. B.; Kittis, A.; Zannis, V.
 Submitted to the EMBL Data Library, July 1989
 A:Reference number: S06064
 A:Accession: S06064
 A:Molecule type: mRNA
 A:Residues: 1-266 <PAR>
 A:Cross-references: EMBL:X15908; NID:g1457; PIDN:CAA34024.1; PID:g1458
 C:Comment: This protein is synthesized in the small intestine.
 C:Superfamily: apolipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem rep
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PRO>
 F:25-266/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 77.3%; Score 430; DB 1; Length 266;
 Best Local Similarity 78.6%; Pred. No. 6.8e-28;
 Matches 88; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 1 OKLHELOEKLSPLGEMDRARAHVDALRTHLAPYSDELQRRLARLEALKEGSGARLAE 60
 DB 155 OKLHELOEKLSPLAEELRDSARTHTVDTLRTKLAPYSDELQRRLARLEALKEGSGARLAE 214
 QY 61 YHAKATEHLSLSEKAKPALEDLRQGLLPVLESEFKVSFLSALEYTKKLNQ 112
 DB 215 YQAKAREHLSVLSSEKARPALEDLRQGLLPVLESEFKVSFLSALEYTKKLNQ 266

RESULT 6

apolipoprotein A-I - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Jun-1998 #sequence_revision 30-Jun-1998 #text_change 31-Dec-1993
 C:Accession: A24998
 R:Yang, C.; Yang, T.; Pownall, H.J.; Gotto Jr., A.M.
 Eur. J. Biochem. 160, 427-431, 1986
 A:Title: The primary structure of apolipoprotein A-I from rabbit high-density lipoprotein
 A:Reference number: A24998; MUID:87030294
 A:Accession: A24998
 A:Molecule type: protein
 A:Residues: 1-241 <YAN>
 C:Superfamily: apolipoprotein A-I
 C:Keywords: HDL; lipid binding; lipoprotein

Query Match 76.4%; Score 425; DB 2; Length 241;
 Best Local Similarity 77.7%; Pred. No. 1.5e-27;
 Matches 87; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 OKLHELOEKLSPLGEMDRARAHVDALRTHLAPYSDELQRRLARLEALKEGSGARLAE 60
 DB 130 OKLHELOEKLSPLAEELRDSARTHTVDTLRTKLAPYSDELQRRLARLEALKEGSGARLAE 189
 QY 61 YHAKATEHLSLSEKAKPALEDLRQGLLPVLESEFKVSFLSALEYTKKLNQ 112
 DB 190 YQAKAREHLSVLSSEKARPALEDLRQGLLPVLESEFKVSFLSALEYTKKLNQ 241

RESULT 7

apolipoprotein A-I precursor (clone PRBA-502) - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999
 C:Accession: S00230; S20557
 R:Pan, T.C.; Hao, Q.L.; Yamin, T.T.; Dai, P.H.; Chen, B.S.; Chen, S.L.; Kroon, P.A.;
 Eur. J. Biochem. 170, 99-104, 1987
 A:Title: Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit apolipoprotein
 A:Reference number: S00230; MUID:88082866
 A:Accession: S00230
 A:Molecule type: mRNA
 A:Residues: 1-265 <PAR>
 A:Cross-references: EMBL:X06658; NID:g1461; PIDN:CAA29857.1; PID:g1462
 A:Note: the authors translated the codon AGC for residue 174 as Arg
 A:Accession: S20557
 A:Molecule type: DNA
 A:Residues: 1-17, 'R', 19-44, 'I', 46-122, 'Y', 124-146, 'V', 148-265 <PAR2>
 A:Cross-references: EMBL:X06659; NID:g1459; PIDN:CAA29858.1; PID:g1460
 C:Comment: This protein is synthesized in the small intestine.
 C:Superfamily: apolipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem r
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PRO>
 F:25-265/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 75.3%; Score 418.5; DB 1; Length 265;
 Best Local Similarity 77.7%; Pred. No. 5.8e-27;
 Matches 87; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 OKLHELOEKLSPLGEMDRARAHVDALRTHLAPYSDELQRRLARLEALKEGSGARLAE 60
 DB 155 OKLHELOEKLSPLAEELRDSARTHTVDTLRTKLAPYSDELQRRLARLEALKEGSGARLAE 213
 QY 61 YHAKATEHLSLSEKAKPALEDLRQGLLPVLESEFKVSFLSALEYTKKLNQ 112
 DB 214 YQAKAREHLSVLSSEKARPALEDLRQGLLPVLESEFKVSFLSALEYTKKLNQ 265

RESULT 8

apolipoprotein A-I precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 05-Jan-1996 #sequence_revision 23-Aug-1997 #text_change 13-Aug-1999
 C:Accession: I45853; A56858; A34649
 R:O'Huigin, C.; Chan, L.; Li, W.
 Mol. Biol. Evol. 7, 327-339, 1990
 A:Title: Cloning and sequencing of bovine apolipoprotein A-I cDNA and molecular evolu
 A:Reference number: I45853; MUID:90348478
 A:Accession: I45853
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-265 <OXH>
 A:Cross-references: GB:M35870; NID:g162677; PIDN:AAA30381.1; PID:g162678
 R:Sparrow, D.A.; Lee, B.R.; Lapidus, P.M.; Audouin, S.; Baughart, D.; Chapman, M.J.;

Biochim. Biophys. Acta 1123, 145-150, 1992
A:Title: Plasma lipid transport in the pre-ruminant calf, Bos spp: primary structure of h
A:Reference number: A56858; MUID:92153895
A:Accession: A56858
A:Status: preliminary
A:Molecule type: protein
A:Residues: 19-184; 'QL', 187-265 <SPA>
A:Experimental source: Friesian-Holstein male calves aged 2-4 weeks
A:Note: sequence extracted from NCBI backbone (NCBI:83520)
R:Aboultou, S.; Sparrow, D.A.; Beaudet, L.; Bauehart, D.; Sparrow, J.T.; Laplaud, P.M.
Biochem. Biophys. Res. Commun. 166, 833-839, 1990
A:Title: Characterization and amino-terminal sequence of apolipoprotein AI from plasma h
A:Reference number: A34649; MUID:90147795
A:Accession: A34649
A:Molecule type: protein
A:Residues: 25-70 <AUB>
A:Experimental source: Friesian-Holstein male calves aged 2-4 weeks
C:Superfamily: apolipoprotein A-I
C:Keywords: lipid binding; lipoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-265/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 74.6%; Score 414.5; DB 2; Length 265;
Best Local Similarity 74.1%; Pred. No. 1.2e-26;
Matches 83; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

OY 1 OKLHELOEKSLPGEMRRARAHVDALRTHLAPYSDELROQLARLEAKENGARLAE 60
DB 155 OKVQELDKSLPLAEPLRDLRAHVEALRQHVAPYSDDLRQRLTARLEAKEGGS-LAE 213
OY 61 YHAKATEHLSTLSEKAPPALEDLROGLLPVLESFVSFLSALEYTKKLTNQ 112
DB 214 YHAKAEOQLKALGEKAKPALEDLROGLLPVLESLKVSILAAIDASKKLTNAQ 265

RESULT 9
apolipoprotein A-I - pig
N:Alternate names: apo-A-I
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 11-May-2000
C:Accession: J06672; P0471; A05311
R:Trileu, V.N.; Patel, B.; Zhan, R.; Black, D.D.
Gene 134, 267-270, 1993
A:Title: Sequence of the porcine apoA-I gene.
A:Reference number: J06672; MUID:94085789
A:Accession: J06672
A:Molecule type: DNA
A:Residues: 1-265 <TRI>
A:Cross-references: EMBL:214124; NID:91893
A:Note: this translation is not annotated in GenBank entry SSAP0AIG, release 111.0; the
R:Trileu, V.N.; Hasler-Kapacz, J.; Kapacz, J.; Black, D.D.
Gene 123, 173-179, 1993
A:Title: Sequences and expression of the porcine apolipoprotein A-I and C-III mRNAs.
A:Reference number: P0471; MUID:93154581
A:Accession: P0471
A:Molecule type: mRNA
A:Residues: 105-265 <TR2>
A:Experimental source: liver
R:Malley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.
Biochemistry 15, 1928-1933, 1976
A:Title: Characterization of the plasma lipoproteins and apoproteins of the Erythrocebus
A:Reference number: A90395; MUID:76184721
A:Accession: A05311
A:Molecule type: protein
A:Residues: 25-34 <MAH>
C:Comment: This protein is the major apolipoprotein of high-density lipoprotein and very
C:Genetics:
A:Gene: apoA-I
A:Introns: 15/1; 66/2
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid metabolism; lip

F:99/Region: ochre stop codon

Query Match 73.5%; Score 408.5; DB 2; Length 265;
Best Local Similarity 74.1%; Pred. No. 3.7e-26;
Matches 83; Conservative 12; Mismatches 16; Indels 1; Gaps 1;

OY 1 OKLHELOEKSLPGEMRRARAHVDALRTHLAPYSDELROQLARLEAKENGARLAE 60
DB 155 OKVQELDKSLPLAEPLRDLRAHVEALRQHVAPYSDDLRQRLTARLEAKEGGS-LAE 213
OY 61 YHAKATEHLSTLSEKAPPALEDLROGLLPVLESFVSFLSALEYTKKLTNQ 112
DB 214 YHAKAEOQLKALGEKAKPALEDLROGLLPVLENLKVSILAAIDASKKLTNAQ 265

RESULT 10
apolipoprotein AI - pig
A:Molecule type: DNA; protein
A:Residues: 1-265 <BIR>
A:Cross-references: GB:L00626; NID:9164358; PID:AAA30992.1; PID:9164359
A:Note: sequence extracted from NCBI backbone (NCBI:129509, NCBI:129511)
C:Superfamily: apolipoprotein A-I

Query Match 72.6%; Score 403.5; DB 2; Length 265;
Best Local Similarity 74.1%; Pred. No. 9.5e-26;
Matches 83; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

OY 1 OKLHELOEKSLPGEMRRARAHVDALRTHLAPYSDELROQLARLEAKENGARLAE 60
DB 155 OKVQELDKSLPLAEPLRDLRAHVEALRQHVAPYSDDLRQRLTARLEAKEGGS-LAE 213
OY 61 YHAKATEHLSTLSEKAPPALEDLROGLLPVLESFVSFLSALEYTKKLTNQ 112
DB 214 YHAKAEOQLKALGEKAKPALEDLROGLLPVLENLKVSILAAIDASKKLTNAQ 265

RESULT 11
apolipoprotein A-I - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 20-Feb-1995 #sequence_revision 22-May-1998 #text_change 13-Aug-1999
C:Accession: S21830
R:Trileu, V.N.; Rohwer-Nuttler, P.; Black, D.D.
Submitted to the EMBL Data Library, May 1991
A:Description: Sequence and developmental expression of porcine ApoA-I mRNA.
A:Reference number: S21830
A:Accession: S21830
A:Molecule type: mRNA
A:Residues: 1-164 <TRI>
A:Cross-references: EMBL:X59414; NID:91891; PID:CAA42050.1; PID:91892
A:Experimental source: liver
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid metabolism; lip

Db 54 OKVLEQEKLSPLGEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEKENGARLAE 112
 QY 61 YHAKATEHLSTLSEKAKPALEDLROGLLPVLESEKVSFLSALEYTKKLNQ 112
 Db 113 YQAKQOEDLKLGEKAKPALEDLROGLLPVLEENKVSITLAIDASKKLNQ 164

RESULT 12

apoliipoprotein A-I - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 28-Oct-1994
 C:Accession: J00704
 R:Weller-Guettler, H.; Sommerfeldt, M.; Papandrikopoulou, A.; Mischek, U.; Bonitz, D.; F. J. Neurochem. 54, 444-450, 1990
 A:Title: Synthesis of apoliipoprotein A-I in pig brain microvascular endothelial cells.
 A:Reference number: J00704; MUID:90132667
 A:Accession: J00704
 A:Molecule type: mRNA
 A:Residues: 1-231 <MET>
 A:Note: the authors translated the codon CAG for residue 124 as His and GAC for residue
 C:Superfamily: apoliipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; lipid binding; lipid transport; lipoprotein; pi

Query Match 72.0%; Score 400.5; DB 2; Length 231;
 Best Local Similarity 74.1%; Pred. No. 1.4e-25;
 Matches 83; Conservative 10; Mismatches 18; Indels 1; Gaps 1;

QY 1 OKLHELOEKLSPLGEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEKENGARLAE 60
 Db 121 OKVLEQEKLSPLGEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEKENGARLAE 179
 QY 61 YHAKATEHLSTLSEKAKPALEDLROGLLPVLESEKVSFLSALEYTKKLNQ 112
 Db 180 YQAKQOEDLKLGEKAKPALEDLROGLLPVLEENKVSITLAIDASKKLNQ 231

RESULT 13

apoliipoprotein A-I - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
 C:Accession: S31394
 R:Moehel, B.; Flach, R.; Weiss, B.; Weller-Guettler, H.; Frey, A.; Zinke, H.; Gassen, H. submitted to the EMBL Data Library, November 1992
 A:Description: Genomic organization of the porcine apoliipoprotein A1 gene and study of
 A:Reference number: S31394
 A:Accession: S31394
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-264 <MOE>
 A:Cross-references: EMBL:X69477; NID:g1889; PIDN:CAA49234.1; PID:g1390
 C:Superfamily: apoliipoprotein A-I

Query Match 72.0%; Score 400.5; DB 2; Length 264;
 Best Local Similarity 74.1%; Pred. No. 1.7e-25;
 Matches 83; Conservative 10; Mismatches 18; Indels 1; Gaps 1;

QY 1 OKLHELOEKLSPLGEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEKENGARLAE 60
 Db 154 OKVLEQEKLSPLGEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEKENGARLAE 212
 QY 61 YHAKATEHLSTLSEKAKPALEDLROGLLPVLESEKVSFLSALEYTKKLNQ 112
 Db 213 YQAKQOEDLKLGEKAKPALEDLROGLLPVLEENKVSITLAIDASKKLNQ 264

RESULT 14
 S22420
 apoliipoprotein A-I precursor - mouse
 C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
 C:Accession: S22420; S22421; A44364
 R:Stoffel, W.; Mueller, R.; Binczek, E.; Hofmann, K. Biol. Chem. Hoppe-Seyler 373, 187-193, 1992
 A:Title: Mouse apoliipoprotein AI. cDNA-derived primary structure, gene organisation a
 A:Reference number: S22420; MUID:92281682
 A:Accession: S22420
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-264 <STO>
 A:Cross-references: EMBL:X64262; NID:g50014; PIDN:CAA45560.1; PID:g50015
 A:Accession: S22421
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-264 <ST>
 A:Cross-references: EMBL:X64263; NID:g50020; PIDN:CAA45561.1; PID:g50021
 R:Janusz, J.L.; Azrolan, N.; O'Connell, A.; Aalto-Setälä, K.; Breslow, J.L. Genomics 14, 1081-1088, 1992
 A:Title: Characterization of the mouse apoliipoprotein Apoa-1/Apoc-3 gene locus: genom
 A:Reference number: A44364; MUID:93122774
 A:Accession: A44364
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-264 <CAN>
 A:Note: sequence extracted from NCBI backbone (NCBIN:122400, NCBI:P:122407)
 C:Genetics:
 A:Introns: 15/1; 66/2
 C:Superfamily: apoliipoprotein A-I

Query Match 53.2%; Score 296; DB 2; Length 264;
 Best Local Similarity 53.6%; Pred. No. 5e-11;
 Matches 60; Conservative 18; Mismatches 32; Indels 2; Gaps 1;

QY 1 OKLHELOEKLSPLGEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEKENGARLAE 60
 Db 155 OKVLEQEKLSPLGEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEKENGARLAE 212
 QY 61 YHAKATEHLSTLSEKAKPALEDLROGLLPVLESEKVSFLSALEYTKKLNQ 112
 Db 213 YHTRATHLKTGEKAKPALEDLRLHSLMPLTETLKTKAOSVIDKASETITLQ 264

RESULT 15

apoliipoprotein A-I precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-1993
 C:Accession: JCI237
 R:Boyle, T.P.; Marotti, K.R. Gene 117, 243-247, 1992
 A:Title: Structure of the murine gene encoding apoliipoprotein A-I.
 A:Reference number: JCI237; MUID:92347700
 A:Accession: JCI237
 A:Molecule type: DNA
 A:Residues: 1-262 <BOY>
 A:Cross-references: GB:M77801
 C:Genetics:
 A:Gene: Apoa-I
 A:Introns: 15/1; 66/2
 C:Superfamily: apoliipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; l
 F:1-24/Domain: signal sequence #status predicted <STG>
 F:25-262/Product: apoliipoprotein A-I #status predicted <MAT>

Query Match 52.2%; Score 290; DB 2; Length 262;
 Best Local Similarity 57.3%; Pred. No. 1.5e-16;
 Matches 59; Conservative 14; Mismatches 28; Indels 2; Gaps 1;

QY 1 OKLHELOEKLSPLGEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEKENGARLAE 60
 Db 155 OKVLEQEKLSPLGEEMDRARAHVDALRTHLAPYSDELRLQRLAARLEKENGARLAE 212

Sun Sep 22 12:10:12 2002

us-09-803-918a-2_copy_156_267.rpr

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QY      61 YHAATEHUHSTSEKAPAEDEDLRGGLPVLEEFKVSFLSALE 103
      || : | | | | | | | | | | : | : | |
DB     213 YHTRAKTHIKTLGEKAPAEDEDLRHSLMPELLETILTKAQSVIE 255

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Search completed: September 22, 2002, 12:06:29
Job time: 324 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:22:18 ; Search time 35.02 Seconds
(without alignments)
123.832 Million cell updates/sec

Title: US-09-803-918A-2_COPY_156_267
Perfect score: 556
Sequence: 1 QKHLQELKSPLEGEKMRD.....SRKVSPLSLAEYTKKLNQ 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	100.0	267	1 APAL_HUMAN	P02647 homo sapien
2	538	96.8	267	1 APAL_MACFA	P15568 macaca fasc
3	449	80.8	266	1 APAL_CANFA	P02648 canis fam11
4	430	77.3	266	1 APAL_RABIT	P09809 oryctolaqus
5	409.5	73.7	265	1 APAL_BOVIN	P15497 bos taurus
6	408.5	73.5	265	1 APAL_PIG	P16648 sus scrofa
7	355	63.8	265	1 APAL_TUPGB	O18759 tupaia glis
8	296	53.2	264	1 APAL_MOUSE	Q00623 mus musculu
9	272	48.9	264	1 APAL_ANAPL	O42296 anas platyr
10	266	47.8	259	1 APAL_CHICK	P08250 gallus gall
11	255	45.9	264	1 APAL_HUMAN	P32818 coturnix co
12	237	42.6	264	1 APAL_COTUA	P06727 homo sapien
13	144	22.3	396	1 APAL_HUMAN	O42363 brachydanio
14	122	21.9	262	1 APAL_BRARE	O46409 sus scrofa
15	119.5	21.5	382	1 AP4A_PIG	P33621 macaca fasc
16	119.5	21.5	429	1 AP4A_MACFA	O57524 oncorhynch
17	116	20.9	262	1 AP12_ONCMW	O57523 oncorhynch
18	115	20.7	262	1 AP11_ONCMW	Q28758 papio anubi
19	113.5	20.4	401	1 AP4A_PAPAN	O91488 salmo trutt
20	111.5	20.1	262	1 APAL_SALTR	O42175 salmo salar
21	107.5	19.3	260	1 APAL_SPANU	P27007 salmo salar
22	105.5	19.0	258	1 APAL_SALSA	P02651 rattus norv
23	103	18.5	391	1 AP4A_RAT	P06728 mus musculu
24	102.5	18.4	395	1 AP4A_MOUSE	P10517 macaca fasc
25	99	17.8	317	1 APPE_MACFA	P05770 papio anubi
26	99	17.8	317	1 APPE_PAPAN	P02650 rattus norv
27	97.5	17.5	107	1 APPE_RAT	Q28995 salmirl sci
28	97	17.4	107	1 APPE_SAISC	Q08226 mus musculu
29	95.5	17.2	311	1 APPE_MOUSE	Q10209 schizosacch
30	93.5	16.8	392	1 YAYI_SCHPO	Q28502 macaca mula
31	93	16.7	107	1 APPE_MACMU	P18649 canis fam11
32	92.5	16.6	305	1 APPE_CANFA	O42364 brachydanio
33	92	16.5	281	1 APPE_BRARE	

34	92	16.5	317	1	APPE_HUMAN	P02649 homo sapien
35	90.5	16.3	3672	1	LM12_CAEL	Q03247 bos taurus
36	90	16.2	316	1	AME_BOVIN	P16785 human cytom
37	89.5	16.1	2241	1	TREGU_HCMVA	P16650 sus scrofa
38	87	15.6	317	1	APPE_PIG	P18287 oryctolaqus
39	85	15.3	311	1	APPE_RABIT	P12883 homo sapien
40	84.5	15.2	1935	1	MYH7_HUMAN	Q08014 giardia lam
41	84	15.1	857	1	MEB8_GIALA	P05661 drosophila
42	84	15.1	2411	1	MYSA_DROME	P23529 cavia porce
43	83	14.9	298	1	APPE_CANPO	P16878 xenopus lae
44	83	14.9	512	1	K2C3_XENLA	P17120 emerice11a
45	83	14.9	1184	1	BIMC_EMENT	

ALIGNMENTS

RESULT	1	APAL_HUMAN	STANDARD	PRT	267 AA.
AC	P02647:	APAL_HUMAN			
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Apolipoprotein A-I precursor (Apo-AI).				
GN	APOL1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84221405; PubMed=6328445;				
RA	Shapiro C.R., Sidoli A., Shelley C.S., Lucero M.A., Shoulders C.C.,				
RA	Baralle F.E.;				
RT	"Human apolipoproteins AI, AII, CII and CIIT. cDNA sequences and mRNA				
RT	abundance.";				
RL	Nucleic Acids Res. 12:3917-3932(1984).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8502665; PubMed=6207999;				
RA	Sellhammer J.J., Protter A.A., Frossard P., Levy-Wilson B.;				
RT	"Isolation and DNA sequence of full-length cDNA and of the entire				
RT	gene for human apolipoprotein AI -- discovery of a new genetic				
RL	polymorphism in the apo AI gene.";				
RL	DNA 3:309-317(1984).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83220822; PubMed=6406984;				
RA	Shoulders C.C., Kornblith A.R., Munro B.S., Baralle F.E.;				
RT	"Gene structure of human apolipoprotein AI.";				
RL	Nucleic Acids Res. 11:2827-2837(1983).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83220772; PubMed=6304641;				
RA	Cheung P., Chan L.;				
RT	"Nucleotide sequence and the encoded amino acids of human				
RT	apolipoprotein A-I mRNA.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 81:66-70(1984).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84119464; PubMed=6198645;				
RA	Law S.W., Brewer H.B., Jr.;				
RT	"Nucleotide sequence and the encoded amino acids of human				
RT	apolipoprotein A-I mRNA.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 81:66-70(1984).				
RN	[6]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=86008382; PubMed=2995392;				
RA	Law S.W., Brewer H.B., Jr.;				
RT	"Tangier disease. The complete mRNA sequence encoding for				
RT	preproapo-A-I.";				
RL	J. Biol. Chem. 260:12810-12814(1985).				
RN	[7]				

- RP SEQUENCE FROM N.A.
RX MEDLINE=84016011; PubMed=6413973;
RA Karathanasis S.K., Zannis V.I., Breslow J.L.;
RT "Isolation and characterization of the human apolipoprotein A-I
gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:6147-6151(1983).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=89377481; PubMed=2673706;
RA Mogilevsky N., Roobol C., Lortiau R., Guillaume J.P., Jacobs P.,
RA Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,
RA Holmquist L., Carlson L.A., Boilen A.;
RT "Production of human recombinant proapolipoprotein A-I in *Escherichia*
coli: purification and biochemical characterization.";
RL DNA 8:429-436(1989).
RN [9]
RP SEQUENCE FROM N.A. (VARIANT TANGIER).
RX MEDLINE=88196137; PubMed=3129297;
RA Makrides S.C., Ruiz-Opazo N., Hayden M., Nussbaum A.L., Breslow J.L.,
RA Zannis V.I.;
RT "Sequence and expression of Tangier apoA-I gene.";
RL Eur. J. Biochem. 173:465-471(1988).
RN [10]
RP SEQUENCE OF 118-267 FROM N.A.
RX MEDLINE=83091059; PubMed=6294659;
RA Breslow J.L., Ross D., McPherson J., Williams H.W., Kurnit D.,
RA Nussbaum A.L., Karathanasis S.K., Zannis V.I.;
RT "Isolation and characterization of cDNA clones for human
apolipoprotein A-I.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6861-6865(1982).
RN [11]
RP SEQUENCE OF 19-27.
RX MEDLINE=83255553; PubMed=6409108;
RA Brewer H.B. Jr., Fairwell T., Kay L., Meng M., Ronan R., Law S.,
RA Light J.A.;
RT "Human plasma proapoA-I: isolation and amino-terminal sequence.";
RL Biochem. Biophys. Res. Commun. 113:626-632(1983).
RN [12]
RP SEQUENCE OF 25-267.
RX MEDLINE=78123731; PubMed=204308;
RA Brewer H.B. Jr., Fairwell T., Larue A., Ronan R., Houser A.,
RA Bronzert T.J.;
RT "The amino acid sequence of human apoA-I, an apolipoprotein isolated
from high density lipoproteins.";
RL Biochem. Biophys. Res. Commun. 80:623-630(1978).
RN [13]
RP SEQUENCE OF 25-267.
RX MEDLINE=75133493; PubMed=164450;
RA Baker H.N., Gotto A.M. Jr., Jackson R.L.;
RT "The primary structure of human plasma high density apolipoprotein
glutamine I (apoA-I). II. The amino acid sequence and alignment of
cyanogen bromide fragments IV, III, and I.";
RL J. Biol. Chem. 250:2725-2738(1975).
RN [14]
RP SEQUENCE OF 25-56.
RX MEDLINE=88331387; PubMed=3047170;
RA Yui Y., Aoyama T., Morishita H., Takahashi M., Takatsu Y., Kawai C.;
RT "Serum proacylglycerin stabilizing factor is identical to apolipoprotein
A-I (apo A-I). A novel function of Apo A-I.";
RL J. Clin. Invest. 82:803-807(1988).
RN [15]
RP SEQUENCE OF 25-48.
RX MEDLINE=89380318; PubMed=2506184;
RA Manjunath P., Marcel Y.L., Uma J., Seidah N.G., Chretien M.,
RA Chapdelaine A.;
RT "Apolipoprotein A-I binds to a family of bovine seminal plasma
proteins.";
RL J. Biol. Chem. 264:16853-16857(1989).
RN [16]
RP SEQUENCE OF 25-43.
RX MEDLINE=88070603; PubMed=3120314;
RA Ptiloi R.P., Ordovas J.M., Rosenberg I., Schaeffer E.J.,
RA Pereira M.E.A.;
RT "Similarity of cruzin, an inhibitor of Trypanosoma cruzi
neuraminidase, to high-density lipoprotein.";
RL Science 238:1417-1419(1987).
RN [17]
RP SEQUENCE OF 25-42.
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
1994.";
RL Electrophoresis 15:1459-1465(1994).
RN [18]
RP PALMITOYLATION.
RX MEDLINE=86140194; PubMed=3005308;
RA Hoeg J.M., Meng M.S., Ronan R., Fairwell T., Brewer H.B. Jr.;
RT "Human apolipoprotein A-I. Post-translational modification by fatty
acid acylation.";
RL J. Biol. Chem. 261:3911-3914(1986).
RN [19]
RP PROCESSING.
RX MEDLINE=83195100; PubMed=6405383;
RA Zannis V.I., Karathanasis S.K., Keutmann H.T., Goldberger G.,
RA Breslow J.L.;
RT "Intracellular and extracellular processing of human apolipoprotein
A-I: secreted apolipoprotein A-I isoprotein 2 is a propeptide.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2574-2578(1983).
RN [20]
RP STRUCTURE BY NMR OF 190-209.
RX MEDLINE=96270776; PubMed=8664326;
RA Wang G., Treleaven W.D., Cushley R.J.;
RT "Conformation of human serum apolipoprotein A-I(166-185) in the
presence of sodium dodecyl sulfate or dodecylphosphocholine by ¹H-NMR
and CD. Evidence for specific peptide-SDS interactions.";
RL Biochim. Biophys. Acta 1301:174-184(1996).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (4.0 ANGSTROMS) OF 67-267.
RX MEDLINE=89024124; PubMed=9356442;
RA Borhani D.W., Rogers D.P., Engler J.A., Brouillette C.G.;
RT "Crystal structure of truncated human apolipoprotein A-I suggests a
lipid-bound conformation.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12291-12296(1997).
RN [22]
RP VARIANT MILANO.
RX MEDLINE=83109095; PubMed=6401735;
RA Welsgraber K.H., Rall S.C. Jr., Bersot T.P., Mahley R.W.,
RA Franceschini G., Sirtori C.R.;
RT "Apolipoprotein A-Milano. Detection of normal A-I in affected
subjects and evidence for a cysteine for arginine substitution in the
variant A-I.";
RL J. Biol. Chem. 258:2508-2513(1983).
RN [23]
RP VARIANT TANGIER.
RX MEDLINE=83300108; PubMed=6412234;
RA Schmitz G., Assmann G., Rall S.C. Jr., Mahley R.W.;
RT "Tangier disease: defective recombination of a specific Tangier
apolipoprotein A-I isoform (pro-apo A-I) with high density
lipoproteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:6081-6085(1983).
RN [24]
RP VARIANT NORMAN.
RX MEDLINE=84289383; PubMed=6432779;
RA Rall S.C. Jr., Welsgraber K.H., Mahley R.W., Ogawa Y., Fielding C.J.,
RA Utermann G., Haas J., Steinmetz A., Menzel H.J., Assmann G.;
RT "Abnormal lecithin:cholesterol acyltransferase activation by a human
apolipoprotein A-I variant in which a single lysine residue is
deleted.";
RL J. Biol. Chem. 259:10063-10070(1984).
RN [25]
RP SEQUENCE OF 25-107 (VARIANT IOWA).
RX MEDLINE=89050104; PubMed=3142462;
RA Nichols W.C., Dwulet F.E., Liepnieks J., Benson M.D.;
RT "Variant apolipoprotein AI as a major constituent of a human
hereditary amyloid.";

Query Match 100.0%; Score 556; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.6e-39;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKHLEIOEKISPLGEERDRARAHVDALRTHLAPYSDELRORLAARLEALKENGARLAE 60
 |||||
 DB 156 OKHLEIOEKISPLGEERDRARAHVDALRTHLAPYSDELRORLAARLEALKENGARLAE 215

QY 61 YHAKATHEHLSTLSEKAPPALEDLROGLLPVLESFKVSFLSALREYTKKLTQ 112
 |||||
 DB 216 YHAKATHEHLSTLSEKAPPALEDLROGLLPVLESFKVSFLSALREYTKKLTQ 267

RESULT 2
 ID APAL_MACFA STANDARD; PRT; 267 AA.
 AC P15568; P17929;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NX NCBI_TaxID=9541, 9557;
 [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=87191989; PubMed=3106152;
 RA Pollitt H.G., Melchior G.W., Castle C.K., Marotti K.R.;
 RT "The primary structure of cynomolgus monkey apolipoprotein A-1
 RL deduced from the cDNA sequence: comparison to the human sequence.";
 RN Gene 49:103-110(1986).
 [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=92305062; PubMed=1610902;
 RA Murray R.W., Marotti K.R.;
 RT "Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene
 RL and corresponding flanking regions.";
 RN Biochim. Biophys. Acta 1131:207-210(1992).
 [3]
 RP SEQUENCE OF 25-48.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=87185451; PubMed=3105581;
 RA Herbert P.N., Bausserman L.L., Lynch K.M., Sartelli A.L.,
 RA Kantor M.A., Nicolosi R.J., Shulman R.S.;
 RT "Homologues of the human C and A apolipoproteins in the Macaca
 RL fascicularis (cynomolgus) monkey.";
 RN Biochemistry 26:1457-1463(1987).
 [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas; TISSUE=Liver;
 RX MEDLINE=89232739; PubMed=2907746;
 RA Hixon J.E., Borenstein S., Cox L.A., Rainwater D.L., Vandenberg J.L.;
 RT "The baboon gene for apolipoprotein A-I: characterization of a cDNA
 RL clone and identification of DNA polymorphisms for genetic studies of
 RL cholesterol metabolism.";
 RN Gene 74:483-490(1988).
 [5]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC SPECIES=M.fascicularis;
 RA Sorci-Thomas M.;
 RL Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M15411; AAA36834.1; -;
 CC EMBL: M83242; AAA36832.1; -;
 CC EMBL: M35634; AAA35380.1; -;
 CC EMBL: M69223; AAA36831.1; -;
 CC PIR: A26529; A26529.
 CC PIR: A26627; A26627.
 CC PIR: J50079; J50079.
 CC PIR: S21335; S21335.
 CC HSSP: P02647; 10DR.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 267
 FT DOMAIN 68 267
 FT REPEAT 68 89
 FT REPEAT 90 111
 FT REPEAT 112 122
 FT REPEAT 123 144
 FT REPEAT 145 166
 FT REPEAT 167 188
 FT REPEAT 189 210
 FT REPEAT 211 232
 FT REPEAT 233 243
 FT REPEAT 244 267
 FT CONFLICT 13 13 L -> P (IN REF. 1).
 SQ SEQUENCE 267 AA; 30735 MW; 869955C024088E21 CRC64;

Query Match 96.8%; Score 538; DB 1; Length 267;
 Best Local Similarity 96.4%; Pred. No. 5e-38;
 Matches 108; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKHLEIOEKISPLGEERDRARAHVDALRTHLAPYSDELRORLAARLEALKENGARLAE 60
 |||||
 DB 156 OKHLEIOEKISPLGEERDRARAHVDALRTHLAPYSDELRORLAARLEALKENGARLAE 215

QY 61 YHAKATHEHLSTLSEKAPPALEDLROGLLPVLESFKVSFLSALREYTKKLTQ 112
 |||||
 DB 216 YHAKATHEHLSTLSEKAPPALEDLROGLLPVLESFKVSFLSALREYTKKLTQ 267

RESULT 3
 ID APAL_CANFA STANDARD; PRT; 266 AA.
 AC P02648;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NX NCBI_TaxID=9615;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=90132271; PubMed=2515239;
 RA Luo C.-C., Li W.-H., Chan L.;

"Structure and expression of dog apolipoprotein A-I, E, and C-I mRNAs: implications for the evolution and functional constraints of apolipoprotein structure.";
 RT J. Lipid Res. 30:1735-1746(1989).
 RN [2]
 RP SEQUENCE OF 25-266.
 RX MEDLINE=82142425; PubMed=6801039;
 RA Chung H., Randolph A., Reardon I., Heinrikson R.L.;
 RT "The covalent structure of apolipoprotein A-I from canine high density lipoproteins.";
 RT J. Biol. Chem. 257:2961-2967(1982).
 RN [3]
 RP SEQUENCE OF 25-57 AND 262-265.
 RX MEDLINE=76210910; PubMed=179887;
 RA Nakai T., Whayne T.F., Tang J.;
 RT "The amino- and carboxyl-terminal sequences of canine apolipoprotein A-1.";
 RT FEBS Lett. 64:409-411(1976).
 RN [4]
 RP SEQUENCE OF 25-37.
 RX TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "Hsc-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins.";
 RT Electrophoresis 18:2795-2802(1997).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF CHOLESTEROL EFFLUX FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- CHROMICONS: SYNTHESIZED IN THE LIVER AND SMALL INTESTINE.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 DR HSSP: P02647; LDPGAL.
 DR HSC-2DPAGE: P02648; DOG.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 266
 FT DOMAIN 67 266
 FT REPEAT 67 266
 FT REPEAT 89 110
 FT REPEAT 111 121
 FT REPEAT 122 143
 FT REPEAT 144 165
 FT REPEAT 166 187
 FT REPEAT 188 209
 FT REPEAT 210 231
 FT REPEAT 232 242
 FT REPEAT 243 266
 FT CONFLICT 168 266
 FT CONFLICT 202 202
 FT CONFLICT 235 235
 FT CONFLICT 264 266
 FT SEQUENCE 266 AA; 30196 MW; A3202620C28A869D CRC64;
 SO

Query Match 80.8%; Score 449; DB 1; Length 266;
 Best Local Similarity 80.4%; Pred. No. 1.2e-30;
 Matches 90; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 QKIHLEOKESPLGEENRRARAHVDAIRTHLAQYSDLEQRQARLEAKENGARLAE 60
 DB 155 QKIQELQEKISPLAEELRDRARTHVDAIRQAQAPYSDDLREKLAARLEAKENGARLAE 214
 QY 61 YHAKATHLSTSEKAPALADLRQGLLPVLESFKVSELSALEEYTKKLNQ 112
 DB 215 YHAKASBOLSALEKAPALADLRQGLLPVLESFKVSLAIDEATKKLNQ 266

RESULT 4
 ID APOA1_RABBIT STANDARD; PRT; 266 AA.
 AC P09809;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22AP AI; TISSUE=Small intestine;
 RA Paraskevopoulou T.B., Kritlis A., Zannis V.I.;
 RL Submitted (JUL-1989) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=88082866; PubMed=3121329;
 RA Pan T.C., Hao Q.L., Yamini T.T., Dai P.H., Chen B.S., Chen S.L.,
 RA Kroon P.A., Chao Y.S.;
 RT "Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit apolipoprotein A-I is synthesized in the intestine but not in the liver.";
 RT Eur. J. Biochem. 170:99-104(1987).
 RN [3]
 RP SEQUENCE OF 25-266.
 RX MEDLINE=87030294; PubMed=3095115;
 RA Yang C., Yang T., Pownall H.J., Gotto A.M., Jr.;
 RT "The primary structure of apolipoprotein A-I from rabbit high-density lipoprotein.";
 RT Eur. J. Biochem. 160:427-431(1986).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF CHOLESTEROL EFFLUX FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC -----
 DR EMBL: X15908; CAA34024.1; -;
 DR EMBL: X06658; CAA29857.1; -;
 DR EMBL: X06659; CAA29858.1; -;
 DR PIR: S06064; LPRB1Z.
 DR PIR: S00230; LPRB1B.
 DR PIR: A24998; A24998.
 DR HSSP: P02647; LAV1.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 266
 FT DOMAIN 67 266
 FT REPEAT 67 266
 FT REPEAT 89 110
 FT REPEAT 111 121
 FT REPEAT 122 143
 FT REPEAT 144 165
 FT REPEAT 166 187
 FT SEQUENCE 166 187

APOLIPOPROTEIN A-I.
 10 X APPROXIMATE TANDEM REPEATS.
 3 (HALF-LENGTH).
 4.
 5.
 6.
 7.
 8.
 9 (HALF-LENGTH).
 10.
 A -> G (IN REF. 2).
 E -> Q (IN REF. 2).
 E -> Q (IN REF. 2).
 NAO -> A (IN REF. 3).

FT	REPEAT	188	209	7.
FT	REPEAT	210	231	8.
FT	REPEAT	232	242	9 (HALF-LENGTH).
FT	REPEAT	243	266	10.
FT	CONFLICT	18	18	A -> R (IN REF. 2; CAA29858).
FT	CONFLICT	44	44	MISSING (IN REF. 3).
FT	CONFLICT	45	45	V -> I (IN REF. 2; CAA29858).
FT	CONFLICT	107	107	E -> Q (IN REF. 3).
FT	CONFLICT	123	123	Y -> F (IN REF. 2; CAA29857).
FT	CONFLICT	147	147	A -> V (IN REF. 2; CAA29858 AND REF. 3).
FT	CONFLICT	150	150	R -> G (IN REF. 2; CAA29858 AND CAA29857).
FT	CONFLICT	191	191	N -> Q (IN REF. 3).
FT	CONFLICT	195	195	MISSING (IN REF. 2; CAA29858 AND CAA29857).
FT	CONFLICT	211	211	S -> K (IN REF. 2; CAA29858 AND CAA29857).
FT	CONFLICT	255	256	VL -> LV (IN REF. 3).
FT	CONFLICT	256	256	L -> V (IN REF. 2; CAA29858 AND CAA29857).
SO	SEQUENCE	266 AA:	30591 MW:	0FF6DB386497C7D2 CRR64;

Query Match	77.3%	Score 430	DB 1	Length 266
Best Local Similarity	78.6%	Pred No. 4.6e-29		
Matches 88, Conservative		8, Mismatches 16	Indels 0	Caps 0

QY	1	ÖKLEHLOEKLSPLGCEEMDRARAVDALRTHLAPYSDELRORLARLEALKENGASRLAE	60
DB	155	ÖKLEHLOEKLSPLAEELRDSARKHVDTLRTKLADYSNELOORLARLESTKEGGASLAE	214

QY	61	YHAKTEHSTLSKRAKPALEDROGLTPEVLESKVSFTLKREYTKLWTO	112
Db	215	YQAKAREHISVLESKRAKPALEDROGLTPEVLESKASVQNVLDKTKKLNTQ	266

RESULT	5
APAI_BOVIN	
ID	APAI_BOVIN
STANDARD;	
PRT:	265 AA.

DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).

OS Bos taurus (Bovine).
OC Eukaryota: Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Ruminantia; Pecora; Bovidea;

RN [1]
RP SEQUENCE FROM N. A.
RX MEDLINE=90348478; PubMed=2117227;

RT molecular evolution of apolipoproteins A-I and B-100.";
 RL Mol. Biol. Evol. 7:327-339 (1990).
 RN [2] *Journal of Molecular Evolution* 35:10-36

RA Sparrow J. A., Lee B. R., Laplaud M. P., Auboliron S., Bauchart D.,
 RA Chapman J. M., Gatto A. M. Jr., Yang C. Y., Sparrow J. T.:
 RT "Plasma lipid transport in the preterm calf, Bos spp: primary

RN [3]
RP SEQUENCE OF 25-70.
RX MEDLINE=90147795; PubMed=2105728;
D Baughart D Searrow T F

RT "Characterization and amino-terminal sequence of apolipoprotein AI
RT from plasma high density lipoproteins in the pre-ruminant calf, *Bos*
RT spp.";

```

CC      BioPhyS, Res. Commun.166:833-839.(1990).
CC      -I- FUNCTION: APOA-I PARTICIPATES IN THE REVERSE TRANSPORT OF
CC      CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC      CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC      THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT) .
CC      -I- SUBCELLULAR LOCATION: Extracellular.
CC      -I- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC      CHYLOMICRONS.
CC      -I- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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CC      or send an email to license@isb-sib.ch).

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DR PIR: A34649; A34649.
DR HSP: P02647; IODR.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein: 1

FT	SIGNAL	1	18	
FT	PROPEP	19	24	
FT	CHAIN	25	265	
FT	DOMAIN	67	265	

APOLIPOPROTEIN A-I.
 10 X APPROXIMATE TANDEM REPEATS.

FT	89	1.10	2.	3. (HALF-LENGTH) .
REPEAT				
FT	111	1.21		
REPEAT				
FT	122	1.43	4.	
REPEAT				
FT	144	1.65	5.	
REPEAT				

FT	18	209	7.
REPEAT	18	209	7.
FT	210	230	8.
REPEAT	210	230	8.
FT	231	241	9 (HALF-LENGTH).
REPEAT	231	241	9 (HALF-LENGTH).
FT	242	265	10
REPEAT	242	265	10

Query Match	73.7%	Score 409.5	DB 1	length 265
SQ	SEQUENCE	265 AA	30276 MW	06A2681EA2ABAS0F CR064

Matches	83;	Conservative	12;	Mismatches	16;	Indels	1;	Gaps	1
QY	1	OKIHLEQEKISPLGEMRRDRAHYDALRTHLAPYSDELFQRLARLEALKENGARLAE	60						

[illegible]

RESULT	6
APAL_PIG	
TD	APAL_PIG
STANDARD:	
PRT:	265 AA.

DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).

05 *Sus scrofa* (Pig) .
06 Chordata; Craniata; Vertebrata; Euteleostomi;
07 Eukaryota; Metazoa;
08 Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus .
09 NCBI TaxID=9823;

RP SEQUENCE FROM N.A.
RX MEDLINE=933224154; PubMed=8468059;
RA Birchbauer A., Knippling G., Juritsch B., Aschauer H., Zechner R.;
RT "Characterization of the apolipoprotein AI and CIII genes in the

RA MEDLINE=93322154; PubMed=8468059;
RX Birchauser A., Knippling G., Juritsch B., Aschauer H., Zechner R.;
RT "Characterization of the apolipoprotein AI and CIII genes in the

RT domestic pig.;
 RL Genomics 15:643-652(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver, and Brain;
 RX MEDLINE=94125128; PubMed=8294940;
 RA Moeckel B., Zinke H., Flach R., Weiss B., Weller-Guettler H.,
 RT Gassen H.;
 "Expression of apolipoprotein A-I in porcine brain endothelium in
 RT vitro";
 RL J. Neurochem. 62:788-798(1994).
 RN [3]
 RP SEQUENCE OF 34-265 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=90132667; PubMed=2105375;
 RA Weller-Guettler H., Sommerfeldt M., Papandikopoulou A., Mischek U.,
 RT Bonitz D., Frey A., Grube M., Scherer J., Gassen H.G.;
 "Synthesis of apolipoprotein A-I in pig brain microvascular
 RT endothelial cells";
 RL J. Neurochem. 54:444-450(1990).
 RN [4]
 RP SEQUENCE OF 105-265 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93154581; PubMed=8428656;
 RA Tieu V.N., Hasler-Rapacz J., Rapacz J., Black D.D.;
 RT "Sequences and expression of the porcine apolipoprotein A-I and C-III
 RN mRNAs";
 RL Gene 123:173-179(1993).
 RN [5]
 RP SEQUENCE OF 25-265.
 RA Hasler-Rapacz J.O., Chaudhary R., Chowdhary B.P., Tieu V.N.,
 RN Jackson K., Gustavsson I., Rapacz J.;
 RL Submitted (OCT-1995) to the SWISS-PROT data bank.
 RP [6]
 RX MEDLINE=76184721; PubMed=178359;
 RA Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;
 RT "Characterization of the plasma lipoproteins and apolipoproteins of the
 RL Erythrocytes of the monkey";
 CC Biochemistry 15:1928-1933(1976).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
 CC THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS. SYNTHESIZED PREDOMINANTLY IN THE INTESTINE AND THE
 CC LIVER.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC -----
 CC EMBL; L00626; AAA3092.1; -
 DR EMBL; X69477; CAA49234.1; -
 DR EMBL; X17057; -; NOT ANNOTATED_CDS.
 DR EMBL; X59414; CAA42050.1; -
 DR PIR; J00704; J00704.
 DR PIR; A05311; A05311.
 DR PIR; A46018; A46018.
 DR PIR; S21830; S21830.
 DR PIR; S31394; S31394.
 DR HSSP; P02647; IODR.
 DR InterPro; IPR000074; Apolipoprotein.
 DR Pfam; PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT PROPEP 19 24

FT CHAIN 25 265
 FT DOMAIN 67 265
 FT REPEAT 67 88
 FT REPEAT 89 110
 FT REPEAT 111 121
 FT REPEAT 122 142
 FT REPEAT 144 165
 FT REPEAT 166 187
 FT REPEAT 188 209
 FT REPEAT 210 230
 FT REPEAT 231 241
 FT REPEAT 242 265
 FT REPEAT 108 108
 FT CONFLICT 143 143
 FT CONFLICT 173 173
 FT CONFLICT 180 180
 FT CONFLICT 185 186
 FT CONFLICT 209 209
 FT CONFLICT 224 224
 SQ SEQUENCE 265 AA; 30325 MW; 2C6E578318ECF69C CRC64;
 Query Match 73.5%; Score 408.5; DB 1; Length 265;
 Best Local Similarity 74.1%; Pred. No. 2.8e-27;
 Matches 83; Conservative 12; Mismatches 16; Indels 1; Gaps 1;
 QY 1 OKHHEQKLSPLGEMRRARAHVDALETHAPISDELROLARLEAKENGARLAE 60
 DB 155 QKQVLEKSLPLAEELRLRAHVAHQVAPYSDLRQMARFALKEGGGS-LAE 213
 QY 61 YHAKTEHLSLEKAKPAPLEDLROGLPVLSEFVSFALEETKLNQ 112
 DB 214 YQAKAQEQKALGEKAKPAPLEDLROGLPVLSEFVSFALEETKLNQ 265
 RESULT 7
 ID APAL_TUPGB STANDARD; PRT; 265 AA.
 AC 018759;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN Tupaia glis belangeri (Common tree shrew).
 OS Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.
 OX NCBI_TaxID=9386;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Lu X., Chen B., Zhao Y., Wang K., Xue H., Zeng W.;
 RT Submitted (MAY-1997) to the EMBL/GenBank/DBP databases.
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
 CC THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF005638; AAB82326.1; -
 DR HSSP; P02647; IAVI.
 DR InterPro; IPR000074; Apolipoprotein.

DR Pfam: PF01442; Apolipoprotein 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT PROPEP 19 24 APOLIPROTEIN A-I.
 FT CHAIN 25 265
 FT DOMAIN 67 265 10 X APPROXIMATE TANDEM REPEATS.
 FT REPEAT 67 88 1.
 FT REPEAT 89 110 2.
 FT REPEAT 111 121 3 (HALF-LENGTH).
 FT REPEAT 122 143 4.
 FT REPEAT 144 165 5.
 FT REPEAT 166 187 6.
 FT REPEAT 188 209 7.
 FT REPEAT 210 231 8.
 FT REPEAT 232 242 9 (HALF-LENGTH).
 FT REPEAT 243 265 10.
 SQ SEQUENCE 265 AA; 30332 MW; 60076BC39FAEA165 CRC64;

Query Match 63.8%; Score 355; DB 1; Length 265;
 Best Local Similarity 62.4%; Pred. No. 7, 6e-23;
 Matches 68; Conservative 18; Mismatches 23; Indels 0; Gaps 0;

QY 1 OKLHELOEKLSPGEMRRARAHVDAALRTHLAPYSDELRLQRLAARLEALKEGARGLA 60
 DB 155 OKLMELOEQLVPLGEDLRDSVAVADTLRTQLAPYSEOMRKTLGARLEAIKEGSGSLAE 214
 QY 61 YHAKATEHLSTLSERAKPALEDRLQGLLPVLESFVSFSALEEYTKRL 109
 DB 215 YHAKASQLSALGKAKPVLEDIHQGLMPWSEKGTGLNVIDEAKKL 263

RESULT 8
 APAL_MOUSE
 ID APAL_MOUSE STANDARD; PRT; 264 AA.
 AC Q00623;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN Apol.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92281682; PubMed=1596360;
 RA Stoffel W., Mueller R., Binczek E., Hofmann K.;
 RT "Mouse apolipoprotein AI. cDNA-derived primary structure, gene
 RT organisation and complete nucleotide sequence.";
 RL Biol. Chem. Hoppe-Seyler 373:187-193(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93122774; PubMed=1478650;
 RA Janusz J.L., Azrolan N., O'Connell A., Aalto-Setälä K., Breslow J.L.;
 RT "Characterization of the mouse apolipoprotein ApoA-I/ApoC-3 gene
 RT locus: genomic, mRNA, and protein sequences with comparisons to other
 RT species.";
 RL Genomics 14:1081-1088(1992).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL EFFLUX FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECTIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X64262; CAA45560.1; -;
 CC DR EMBL: X64263; CAA45561.1; -;
 CC DR EMBL: L04149; -; NOT_ANNOTATED_CDS.
 CC DR EMBL: L04151; -; NOT_ANNOTATED_CDS.
 CC DR PIR: S22420; S22420.
 CC DR PIR: A44364; A44364.
 CC DR HSSP: P02647; IAVI.
 CC DR SWISS-2DPAGE: Q00623; MOUSE.
 CC DR MGD: MGI:88049; Apol.
 CC DR InterPro: IPR000074; Apol.
 CC DR Pfam: PF01442; Apolipoprotein 1.
 CC KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT PROPEP 19 24 APOLIPROTEIN A-I.
 FT CHAIN 25 264 APOLIPROTEIN A-I.
 FT DOMAIN 67 264 10 X APPROXIMATE TANDEM REPEATS.
 FT REPEAT 67 88 1.
 FT REPEAT 89 110 2.
 FT REPEAT 111 121 3 (HALF-LENGTH).
 FT REPEAT 122 143 4.
 FT REPEAT 144 165 5.
 FT REPEAT 166 187 6.
 FT REPEAT 188 207 7 (INCOMPLETE).
 FT REPEAT 208 229 8.
 FT REPEAT 230 240 9 (HALF-LENGTH).
 FT REPEAT 241 264 10.
 SQ SEQUENCE 264 AA; 30587 MW; C453FF2019634AAC CRC64;

Query Match 53.2%; Score 296; DB 1; Length 264;
 Best Local Similarity 53.6%; Pred. No. 5, 9e-18;
 Matches 60; Conservative 18; Mismatches 32; Indels 2; Gaps 1;

QY 1 OKLHELOEKLSPGEMRRARAHVDAALRTHLAPYSDELRLQRLAARLEALKEGARGLA 60
 DB 155 OKLMELOEQLVPLGEDLRDSVAVADTLRTQLAPYSEOMRKTLGARLEAIKEGSGSLAE 214
 QY 61 YHAKATEHLSTLSERAKPALEDRLQGLLPVLESFVSFSALEEYTKRL 112
 DB 213 YHAKATEHLSTLSERAKPALEDRLQGLLPVLESFVSFSALEEYTKRL 264

RESULT 9
 APAL_ANAPL
 ID APAL_ANAPL STANDARD; PRT; 264 AA.
 AC O42296;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN Anas platyrhynchos (Domestic duck).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=8839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PERIN BREED; TISSUE=Liver;
 RA Chen B., Lu X., Wang K., Xue H., Zeng W., Zhu D., Chi L.;
 RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL EFFLUX FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECTIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----

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 CC -----
 DR EMBL; U86131; AAB64381.1; -
 DR HSSP; P02647; 10DR.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KM Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL
 FT PROPEP 19 24 BY SIMILARITY.
 FT CHAIN 25 264 APOLIPOPROTEIN A-I.
 FT DOMAIN 67 264 10 X APPROXIMATE TANDEM REPEATS.
 FT REPEAT 67 88 1.
 FT REPEAT 89 110 2. (HALF-LENGTH).
 FT REPEAT 111 121 3 (HALF-LENGTH).
 FT REPEAT 122 143 4.
 FT REPEAT 144 165 5.
 FT REPEAT 166 187 6.
 FT REPEAT 188 209 7.
 FT REPEAT 210 231 8.
 FT REPEAT 232 242 9 (HALF-LENGTH).
 FT REPEAT 243 264 10.
 SQ SEQUENCE 264 AA; 30659 MW; 7546F4BAF246900 CRC64;
 Query Match 48.9%; Score 272; DB 1; Length 264;
 Best Local Similarity 49.5%; Pred. No. 5.8e-16;
 Matches 53; Conservative 20; Mismatches 34; Indels 0; Gaps 0;
 QY 1 OKLHELOEKISPLGEEMDRARAHVDAIRTHLAPYSDELRLAARLEALKENGARLAE 60
 DB 155 QKVELMOCKLTPVAEAEADRLRGHVEELKRNAPYSDELRLKSLKELEIRKGIPOAE 214
 QY 61 YHAKATEHLSTSEKAKPALEDLROGLPLVLESEKVSLSALEEYTK 107
 DB 215 YQAKVEQLSNIREKMTPLVODFKERLTPYAEKLTREISLDELQK 261
 RESULT 10
 APAL_RAT STANDARD; PRT; 259 AA.
 AC P04639;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=84207987; PubMed=6426956;
 RA Poncelet J.E., Martial J.A., Gielem J.E.;
 RT "Cloning and structure analysis of the rat apolipoprotein A-I cDNA.";
 RL Eur. J. Biochem. 140:493-498(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87008540; PubMed=3020028;
 RA Haddad I.A., Ordovas J.M., Fitzpatrick T., Karathanasis S.K.;
 RT "Linkage, evolution, and expression of the rat apolipoprotein A-I, C-
 RT III, and A-IV genes.";
 RL J. Biol. Chem. 261:13268-13277(1986).
 RN [3]
 RP SEQUENCE OF 1-45.
 RC STRAIN=SPRAGUE-DAWLEY;
 RX MEDLINE=82098162; PubMed=6798036;

RA Gordon J.I., Smith D.P., Andy R., Alpers D.H., Schonfeld G.,
 RA Straus A.W.;
 RT "The primary translation product of rat intestinal apolipoprotein A-I
 RT mRNA is an unusual preproprotein.";
 RL J. Biol. Chem. 257:971-978(1982).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHROMATOCYTES
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC -----
 DR EMBL; M00001; AAA40749.1; -
 DR EMBL; X00558; CAA25224.1; -
 DR EMBL; J02597; AAA40745.1; -
 DR PIR; A24700; A24700.
 DR HSSP; P02647; 1AVL.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KM Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL
 FT PROPEP 19 24
 FT CHAIN 25 259
 FT DOMAIN 67 259
 FT REPEAT 67 88
 FT REPEAT 89 110
 FT REPEAT 111 121
 FT REPEAT 122 143
 FT REPEAT 144 161
 FT REPEAT 162 183
 FT REPEAT 184 203
 FT REPEAT 204 225
 FT REPEAT 226 236
 FT REPEAT 237 259
 FT CONFLICT 201 201 R -> K (IN REF. 2).
 FT CONFLICT 214 214 G -> S (IN REF. 2).
 FT CONFLICT 218 218 R -> K (IN REF. 2).
 SQ SEQUENCE 259 AA; 30088 MW; 2EBD5EB45FEAE88 CRC64;
 Query Match 47.8%; Score 266; DB 1; Length 259;
 Best Local Similarity 49.6%; Pred. No. 1.8e-15;
 Matches 56; Conservative 18; Mismatches 33; Indels 6; Gaps 2;
 QY 2 KLN-----ELQEKISPLGEEMDRARAHVDAIRTHLAPYSDELRLAARLEALKENGAR 57
 DB 148 ELHKNKAKEMQRLKVAEAEFRDMRVNADALRAKFGVLSYSDQMEINLAQRLTEIRNH--PT 205
 QY 58 LAEYHAKATEHLSTSEKAKPALEDLROGLPLVLESEKVSLSALEEYTKLN 110
 DB 206 LIEYHKAGSHLTLGEKAKPALDDLGQGLMPVLEAKKAKINSMIDAKKLN 258
 RESULT 11
 APAL_CHICK STANDARD; PRT; 264 AA.
 AC P08250;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86049703; PubMed=3118875;
 RA Byrnes L., Luo C.-C., Li W.-H., Yang C.-Y., Chan L.;
 RT "Chicken apolipoprotein A-I: cDNA sequence, tissue expression and
 RT evolution.";
 RL Biochem. Biophys. Res. Commun. 148:485-492(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=88152500; PubMed=3126099;
 RA Ferrari S., Tarugi P., Drusiani E., Calandra S., Fregni M.;
 RT "The complete sequence of chick apolipoprotein AI mRNA and its
 RT expression in the developing chick.";
 RL Gene 60:39-46(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=8722301; PubMed=3108248;
 RA Rajavashisth T.B., Dawson P.A., Williams D.L., Shackelford J.E.,
 RA Leberer H., Lusis A.J.;
 RT "Structure, evolution, and regulation of chicken apolipoprotein A-I.";
 RL J. Biol. Chem. 262:7058-7065(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92381402; PubMed=1512510;
 RA Lamou-Fava S., Sastre R., Ferrari S., Rajavashisth T.B.,
 RA Lusis A.J., Karathanasis S.K.;
 RT "Evolutionary distinct mechanisms regulate apolipoprotein A-I gene
 RT expression: differences between avian and mammalian apoA-I gene
 RT transcription control regions.";
 RL J. Lipid Res. 33:831-842(1992).
 RN [5]
 RP SEQUENCE OF 25-44.
 RA MEDLINE=83213468; PubMed=6406496;
 RA Shackelford J.E., Leberer H.C.;
 RT "Synthesis and secretion of apolipoprotein A1 by chick breast
 RT muscle.";
 RL J. Biol. Chem. 258:7175-7180(1983).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECTITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC -----
 DR EMBL: M17961; AAA48593.1; -;
 DR EMBL: M18746; AAA48594.1; -;
 DR EMBL: M25559; AAA48592.1; -;
 DR EMBL: M96012; AAA48597.1; -;
 DR PIR: S01453; LPPCHAL1;
 DR PIR: JH04731; JH0471.
 DR HSSP: P02647; IODR.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 264
 FT DOMAIN 67 264
 FT REPEAT 67 88
 FT 1. APOLOPOPROTEIN A-I.
 FT 10 X APPROXIMATE TANDEM REPEATS.

FT REPEAT 89 110 2. (HAIF-LENGTH).
 FT REPEAT 111 121 3. (HAIF-LENGTH).
 FT REPEAT 122 143 4.
 FT REPEAT 144 165 5.
 FT REPEAT 166 187 6.
 FT REPEAT 188 209 7.
 FT REPEAT 210 231 8.
 FT REPEAT 232 242 9. (HAIF-LENGTH).
 FT REPEAT 243 264 10.
 FT CONFLICT 16 16 T -> I (IN REF. 4).
 FT CONFLICT 148 148 E -> K (IN REF. 3).
 SQ SEQUENCE 264 AA; 30680 MW; 968320E81E2AC5C2 CRC64;
 QY Query Match 45.98; Score 255; DB 1; Length 264;
 Db Best Local Similarity 46.8%; Pred. No. 1.5e-14;
 Matches 51; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
 QY 1 OKLHEIGKSLPIGEERDRARAHVDALRTHLAPYSDLRQRLAALDLKENGARLAE 60
 Db 155 QKVELMQAKLPVAEARDRLRGVEELKRLNLAQYSDLRQRLAALDLKENGARLAE 214
 QY 61 YHAKATEHLSTSEKAPPALEDLROGLPLVLESFKVSFSALEEYTKL 109
 Db 215 YQAKVMEQLSNLREKMPPLVQEFERLTPYAEVNLKRLISFLDELQKSV 263
 RESULT 12
 ID APAL_COTUA STANDARD; PRT; 264 AA.
 AC P32918;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Coturnix.
 OX NCBI_TaxID=93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=97212027; PubMed=9058967;
 RA Oku H., Toda T., Nagata J., Ishikawa M., Neyazaki K., Shinjo C.,
 RA Chinen I.;
 RT "Apolipoprotein A-1 of Japanese quail: cDNA sequence and modulation of
 RT tissue expression by cholesterol feeding.";
 RL Biosci. Biotechnol. Biochem. 61:286-290(1997).
 RN [2]
 RP SEQUENCE OF 25-60.
 RA MEDLINE=93213845; PubMed=8461329;
 RA Oku H., Ishikawa M., Nagata J., Toda T., Chinen I.;
 RT "Lipoprotein and apoprotein profile of Japanese quail.";
 RL Biochim. Biophys. Acta 1167:22-28(1993).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECTITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF VLDL, HDL, LDL AND IN
 CC CHYLOMICRONS. EXPRESSED IN A NUMBER OF TISSUES INCLUDING LIVER,
 CC SMALL INTESTINE, LUNG, KIDNEY, HEART AND MUSCLE WITH HIGHEST
 CC EXPRESSION IN LIVER AND SMALL INTESTINE.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----
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RA Kamboh M.I., Williams E.R., Law J.C., Aston C.E., Bunker C.H.,
 RA Ferrell R.E., Pollitzer W.S.;
 RT "Molecular basis of a unique African variant (A-IV 5) of human
 RT apolipoprotein A-IV and its significance in lipid metabolism";
 RL Genet. Epidemiol. 9:379-388(1992).
 RP (151)
 RP VARIANTS IYS-44 (BUDAPEST-2); CYS-305 AND SER-367 (BUDAPEST-1).
 RX MEDLINE-95245341; PubMed-7728150;
 RA Menzel H.J., Dieplinger H., Sandholzer C., Karadi I., Utermann G.,
 RA Csaszar A.;
 RT "Apolipoprotein A-IV polymorphism in the Hungarian population: gene
 RT frequencies, effect on lipid levels, and sequence of two new
 RT variants";
 RL Hum. Mutat. 5:58-65(1995).
 RN [161]
 RP VARIANTS FCHL SEATTLE SER-161; LEU-178 AND GLN-264.
 RX MEDLINE-97114287; PubMed-8956036;
 RA Deeb S.S., Nevin D.N., Iwasaki L., Brunzell J.D.;
 RT "Two novel apolipoprotein A-IV variants in individuals with familial
 RT combined hyperlipidemia and diminished levels of lipoprotein lipase
 RT activity";
 RL Hum. Mutat. 8:319-325(1996).
 CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
 CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
 CC LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
 CC COMPONENT OF HDL AND CHYLOMICRONS.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE INTESTINE.
 CC -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
 CC MERG) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
 CC HELICAL, AND MANY OF THESE HELICES ARE PREDICTED TO BE HIGHLY ALPHA-
 CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL
 CC ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES
 CC -1- POLYMORPHISM: EIGHT ALLELES HAVE BEEN CHARACTERIZED (APOA-IV*0
 CC TO APOA-IV*7). APOA-IV*1 IS THE MAJOR ALLELE (90%), IV*2 IS ALSO
 CC COMMON (8%). THE OTHERS ARE RARE ALLELES.
 CC -1- DISEASE: DEFECTS IN APOA4 MAY CONTRIBUTE, ALONG WITH DEFECTS IN
 CC OTHER GENES OR ENVIRONMENTAL FACTORS, TO THE DEVELOPMENT OF
 CC FAMILIAL COMBINED HYPERLIPIDEMIA (FCHL).
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC
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 CC -----
 DR EMBL: M14642; AAA51745.1; -
 DR EMBL: X13629; CAA31955.1; -
 DR EMBL: M14566; AAA51748.1; -
 DR EMBL: J02758; AAA96731.1; -
 DR EMBL: M13654; AAA51744.1; -
 DR PIR: A26481; LPHU04.
 DR PIR: A24449; A24449.
 DR PIR: A29330; A29330.
 DR PIR: A26280; A26280.
 DR PIR: S02715; S02715.
 DR HSSP: P02649; INFO.
 DR SWISS-2DPAGE: P06727; HUMAN.
 DR MIM: 107690; -
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal;
 KW Disease mutation; Polymorphism.
 FT SIGNAL 1 20
 FT CHAIN 21 396 APOLOPROTEIN A-IV.
 FT DOMAIN 33 330 13 X 22 AA APPROXIMATE TANDEM REPEATS.
 FT REPEAT 33 54 1.
 FT REPEAT 60 81 2.

FT REPEAT 82 103 3.
 FT REPEAT 115 136 4.
 FT REPEAT 137 158 5.
 FT REPEAT 159 180 6.
 FT REPEAT 181 202 7.
 FT REPEAT 203 224 8.
 FT REPEAT 225 246 9.
 FT REPEAT 247 268 10.
 FT REPEAT 269 287 11.
 FT REPEAT 287 308 12.
 FT REPEAT 309 330 13.
 FT DOMAIN 372 389 GLU/GLN-RICH.
 FT VARIANT 13 V->M (IN APOA-IV*1D).
 FT VARIANT 44 /FTID-VAR_000626.
 FT VARIANT 44 E->K (IN BUDAPEST-2).
 FT VARIANT 147 /FTID-VAR_000627.
 FT VARIANT 147 N->S (IN APOA-IV*1B).
 FT VARIANT 161 /FTID-VAR_000628.
 FT VARIANT 161 A->S (IN SEATTLE-3; IN FCHL).
 FT VARIANT 161 /FTID-VAR_000629.
 Query Match 22.3%; Score 124; DB 1; Length 396;
 Best Local Similarity 28.6%; Pred. No. 0.0017;
 Matches 30; Conservative 22; Mismatches 53; Indels 0; Gaps 0;
 QY 5 ELOEKSPGCEMRDRARAHVDALEKRLHAPVSDLEKRLAARLEAKENGARLAERYHAK 64
 DB 53 ELTQQLNALFQDKLGEVNTYAGDLQKLVFATLEHRLAKSEKLEIGKELEELRAR 112
 QY 65 ATCHLSTSEKAKPALEDRLQGLPLVESFKVSFLSALEYTKKL 109
 DB 113 LPHANEVSKIKDNLRELQRLPEYADOLRQVNTQABOLRRL 157
 RESULT 14
 ID APAL_BRARE STANDARD; PRT; 262 AA.
 AC 042363;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA.
 OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA MEDLINE-97385153; PubMed-9238027;
 RA Babin F.J., Thisse C., Durillat M., Andre M., Akimenko M.-A.,
 RA Thisse B.;
 RT "Both apolipoprotein E and A-I genes are present in a nonmammalian
 RT vertebrate and are highly expressed during embryonic development";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:8622-8627(1997).
 CC -1- FUNCTION: APOA-I PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT) (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN THE YOLK SYNCTIAL LAYER
 CC DURING EMBRYONIC (STARTING AT THE GASTRULA STAGE) AND EARLY LARVAL
 CC DEVELOPMENT. AN EXTRAMEMBRYONIC STRUCTURE IMPLICATED IN EMBRYONIC
 CC AND LARVAL NUTRITION.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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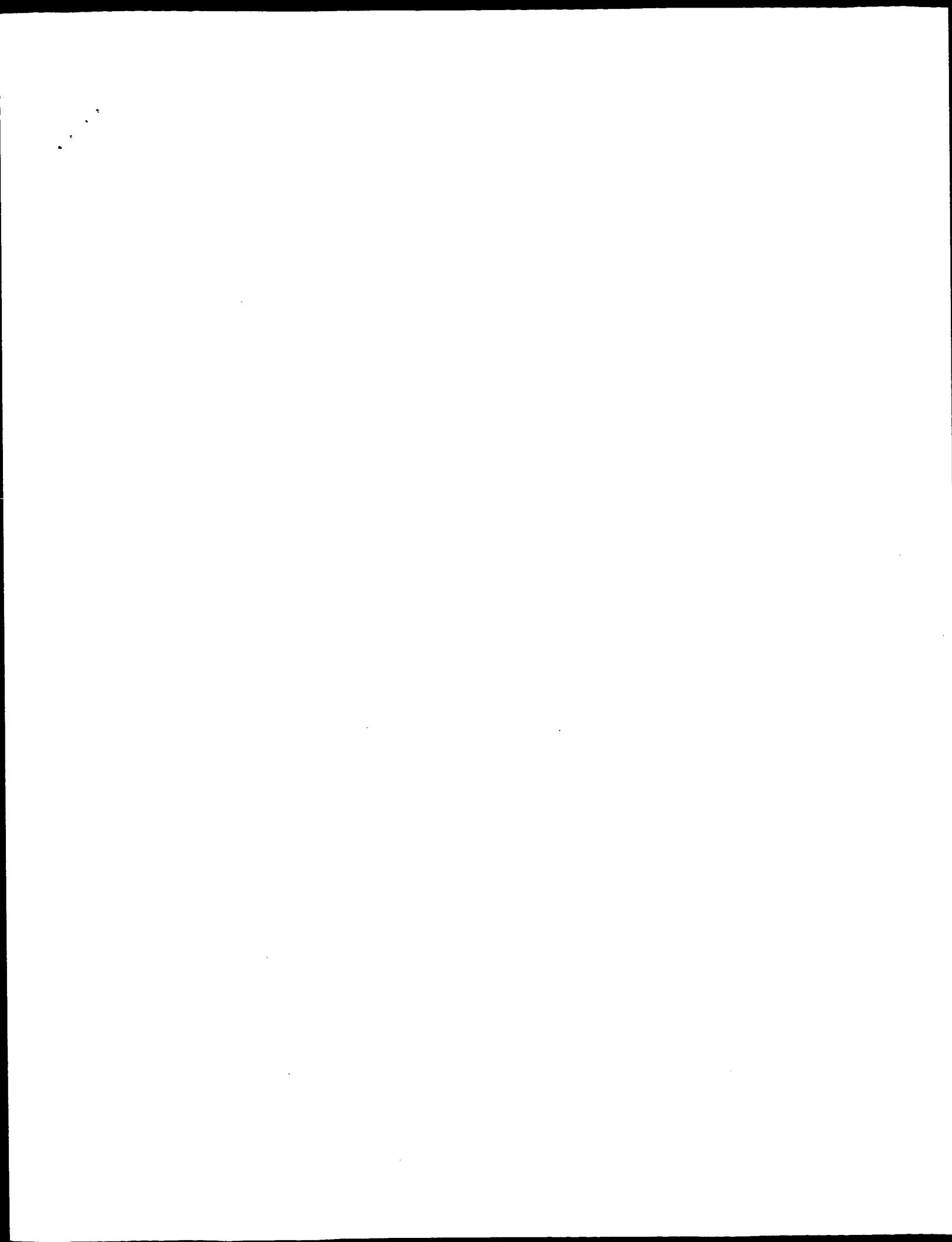
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 CC -----
 DR EMBL: Y13653; CAA74004.1; -
 DR ZFIN: ZDB-GENE-990415-14; apoA.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 23
 FT CHAIN 24 262
 FT DOMAIN 32 63
 FT DOMAIN 64 262
 FT REPEAT 64 85
 FT REPEAT 87 107
 FT REPEAT 108 118
 FT REPEAT 119 140
 FT REPEAT 141 162
 FT REPEAT 163 184
 FT REPEAT 185 206
 FT REPEAT 207 228
 FT REPEAT 229 239
 FT REPEAT 240 262
 SQ SEQUENCE 262 AA; 30256 MW; BB839A0A815365B9 CRC64;
 Query Match 21.9%; Score 122; DB 1; Length 262;
 Best Local Similarity 23.9%; Pred. No. 0.0016;
 Matches 26; Conservative 27; Mismatches 56; Indels 0; Gaps 0;
 Oy 1 OKHLEOEKLSPLGEEMDRARAHVDAALRTHLAPYSDELRORLAARLEAKENGARLAE 60
 Db 152 QNADLPAKAEPLDDDRKAPESNIEETKSKVPMVAEVTKLTREEDRTMAAYAE 211
 Oy 61 YHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKVSFLSALFEYTKL 109
 Db 212 YKEDLVAVAEARKIAPIHODLTREPEYMEVNTTFEQMYETIAKAI 260
 RESULT 15
 APAA_PIG STANDARD; PRT; 382 AA.
 ID APAA_PIG
 AC 046409;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV).
 GN APOA4.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Osada J., Iturriale M., Calleja L., Gonzalez N., Pineiro A.;
 RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
 CC -! FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
 CC CARBOHYDRATE METABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
 CC LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
 CC COMPONENT OF HDL AND CHYLOMICRONS.
 CC -! SUBCELLULAR LOCATION: Extracellular.
 CC -! TISSUE SPECIFICITY: SECRETED IN PLASMA.
 CC -! DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
 CC 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
 CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
 CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
 CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL
 CC ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
 CC -! SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----
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 CC -----
 DR EMBL: AJ22966; CAA11020.1; -
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 382
 FT DOMAIN 33 330
 FT REPEAT 33 54
 FT REPEAT 60 81
 FT REPEAT 82 103
 FT REPEAT 115 136
 FT REPEAT 137 158
 FT REPEAT 159 180
 FT REPEAT 181 202
 FT REPEAT 203 224
 FT REPEAT 225 246
 FT REPEAT 247 268
 FT REPEAT 269 286
 FT REPEAT 287 308
 FT REPEAT 309 330
 FT DOMAIN 360 377
 SQ SEQUENCE 382 AA; 43294 MW; ZACAB8A02D4379EF CRC64;
 Query Match 21.5%; Score 119.5; DB 1; Length 382;
 Best Local Similarity 24.6%; Pred. No. 0.0039;
 Matches 34; Conservative 28; Mismatches 47; Indels 29; Gaps 2;
 Oy 1 OKHLEOEKLSPLGEEMDRARAHVDAALRTHLAPYSDELRORLAARLEAKENGARLAE 60
 Db 192 QNVEELKSGITPYAEELAKIDQNVIELRSLAPYAQDVQKLNHQGLAFQKKQAE 251
 Oy 61 YHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKVSFLSALFEYTKL 109
 Db 252 LKAKISANADELROKLIVPAEENVHGLKNGTEGLOKSLLELRSHLDQVVEERLKEVEYG 311
 Oy 92 ESEFKVSFLSALFEYTKL 109
 Db 312 ETFNKALVQVQVEDLRKGL 329

Search completed: September 22, 2002, 12:22:18
 Job time: 1018 sec

Sun Sep 22 12:10:13 2002

us-09-803-918a-2_copy_156_267.rsp



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:21:37 ; Search time 111.17 Seconds
(without alignments)
174.287 Million cell updates/sec

Title:	US-09-803-918A-2_COPY_156_267
Perfect score:	556
Sequence:	1 QRIHELQEKLSPLCEMRDR.....SPKVSFLSAIEEYTKLINTQ 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Searched:      562222 segs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Maximum Match 100%
Listing first 45 summaries

Database :

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1:  SETPRIMBL_19: *
2:  2:  sp.bacteria: *
3:  3:  sp.fungi: *
4:  4:  sp.human: *
5:  5:  sp.invertebrate: *
6:  6:  sp.mammal: *
7:  7:  sp.minc: *
8:  8:  sp.organelle: *
9:  9:  sp.phase: *
10: 10: sp.plant: *
11: 11: sp.rodent: *
12: 12: sp.virus: *
13: 13: sp.vertebrate: *
14: 14: sp.unclassified: *
15: 15: sp.virus: *
16: 16: sp.zoonotic: *
17: 17: sp.archaea: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	367	66.0	264	11	Q9Z2L4	Q9Z2L4	mesocricetus
	2	327	58.8	67	4	Q9T355	Q9T355	homo sapien
	3	297	53.4	263	11	Q08855	Q08855	mus musculus
	4	296	53.2	263	11	Q09042	Q09042	mus musculus
	5	287.5	51.7	241	6	Q9T549	Q9T549	crinaceus e
	6	273	49.1	258	11	Q09054	Q09054	rattus norv
	7	271	48.7	258	11	Q08877	Q08877	rattus norv
	8	132	23.7	263	13	Q98T66	Q98T66	anguilla ja
	9	130.5	23.5	366	13	Q93601	Q93601	gallus galli
	10	113	20.3	174	13	Q98S13	Q98S13	cyprinus ca
	11	112.5	20.2	244	4	Q13784	Q13784	homo sapien
	12	111	20.0	1547	5	Q26471	Q26471	schistocerc
	13	109.5	19.7	102	13	Q98T79	Q98T79	platichthys
	14	102.5	18.4	395	11	Q9D8N0	Q9D8N0	mus musculus
	15	102.5	18.4	395	11	Q91X58	Q91X58	mus musculus
	16	102.5	18.4	435	11	Q01458	Q01458	mus musculus

17	97.5	17.5	224	13	0.9P73	09c173 scopthalmi
18	97	17.4	317	6	0.9GLM8	09g1m8 gotilla gor
19	95	17.1	313	6	0.9GLC0	09g1c0 tupia glis
20	93	16.7	317	6	0.9GLJ3	09g1j3 pan troglod
21	93	16.7	317	6	0.9GLM7	09g1m7 pongo pygma
22	93	16.7	317	6	0.9GLM6	09g1m6 hylobates c
23	91.5	16.5	113	3	0.08245	0.08245 saccharomyc
24	90.5	16.3	1518	5	0.21442	0.21442 caenorhabdi
25	90.5	16.3	3704	5	P91904	P91904 caenorhabdi
26	89.5	16.1	1845	12	0.9w128	0.9w128 human cytom
27	88	15.8	363	4	0.9B0J3	0.9B0J3 homo sapien
28	87.5	15.7	194	11	0.94D29	0.94D29 mus musculu
29	87	15.6	229	16	0.9CNI8	0.9CNI8 pasteurella
30	87	15.6	2310	5	0.9NKR1	0.9NKR1 leishmania
31	87	15.6	2354	5	0.9NKR19	0.9NKR19 leishmania
32	86.5	15.6	240	11	0.9RXI9	0.9RXI9 delnoccusu
33	86	15.5	457	11	0.9DCV7	0.9dcv7 mus musculu
34	86	15.5	731	5	0.9N8D2	0.9n8d2 trypanosoma
35	85.5	15.4	585	4	0.9UHM5	0.9uhm5 homo sapien
36	85.5	15.4	585	4	0.9P028	0.9p028 homo sapien
37	85.5	15.4	603	4	0.75135	0.75135 homo sapien
38	84.5	15.2	500	5	0.9GT16	0.9gt16 wuchereria
39	84.5	15.2	585	11	0.98443	0.98443 mus musculu
40	84	15.1	259	13	0.987G5	0.987g5 anguilla japa
41	84	15.1	1175	5	0.9T12	0.9t12 drosophila
42	84	15.1	1201	5	0.8392	0.8392 drosophila
43	84	15.1	1411	4	0.15075	0.15075 homo sapien
44	84	15.1	2067	5	0.9VJ13	0.9v13 drosophila
45	83.5	15.0	1164	5	P92021	P92021 caenorhabdi

ALIGNMENTS

RESULT	1	
0922L4		
ID	0922L4	PRELIMINARY; PRT; 264 AA.
AC	0922L4;	
DT	01-MAY-1999 (TREMBLrel. 10, Created)	
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE	APOLIPOPROTEIN A-I.	
GN	APOAI.	
OS	Mesocricetus auratus (Golden hamster).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;	
OC	Mesocricetus.	
OX	NCBI_TaxID=10036;	
OX	[1]	
RP	SEQUENCE FROM N.A.	
RC	SPRAIN-GOLDEN SYRIAN; TISSUE=INTESTINE;	
RX	MEDLINE=99061559; PubMed=9843713;	
RA	Wu J.Y., Reeves S.K., Wang Y.R., Wu Y., Lei P.P., Lei K.Y.;	
RT	"Amino deficiency decreases plasma level and hepatic mRNA abundance of	
RL	Apolipoprotein A-I in rats and hamsters."	
RL	Am. J. Physiol. 275:C1516-C1525(1998).	
DR	EMBL; AF046919; AAC98484.1; -.	
DR	HSSP; P02647; IAVI.	
DR	InterPro; IPR000074; Apolipoprotein.	
DR	Pfam; PF01442; Apolipoprotein; 1.	
DR	lipoprotein.	
DR	SEQUENCE 264 AA; 30739 MW; 280B22F4C0F0B129 CRC64;	

Query Match	66.0%;	Score 367;	DB 11;	Length 264;
Best Local Similarity	65.2%;	Pred. No. 4e-23;		
Matches 73;	Conservative 13;	Mismatches 24;	Indels 2;	Gaps 1

[illegible]

DB 213 YHTRAKADHLKAFGEKAKPALEDLROGLMPVSEFKTRIMSVNEFSKLTNAQ 264

RESULT 2
ID 09Y355 PRELIMINARY: PRT: 67 AA.

AC 09Y355: 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)
DE APOLIPROTEIN A1 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
RX MEDLINE=99216322; PubMed=10198255;
RA Hamidi Asl K., Liepinieks J.J., Nakamura M., Parker F., Benson N.D.;
RT "A novel apolipoprotein A-1 variant, Arg173Pro, associated with
RL cardiac and cutaneous amyloidosis";
RT Biochem. Biophys. Res. Commun. 257:584-588(1999).
DR EMBL; AF148963; AAD34604.1; -.
DR HSSP; P02647; IAV1.
KW Lipoprotein.
FT NON_TER 1 1
FT SEQUENCE 67 AA; 7433 MW; 525ELFER7BD5AFB CRC64;

Query Match 58.8%; Score 327; DB 4; Length 67;
Best Local Similarity 98.5%; Pred. No. 1.8e-20;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 LSPLEEMDRARAHVDAIRTHLAPYSDELRLAARLEALKENGARLAELHAKATHTL 69
DB 1 LSPLEEMDRARAHVDAIRTHLAPYSDELRLAARLEALKENGARLAELHAKATHTL 60

QY 70 STLSEKA 76
DB 61 STLSEKA 67

RESULT 3
ID 008855 PRELIMINARY: PRT: 263 AA.

AC 008855: 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE APOLIPROTEIN A-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=SPLEEN;
RX MEDLINE=98077648; PubMed=9415807;
RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
RT "Repetitive elements in the third intron of murine apolipoprotein A-1
RT gene";
RT Biochem. Mol. Biol. Int. 43:989-996(1997).
DR EMBL; U79574; AAB58426.1; -.
DR HSSP; P02647; IAV1.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Lipoprotein.
SO SEQUENCE 263 AA; 30544 MW; 7825DF7483A5B24A CRC64;

Query Match 53.4%; Score 297; DB 11; Length 263;

Best Local Similarity 53.6%; Pred. No. 2.7e-17;
Matches 60; Conservative 18; Mismatches 32; Indels 2; Gaps 1;

QY 1 OKLHEIOEKISPLGEEMDRARAHVDAIRTHLAPYSDELRLAARLEALKENGARLAEL 60
DB 154 OKLHEIOEKISPLGEEMDRARAHVDAIRTHLAPYSDELRLAARLEALKENGARLAEL 211

QY 61 YHAKATEHLSTSEKAKPALEDLROGLMPVSEFKTRIMSVNEFSKLTNAQ 112
DB 212 YHTRAKTHLKTGKAKPALEDLROGLMPVSEFKTRIMSVNEFSKLTNAQ 263

RESULT 4
ID 009042 PRELIMINARY: PRT: 263 AA.

AC 009042: 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
DE APOLIPROTEIN A-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.
RC STRAIN=ICR AND BALB/C, AND C3H; TISSUE=SPLEEN;
RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
RL Submitted (JUN-1997) to the EMBL/Genbank/DDb databases.
DR EMBL; U79575; AAB58427.1; -.
DR EMBL; U79572; AAB58424.1; -.
DR EMBL; U79573; AAB58425.1; -.
DR HSSP; P02647; IAV1.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Lipoprotein.
SO SEQUENCE 263 AA; 30516 MW; E245DF7483A5B0DD CRC64;

Query Match 53.2%; Score 296; DB 11; Length 263;
Best Local Similarity 53.6%; Pred. No. 3.3e-17;
Matches 60; Conservative 18; Mismatches 32; Indels 2; Gaps 1;

QY 1 OKLHEIOEKISPLGEEMDRARAHVDAIRTHLAPYSDELRLAARLEALKENGARLAEL 60
DB 154 OKLHEIOEKISPLGEEMDRARAHVDAIRTHLAPYSDELRLAARLEALKENGARLAEL 211

QY 61 YHAKATEHLSTSEKAKPALEDLROGLMPVSEFKTRIMSVNEFSKLTNAQ 112
DB 212 YHTRAKTHLKTGKAKPALEDLROGLMPVSEFKTRIMSVNEFSKLTNAQ 263

RESULT 5
ID 09TS49 PRELIMINARY: PRT: 241 AA.

AC 09TS49: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
DE APOLIPROTEIN A-1, APOA-I-CHOLESTEROL TRANSPORTER.
OS Erinnaceus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.
OX NCBI_TaxID=9365;
RN 11
RP SEQUENCE.
RX MEDLINE=95294458; PubMed=7775860;
RA Sparrow D.A., Laplaud P.M., Saboureau M., Zhou G., Dolphin P.J.,
RA Goto A.M.Jr., Sparrow J.T.;
RT "Plasma lipid transport in the hedgehog: partial characterization of
RT structure and function of apolipoprotein A-I";
RT J. Lipid Res. 36:485-495(1995).
DR HSSP; P02647; IAV1.

DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 SQ SEQUENCE 241 AA; 27630 MW; 2EF00F2B69210535 CRC64;

Query Match 51.7%; Score 287.5; DB 6; Length 241;
 Best Local Similarity 53.6%; Pred. No. 1.5e-16;
 Matches 60; Conservative 14; Mismatches 37; Indels 1; Gaps 1;
 QY 1 OKLHEKLSPLGEMDRARAHVDAALRTHLAPYSDELROQLARLEALKENGARLAE 60
 DB 131 QKAEHLKQAGELQORRRVTHVDAALRTDLAPYGEERKLLLDIDIKAKSG-DLAE 189
 QY 61 YHAKATEHLSTLSEKAPALDELROGLLPVLESFVFSLSALEEYTKLN 112
 DB 190 YQTKLSEHLKSFGEKAPQPTLDLRGLLEPTMGITAGAMSMLEELGKKLN 241

RESULT 6
 ID 009054 PRELIMINARY; PRT; 258 AA.
 AC 009054;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE Apolipoprotein A-I.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WKT, AND SHRSP; TISSUE=SPLEEN.
 RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U79578; AAB58430.1; -
 DR EMBL: U79577; AAB58429.1; -
 DR HSSP: P02647; IAV1.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 SQ SEQUENCE 258 AA; 29918 MW; 093B6EF2E629C0C8 CRC64;

Query Match 49.1%; Score 273; DB 11; Length 258;
 Best Local Similarity 50.4%; Pred. No. 2.6e-15;
 Matches 57; Conservative 18; Mismatches 32; Indels 6; Gaps 2;

QY 2 KLH----ELQELSLPLGEMDRARAHVDAALRTHLAPYSDELROQLARLEALKENGAR 57
 DB 147 ELHNNAKEMQRLKVAEERDRKRVADALRAKFGLYSDQRENLAQRLTEIKNH--PT 204
 QY 58 LAEYHAKATEHLSTLSEKAPALDELROGLLPVLESFVFSLSALEEYTKLN 110
 DB 205 LIEVHTKASDHLKTLGKAKPALDLDLGIMPLVLEAVKAKIMSIDAKKKLN 257

RESULT 7
 ID 008877 PRELIMINARY; PRT; 258 AA.
 AC 008877;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Apolipoprotein A-I.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SHR; TISSUE=SPLEEN;
 MEDLINE=98077648; PubMed=9415807;

RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
 RT "Repetitive elements in the third intron of murine apolipoprotein A-I
 RT gene.";
 RL Biochem. Mol. Biol. Int. 43:989-996(1997).
 DR EMBL: U79576; AAB58428.1; -
 DR HSSP: P02647; IAV1.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 SQ SEQUENCE 258 AA; 29831 MW; 093FB582E629C0C8 CRC64;

Query Match 48.7%; Score 271; DB 11; Length 258;
 Best Local Similarity 50.4%; Pred. No. 3.9e-15;
 Matches 57; Conservative 17; Mismatches 33; Indels 6; Gaps 2;
 QY 2 KLH----ELQELSLPLGEMDRARAHVDAALRTHLAPYSDELROQLARLEALKENGAR 57
 DB 147 ELHNNAKEMQRLKVAEERDRKRVADALRAKFGLYSDQRENLAQRLTEIKNH--PT 204
 QY 58 LAEYHAKATEHLSTLSEKAPALDELROGLLPVLESFVFSLSALEEYTKLN 110
 DB 205 LIEVHTKASDHLKTLGKAKPALDLDLGIMPLVLEAVKAKIMSIDAKKKLN 257

RESULT 8
 ID 098TG6 PRELIMINARY; PRT; 263 AA.
 AC 098TG6;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
 DE 28KDa-2 Apolipoprotein.
 OS Anguilla japonica (Japanese eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillioidei;
 OC Anguillidae; Anguilla.
 OX NCBI_TaxID=7937;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=21175592; PubMed=11278178;
 RA Kondo H., Kawazoe I., Nakuchi K., Aida K., Watabe S.;
 RT "The novel sequences of major plasma apolipoproteins in the eel
 RT Anguilla japonica.";
 RL Biochim. Biophys. Acta 1531:132-142(2001).
 DR EMBL: AB046203; BAB40960.1; -
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 SQ SEQUENCE 263 AA; 30087 MW; DB8CB0AF30EB6B1 CRC64;

Query Match 23.7%; Score 132; DB 13; Length 263;
 Best Local Similarity 29.0%; Pred. No. 0.0015;
 Matches 31; Conservative 26; Mismatches 48; Indels 2; Gaps 1;

QY 1 OKLHEKLSPLGEMDRARAHVDAALRTHLAPYSDELROQLARLEALKENGARLAE 60
 DB 155 QEMELKTKLQVVEDLRRIQVNEETKSKVPIVERAIRALTRELRLETPYVOE 214
 QY 61 YHAKATEHLSTLSEKAPALDELROGLLPVLESFVFSLSALEEYTK 107
 DB 215 YKDHLSEALTVKDKVGG--EDLQSKLPYAEELKTKVALMESLSQ 259

RESULT 9
 ID 093601 PRELIMINARY; PRT; 366 AA.
 AC 093601;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DE APOLOPROTEIN AIV.
 GN APOAIV.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98221191; PubMed=9553114;
 RX Steilmetz A., Hermann M., Nimpt J., Aebersold R., Ducret A.,
 RA Weinberg R.B., Schneider W.J.;
 RT "Expression and conservation of apolipoprotein AIV in an avian
 RT species";
 RL J. Biol. Chem. 273:10543-10549(1998).
 DR EMBL: Y16534; CAA6273.1;
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 SO SEQUENCE 366 AA; 40852 MW; B47DB49F3E8D91CE CRC64;

Query Match 23.5%; Score 130.5; DB 13; Length 366;
 Best Local Similarity 25.9%; Pred. No. 0.0029;
 Matches 36; Conservative 27; Mismatches 43; Indels 33; Gaps 2;

QY 6 LQKLSPLGEMDRARAHDALRTHLAPYSDEL-----QRLARLEALKEKGASRL 58
 DB 196 LKGLPLADLEKQVAVSVEGLKGLSPFAQEVQDGLNRQSLAOMERAAEELRSL 255
 QY 59 AEYAKATEHLSTLSEKAKPAL-----EDLRGGLLPVL 92
 DB 256 AASEEMRAQSLPLAQALRGDAEAMQRLAPLAQDLERLAQVFAFRQAAPISE 315
 QY 93 SFKVSFLSALEETKRLNT 111
 DB 316 TFRQOLVORLEEMKOKLES 334

RESULT 10
 Q98S13 PRELIMINARY; PRT; 174 AA.
 AC Q98S13;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE APOLOPROTEIN A-I (FRAGMENT).
 GN APOA1.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RA Concha M.I., Villanueva J., Amthauer R.J.;
 RT "Synthesis and secretion of apolipoprotein A-I in the carp skin: A
 RT possible defensive mechanism";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ308993; CAC34942.1;
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 FT NON_TER
 SO SEQUENCE 174 AA; 20810 MW; 435FC05AE0EA0578 CRC64;

Query Match 20.3%; Score 113; DB 13; Length 174;
 Best Local Similarity 23.4%; Pred. No. 0.035;
 Matches 30; Conservative 27; Mismatches 51; Indels 20; Gaps 2;

QY 3 LHELOKLSPLGEMDRARAHDALRTHLAP-----YSDELRLARLEALK 51

DB 41 VEEELRKKTEPPRAELROVLEKHLQEXRDELKPEVEEYLTKEHQFLDEMRKTEPPYKSLR 100
 QY 52 ENGGAFLAEYHAKATEHLSTLSEKAKPALEDRLQGLLPVLESFVSLSALEY----- 105
 DB 101 EKFGPPNMEETKSKMLPLEAVREKVAHEDLDKLLKLEPPYQDYRDEMGKAGQEFQSVKS 160
 QY 106 ---TRKLN 110
 DB 161 GELRKKMN 168

RESULT 11
 Q13784 PRELIMINARY; PRT; 244 AA.
 ID Q13784;
 AC Q13784;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE APOA4 PROTEIN (FRAGMENT).
 GN APOA4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=86016704; PubMed=3931073;
 RA Karathanasis S.K.;
 RT "Apolipoprotein multigene family: tandem organization of human
 RT apolipoprotein AI, CII, and AIV genes";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6374-6378(1985).
 DR EMBL: M10373; AAB59516.1;
 DR HSSP: P02649; I824.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 FT NON_TER
 SO SEQUENCE 244 AA; 28157 MW; 01616ACB53F12734 CRC64;

Query Match 20.2%; Score 112.5; DB 4; Length 244;
 Best Local Similarity 25.4%; Pred. No. 0.057;
 Matches 35; Conservative 27; Mismatches 47; Indels 29; Gaps 3;

QY 1 OKLHELOKLSPLGEMDRARAHDALRTHLAPYSDELRLARLEAL-----KENGGA 56
 DB 58 QNVEELKRLTPYADEFKYKIDQVLEELRSLAPYAQDTQELKLNQLEGLFPQKKNAE 117
 QY 57 RLAEYHAKATE--HLSTLSEKAKPAL-----EDLRGGLLPVL 91
 DB 118 LKARISASAEELRQRLAPLEAVRGNLKNTEGLQSLAEIGHLDQVEEFRVRVEPYG 177
 QY 92 ESFVSFLSALEETKRL 109
 DB 178 ENFNKALVOQMQLROKL 195

RESULT 12
 Q26471 PRELIMINARY; PRT; 1547 AA.
 ID Q26471;
 AC Q26471;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE BLACKJACK PROTEIN.
 OS Schistocerca americana (American grasshopper).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Schistocerca.
 OX NCBI_TaxID=7009;
 RN (1)
 RP SEQUENCE FROM N.A.

RX	Tissue-embryo: MEDLINE=96393048; PubMed=8799836;
RA	Zachow K.R., Bentley D.; "Blackjack, a novel protein associated with microtubules in embryonic neurons";
RT	J. Cell Sci. 109:1497-1507(1996).
RL	-I- SUBCELLULAR LOCATION: MICROTUBULE ASSOCIATED.
CC	-I- TISSUE SPECIFICITY: IN THE EMBRYO, HEAVILY EXPRESSED IN CNS AND PNS AXONS. EXPRESSED AT LOWER LEVELS IN EPITHELIAL AND MESODERMAL CELLS.
DR	EMBL: U76606; AAC37266.1; -; InterPro: IPR004155; HEST PBS. DR Pfam: PF03130; HEST PBS: 7.
KW	Coupled coil: Microtubules; Rept.
FT	DOMAIN 630 860 21 x 11 AA TANDEM REPEATS OF P-L-E-E-L-R
FT	REPEAT 630 640 1. K-D-A-A-E.
FT	REPEAT 641 651 2.
FT	REPEAT 652 662 3.
FT	REPEAT 663 673 4.
FT	REPEAT 674 684 5.
FT	REPEAT 685 695 6.
FT	REPEAT 696 706 7.
FT	REPEAT 707 717 8.
FT	REPEAT 718 728 9.
FT	REPEAT 729 739 10.
FT	REPEAT 740 750 11.
FT	REPEAT 751 761 12.
FT	REPEAT 762 772 13.
FT	REPEAT 773 783 14.
FT	REPEAT 784 794 15.
FT	REPEAT 795 805 16.
FT	REPEAT 806 816 17.
FT	REPEAT 817 827 18.
FT	REPEAT 828 838 19.
FT	REPEAT 839 849 20.
FT	REPEAT 850 860 21.
FT	DOMAIN 631 860 COILED COIL (POTENTIAL).
SQ	SEQUENCE 1547 AA; 169310 MW; 94F3D243768BFDEB CRC64;

Query Match 20.0%; Score 111; DB 5; Length 1547;
Best Local Similarity 31.8%; Pred. No. 0.62;
Matches 34; Conservative 16; Mismatches 57; Indels 0; Gaps

```

QY      1 QKIHLELOEKLSPLGEENRDRARAHVDAPTHLLAPYSDELROKLARLDLAKENGCAFLAE 60
          :|::: |::| |:: ||::||::||::||::||::||::||::||::||::||::||::||
DB       640 EPLEELRKDAEPELELRKDAAEPLEELRKDAEPELELRKDAAEPLEELRKDAEPELEE 699
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      61 YHAKTEHLSTLSKAKPALEDLROGILLPYLESFKVSFLALEEYTK 107
          ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB       700 LKKDAEPELELRKDAAEPLEELRKDAEPELELRKDAAEPLEELRKDAEPELELRK 746
          ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
    
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RESULT 13

ID	O98JT9	PRELIMINARY;	PRT;	102 AA.
AC	O98JT9;			
DT	01-JUN-2001 (TREMBREL, 17, Created)			
DT	01-JUN-2001 (TREMBREL, 17, Last sequence update)			
DT	01-DEC-2001 (TREMBREL, 19, Last annotation update)			
DE	APOLIPOPOTEIN AI (FRAGMENT).			
GN	APOL1.			
OS	Platichthys flesus (European flounder).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neoplecyti; Teleostei; Euteleostei; Neoteleostei;			
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;			
OC	Pleuronectoidei; Pleuronectidae; Platichthys.			
OX	NCBI_TaxId=8260;			
ON	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RA	Williams T.D., Chipman J.K.;			

RT "A DNA array to monitor the effects of environmental pollution on
RT European flounder (*Platichthys flesus*).";
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ110423; CAC27154.1; -.
KW Lipoprotein.
FT NON TER 1 1
SO SEQUENCE 102 AA; 11248 MW; 8F0EB2150625EDFA CRC64;

Query Match	19.7%;	Score 109.5;	DB 13;	Length 102;
Best Local Similarity	27.6%;	Pred. No. 0.038;		
Matches	27;	Conservative	20;	Mismatches 40;
				Indels 11.
				Gap 1

```
QY 12 PLGEHMDRARAHVDLRLTHLAPYSDCLRORLARLEALKENGSGARLAEE----- 61
Db 2 PVDADAKTSTAAANVEETTKATLALPIESYRAKTSLESLKEMATPYGEYKKDOLKOAYGO 61
QY 62 -HAKKATHEHSTLSEKAKPALLEDLRQGLLPVLESKVSF 98
Db 62 AQAVKPEDDIALKEKISPAEVEVKAKVEMEEAATAAF 99
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RESULT	14
ID	Q9DBNO
Q9DBNO	PRELIMINARY:
Q9DBNO	PRT: 395 AA.
DT	01-JUN-2001 (TREMBLrel. 17, Created)
DY	01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE	ADULT MALE LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE	CLONE:1300002K10, FULL INSERT SEQUENCE.
OS	APOLAL.
GN	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=LIVER.
RX	MEDLINE=21085660; PubMed=11217851;
RA	Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA	Arakawa T., Hara A., Fukunishi Y., Komio H., Adachi T., Fukuda S.,
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA	Saito T., Okazaki Y., Gotojohri T., Bono H., Kasukawa T., Saito R.,
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Koehne H.,
RA	Kuehl P., Lewis S., Matsuo Y., Niklido I., Pesole G., Quackenbush J.,
RA	Schimi L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA	Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA	Gustincich S., Hill D., Hoffman M., Hume D.A., Kamiya M., Lee N.H.,
RA	Lyons F., Marchionni L., Mashima J., Mazzarelli J., Mombeerts P.,
RA	Nordone P., Ring B., Ringwald C., Seya T., Shibata Y., Storch K.-F.,
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA	Suzuki H., Toyokawa K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA	Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kozitski S.,
RA	Yashizaki Y.;
RT	"Functional annotation of a full-length mouse cDNA collection.";
RT	Nature 409:665-690(2001).
DR	EMBL: AK004856, BAB23620.1; -;
DR	MCD: MGI:88051; Apolal.
DR	InterPro: IPR000074; Apolipoprotein.
DR	Protein: P01442; Apolipoprotein; 1.
SO	SEQUENCE 395 AA; 45044 MW; 410284ACG0D182A CRC64.

	Query Match	18.4%	Score 102.5	DB 11	Length 395	
	Best Local Similarity	19.8%	Pred. No. 0.67			
	Matches	23	Conservative	39	Mismatches	47
					Indels	7
					Gaps	
QY	1	OKHLEOERKSPGEMDRBRNRHVDALRTHLAFPSDLRLRLAREDAIKENGARLAE	60			1
		:::: :	:	:	: :	:::: :

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:05:15 ; Search time 139.03 Seconds

(without alignments)
89.479 Million cell updates/sec

Title: US-09-803-918a-2_COPY_156_267

Perfect score: 536

Sequence: 1 OKLHELQKLSPLGEMRDR.....SFKVSFLSALEHYTKINTQ 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

Maximum Match 100%

Listing first 45 summaries

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21:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:**
22:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	100.0	243	9	AA1982
2	556	100.0	244	22	AAU28184
3	556	100.0	267	7	AA191079
4	556	100.0	267	9	AA192128
5	556	100.0	267	14	AA1934032
6	556	100.0	267	16	AA192705
7	556	100.0	267	20	AA191875
8	556	100.0	267	22	AA1947620
9	548	98.6	267	9	AA190668
10	548	98.6	267	18	AA1906602
11	545	98.0	264	15	AA195663

Result No.	Score	Query Match	Length	ID	Description
12	545	98.0	264	15	AA195664
13	522	93.9	299	22	AAU33170
14	496.5	89.3	359	22	AAU30470
15	409.5	73.7	318	22	AAU30268
16	376	67.6	221	22	AAU29835
17	194	34.9	151	22	AAU02278
18	187.5	33.7	119	22	AAU30468
19	125	22.5	333	14	AA193497
20	125	22.5	333	14	AA193498
21	125	22.5	336	22	AA190664
22	124	22.3	183	14	AA193482
23	124	22.3	333	14	AA193481
24	124	22.3	333	14	AA193488
25	124	22.3	333	14	AA193490
26	124	22.3	333	14	AA193495
27	124	22.3	337	14	AA193492
28	124	22.3	342	14	AA193487
29	124	22.3	342	14	AA193489
30	124	22.3	342	14	AA193491
31	124	22.3	342	14	AA193496
32	124	22.3	346	14	AA193493
33	124	22.3	363	14	AA193479
34	124	22.3	373	14	AA193478
35	124	22.3	377	14	AA193486
36	124	22.3	377	14	AA193443
37	124	22.3	377	14	AA193502
38	124	22.3	377	14	AA193501
39	124	22.3	377	14	AA195242
40	124	22.3	377	14	AA195243
41	122	21.9	337	14	AA195244
42	121	21.8	377	14	AA194944
43	120.5	21.7	328	14	AA1939500
44	120.5	21.7	337	14	AA1939484
45	120.5	21.7	363	14	AA1939485

ALIGNMENTS

RESULT 1

AA1982 standard; protein; 243 AA.

AA1982:

14-JAN-1991 (first entry)

Sequence of mature human apolipoprotein AI (apoAI).

Atherosclerosis; therapy; cardiovascular disease.

Homo sapiens.

W08803166-A.

05-MAY-1988.

21-OCT-1987; 87WO-EP00621.

23-OCT-1986; 86GB-0025435.

(FARM) FARMITALIA C ERBA SPA.

Loenzetti R, Monaco L, Soria M, Palomba R, Isacchi A, Sarmientos P; WPI: 1988-133240/19.

N-PSDB; AAN80243.

Recombinant human apo:lipoprotein AI - used to lower plasma cholesterol and/or tri glyceride levels and to combat atherosclerosis and cardiovascular diseases

Disclosure; Fig 1; 51pp; English.

XX The protein comprising apo AI genetic variants may be used to lower
 CC plasma cholesterol and/or triglyceride levels. They may also be used to
 CC combat atherosclerosis and cardiovascular diseases such as coronary
 CC heart disease. Peptide proteins are Met-apo AI, Met-apo AI-T6, Met-apo
 CC AI-MI and Met-apo AI-T6/MI.

XX Sequence 243 AA;

Query Match 100.0%; Score 556; DB 9; Length 243;
 Best Local Similarity 100.0%; Pred. No. 9.6e-49;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OKLHELOEKLSPGEMRRARAHVDALRTHLAPYSDELRIQRLAARLEALKEKGARLAE 60
 DB 132 qkheqekispigemdrarahvdalrthlapydelrqrtaarleaalkengarlalae 191

OY 61 YHAKATEHLSTSEKAPALDELROGLLPVLESFVSTLSALEEYTKKLNQ 112
 DB 192 ynakatehlstsekapaledlrqglpvlsefkvsflsaeleeytkklnq 243

RESULT 2

AAU28184 standard; Protein; 244 AA.

AAU28184;

18-DEC-2001 (first entry)

Novel human secretory protein, Seq ID No 353.

Human: secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.

OS Homo sapiens.

MO20016689-A2.

13-SEP-2001.

05-MAR-2001; 2001MO-US04942.

07-MAR-2000; 2000US-0519705.
 19-MAY-2000; 2000US-0574454.
 17-JUN-2000; 2000US-0596193.
 14-JUL-2000; 2000US-0616847.
 19-SEP-2000; 2000US-0665363.
 20-OCT-2000; 2000US-0693267.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Dimaenac RT, Zhang J, Chen R, Xue AJ, Wang J;
 DR N-PSDB; AAS45084.
 WPI; 2001-589934/66.

Novel polypeptides and nucleic acids obtained from cDNA libraries
 prepared from various human tissues, for diagnosis and treatment of
 cancer, neurological, inflammatory, and autoimmune disorders.

Example 5; SEQ ID No 353; 107pp; English.

The invention relates to novel isolated human secreted polypeptides (I)

CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischemia-reperfusion injury, shock, sepsis, immune response, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity; regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention.

Sequence 244 AA;

Query Match 100.0%; Score 556; DB 22; Length 244;
 Best Local Similarity 100.0%; Pred. No. 9.7e-49;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OKLHELOEKLSPGEMRRARAHVDALRTHLAPYSDELRIQRLAARLEALKEKGARLAE 60
 DB 132 qkheqekispigemdrarahvdalrthlapydelrqrtaarleaalkengarlalae 192

OY 61 YHAKATEHLSTSEKAPALDELROGLLPVLESFVSTLSALEEYTKKLNQ 112
 DB 193 ynakatehlstsekapaledlrqglpvlsefkvsflsaeleeytkklnq 244

RESULT 3

AAU281079 standard; Protein; 267 AA.

AAU281079;

07-OCT-1991 (first entry)

Assumed human apolipoprotein A-1 derivative gene product.

Hyperlipaemia; arteriosclerosis.

Homo sapiens.

JP61096998-A.

15-MAY-1986.

16-OCT-1984; 84UP-0216988.

16-OCT-1984; 84UP-0216988.

(MITU) MITSUBISHI CHEM IND KK.

DR WPI: 1986-165025/26.
 DR N-PSDB: AAN60886.
 XX Human apo:lipoprotein A-I (deriv.) prepn. - by providing DNA
 PT fragment in cloning site downstream of expression vector promoter
 PT and introducing into host microorganism.
 XX
 PS Disclosure; Fig 2; 9pp; Japanese.
 XX
 CC The human apolipoprotein may be produced by a suitable transformed
 CC host, it is effective in treating hyperlipaemia and arteriosclerosis.
 CC
 XX
 SQ Sequence 267 AA;
 Query Match 100.0%; Score 556; DB 7; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.1e-48;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 OKLHELOEKLSPGEMDRARAHVDALRTHLAPYSDLRQRLARLEALKENGARLAE 60
 DB 156 qklhelgeklspgsemrdraravdalrthlapyssdelrqlaarlealkenggarlae 215
 QY 61 YHAKATEHLSTSEKAPALDLROGLLPVLESFVSTLSALEEYTKKLNQ 112
 DB 216 yhakatehlstsekakpaledlrqgllpylesfkvsfslsaleeytkklnq 267
 RESULT 4
 AAP82128
 ID AAP82128 standard; protein: 267 AA.
 AC AAP82128;
 DF 24-OCT-1990 (first entry)
 DE Entire human preproapoprotein A1.
 XX human preproapoprotein A1; high density lipoprotein deficiency; ss.
 KM human preproapoprotein A1; high density lipoprotein deficiency; ss.
 XX
 OS synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT Peptide /label=precursor
 FT Peptide 19..24
 FT Peptide /label=propeptide
 FT Protein 25..267
 FT /label=mature apoprotein
 PN EP293357-A.
 PD 30-NOV-1988.
 PF 24-MAY-1988; 88BP-0870095.
 PR 28-MAY-1987; 87GB-0012540.
 XX (UNIO) UCB SA.
 PA Bollen A, Gobert J, Wulfert E;
 PI WPI: 1988-339891/48.
 DR N-PSDB: AAN82064.
 XX
 PT New DNA encoding human preproapoprotein A1 -
 PT modified to eliminate hairpin structures
 XX
 PS Disclosure; ; P; French.
 CC The cDNA 878bp fragment encoding preproapoprotein A1 was detected
 CC in clone PUB1609 derived from human liver cells.
 CC See also AAN81258.

XX
 SQ Sequence 267 AA;
 Query Match 100.0%; Score 556; DB 9; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.1e-48;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 OKLHELOEKLSPGEMDRARAHVDALRTHLAPYSDLRQRLARLEALKENGARLAE 60
 DB 156 qklhelgeklspgsemrdraravdalrthlapyssdelrqlaarlealkenggarlae 215
 QY 61 YHAKATEHLSTSEKAPALDLROGLLPVLESFVSTLSALEEYTKKLNQ 112
 DB 216 yhakatehlstsekakpaledlrqgllpylesfkvsfslsaleeytkklnq 267
 RESULT 5
 AAR34032
 ID AAR34032 standard; Protein: 267 AA.
 AC AAR34032;
 DT 13-AUG-1993 (first entry)
 DE Sequence of apo A1.
 XX
 KM Lipoprotein; apoprotein; B-100; A-I; LDL; HDL; assay.
 XX
 OS Homo sapiens.
 PN WC9307165-A.
 PD 15-APR-1993.
 PF 09-OCT-1992; 92WC-US08634.
 PR 09-OCT-1991; 91US-0774633.
 PR 08-OCT-1992; 92US-055555.
 PR 28-JUN-1992; 92US-0901706.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Curtiss LK, Koduri KR, Smith RS, Wiltzium JL, Young SG;
 DR WPI: 1993-134378/16.
 DR N-PSDB: AAO40030.
 XX Polypeptide mimic of native apo B-100 and native apo A-I - useful
 PT in assays for LDL and HDL in plasma samples
 PS Claim 19; Pages 105-106; 137pp; English.
 XX
 CC The inventors claim a portion of the polypeptide contg. apo B-100
 CC that immunoreacts with antibodies secreted by the hybridoma MB47
 CC having ATCC Accession No. 8746. Polypeptides specifically claimed
 CC include residues 217-297, 216-310, 216-331, 216-352, 216-377, 1-377,
 CC 205-297, 173-297, 140-297. DNA sequences encoding the polypeptides
 CC are also claimed. Also claimed are a fusion polypeptide that
 CC contains: (a) a first amino acid residue sequence up to 250 residues
 CC in length that includes residues 120-135 of apo A-I, (b) a second
 CC amino acid residue sequence up to 375 residues in length that
 CC includes residues 217-297 of apo B-100 and DNA encoding it.
 CC
 XX
 SQ Sequence 267 AA;
 Query Match 100.0%; Score 556; DB 14; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.1e-48;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 OKLHELOEKLSPGEMDRARAHVDALRTHLAPYSDLRQRLARLEALKENGARLAE 60
 DB 156 qklhelgeklspgsemrdraravdalrthlapyssdelrqlaarlealkenggarlae 215

Db 156 qkhlheqekispjgeemrdrarahvdalrthlapydelrqlraarleaalkenggarlae 215

OY 61 YHAKATEHLSTSEKAPALEDLROGLIPVLESFVKVSFLSALEYTKKLNQ 112
 |||||
 Db 216 yhakatehstlsekakpaledlrgllypvesfkvsflsaeeytkklnq 267

RESULT 6

AA72705 standard; Protein; 267 AA.

AC AAR72705;

DT 31-OCT-1995 (first entry)

DE Human apo A-I including signal and propeptide sequences.

KW Apo A-I; LDL cholesterol; low density lipoprotein; lipid.

OS Homo sapiens.

XX

FT Key Location/Qualifiers

FT Peptide 1..18

FT Peptide /label= presignal

FT Peptide 19..24

FT Peptide /label= propeptide

FT Peptide 120..135

FT Peptide /label= claimed

FT Peptide /note= "as part of fusion polypeptide"

FT Peptide /label= claimed

FT Peptide /note= "as part of fusion polypeptide"

PN US5408038-A.

XX 18-APR-1995.

PF 09-OCT-1991; 91US-0774633.

PR 09-OCT-1991; 91US-0774633.

PR 18-JUN-1992; 92US-0901706.

PR 08-OCT-1992; 92US-0959946.

XX

PA (SCRI) SCRIPPS RES INST.

PI Curtiss LK, Koduri KR, Smith RS, Wiltz JL, Young SG;

XX

DR WPI: 1995-161146/21.

DR N-PSDB: AAQ89634.

XX

PT New apo: lipoprotein B-100 peptide(s) and fusion peptide(s) - used

PT in assay systems for detecting LDL and HDL cholesterol levels in

PT body fluids.

XX

PS Claim 10: Fig 2: 41pp; English.

XX

CC AAA89634 and AAR72705 depict the AA sequence of human apo A-I and its

CC corresp. cDNA, including presignal residues and propeptide

CC residues, according to Seilhamer et al., DNA 3(4):309 (1984).

CC A dispersible apo A-I/B-100 fusion polypeptide is claimed which

CC contains a first AA sequence of apo A-I and that includes at

CC least AA sequence positions 120-135 (see AAR72606) and which reacts

CC with pan anti-apo A-I antibodies such as: AI-4 ATCC HB8744; AI-7

CC ATCC HB 8745; AI-9 ATCC HB 8741; AI-10 ATCC HB 9200; AI-11 ATCC

CC HB 9201; AI-12 ATCC HB 9202; AI-13 ATCC HB 9203; AI-14 ATCC HB

CC 9204; AI-18 ATCC HB 9507.

XX

SO Sequence 267 AA;

Query Match 100.0%; Score 556; DB 16; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.1e-48;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OKHLEQKSLPBGEMDRARAHVDALRTHLAPYSELRORLAARLEALKENGARLAE 60
 |||||
 Db 156 qkhlheqekispjgeemrdrarahvdalrthlapydelrqlraarleaalkenggarlae 215

OY 61 YHAKATEHLSTSEKAPALEDLROGLIPVLESFVKVSFLSALEYTKKLNQ 112
 |||||
 Db 216 yhakatehstlsekakpaledlrgllypvesfkvsflsaeeytkklnq 267

RESULT 7

AA18675 standard; Protein; 267 AA.

AC AAY18675;

DT 09-JUL-1999 (first entry)

DE Human apolipoprotein AI protein sequence.

KW Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder;

KW ApoA-I; cardiovascular disease; atherosclerosis; restenosis; LCAT;

KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.

OS Homo sapiens.

XX

PN MO9916409-A2.

XX 08-APR-1999.

PF 28-SEP-1998; 98WO-US20329.

PR 29-SEP-1997; 97US-0940136.

XX

PA (BUTT/) BUTTNER K.

PA (CORN/) CORNUT I.

PA (DASE/) DASSEUX J.

PA (DUFO/) DUFOURCO J.

PA (METZ/) METZ G.

PA (SEKU/) SEKUL R.

PI Butner K, Cornut I, Dasseux J, Dufourcq J, Metz G;

PI Sekul R.

XX

DR WPI: 1999-254921/21.

DR N-PSDB: AAX55971.

XX

PT Nucleic acid encoding apolipoprotein A-I agonist peptides

XX

PS Example: Fig 1: 232pp; English.

XX

CC The present invention describes a nucleic acid (A) encoding an

CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,

CC which forms an amphipathic alpha-helix in presence of lipids. (A),

CC optionally as a complex with lipids, and host cells that contain (A),

CC are useful for gene therapy, or prevention, of diseases associated with

CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,

CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I

CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat

CC endotoxemia (septic shock). Host cells containing (A) can also be used

CC to study the role of apoA-I in lipid metabolism. (B) can also be used

CC diagnostically, e.g. to measure serum HDL (particularly its

CC subpopulation involved in retrograde cholesterol transport) and for

CC imaging the circulatory system or HDL accumulations at fatty streaks.

CC The present sequence represents human apoA-I.

XX

SO Sequence 267 AA;

Query Match 100.0%; Score 556; DB 20; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.1e-48;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKLHELOEKLSPLGEMRRARAHVDALRTHLAPYSDCLRORLAARLEALKENGARLAE 60
 DB 156 qkLheqeklsplgeemrdrarahvdalrthlapydelrqlraarleaalkengarlae 215
 QY 61 YHAKATEHLSTSEKAPALDELROGLLPVLESFKVSFSALEEYTKKINTQ 112
 DB 216 yHakatehltstsekakpaledlrqglpvlsefkvsfisaaleeytkkintq 267

RESULT 8
 AAB47620
 ID AAB47620 standard; Protein; 267 AA.
 XX
 AC AAB47620;
 XX
 DT 21-JAN-2002 (first entry)
 XX
 DE Full length Apo-A1.
 XX
 KW Apolipoprotein; Apo-A1; Apo-A-I fragment T-cell activation inhibitor;
 KW AFTI; monocyte; IL-1; interleukin 1; TNF; tumor necrosis factor;
 KW acute pancreatitis; Alzheimer's disease; asthma; cancer; fever;
 KW inflammatory bowel disease; ischemia; multiple sclerosis; osteoporosis;
 KW Parkinson's disease; psoriasis; probe.
 XX
 OS Homo sapiens.
 XX
 Key location/Qualifiers
 FH 44..65
 FT Binding-site /label= Helical lipid binding domain
 FT Binding-site 220..241
 FT /label= Helical lipid binding domain
 FT 74..111
 FT /note= "Involved in lipoprotein-mediated cholesterol
 Binding-site 149..219
 FT /label= Receptor binding domain
 FT 99..120
 FT /label= Major antigenic epitope domain
 FT 99..143
 FT /label= Hinged domain
 FT 66..120
 FT /label= phylogenetically conserved domain
 FT 90..111
 FT /note= "Involved in lectin-cholesterol acyltransferase
 activity"
 FT 44..65
 FT /label= Amphipathic helix
 FT 66..98
 FT /label= Amphipathic helix
 FT 99..120
 FT /label= Amphipathic helix
 FT 121..142
 FT /label= Amphipathic helix
 FT 143..164
 FT /label= Amphipathic helix
 FT 165..208
 FT /label= Amphipathic helix
 FT 209..219
 FT /label= Amphipathic helix
 FT 220..241
 FT /label= Amphipathic helix
 FT 25..194
 FT /label= AFTI
 FT /note= "18 kD N-terminal fragment"
 FT 25..144
 FT /label= AFTI
 FT /note= "13 kD N-terminal fragment"
 FT 136..267
 FT /label= AFTI
 FT /note= "13 kD C-terminal fragment"
 XX
 PN WO200168852-A2.

XX 20-SEP-2001.
 FD 13-MAR-2001; 2001WO-US07826.
 PF 13-MAR-2000; 2000US-189008P.
 PR 13-MAR-2000; 2000US-189008P.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Edwards CK, Burger D, Dayer J, Kohno T;
 XX WPI: 2001-596908/67.
 DR N-PSDB; AAM43623.
 XX
 PT Apo-A-I fragment T-cell activation inhibitor (AFTI) polynucleotides,
 PT useful for treating, diagnosing, ameliorating diseases associated with
 PT IL-1 and/or TNF activity, e.g. acute pancreatitis, Alzheimer's disease
 PT and asthma -
 XX
 PS Claim 1; Fig 1a; 132pp; English.
 XX
 CC This sequence shows full length apolipoprotein (Apo-A1). Fragments
 CC of Apo-A1 may be used as Apo-A-I fragment T-cell activation inhibitors
 CC (AFTI). These fragments are selected from an 18 kD N-terminal fragment
 CC (amino acids 25-194), a 13 kD N-terminal fragment (amino acids 25-144)
 CC and a 13 kD C-terminal fragment (amino acids 156-267). The AFTI
 CC polypeptides and polynucleotides are useful for regulating T-cell
 CC mediated activation of monocytes and for treating, diagnosing,
 CC ameliorating diseases associated with IL-1 and/or TNF activity.
 CC The diseases are acute pancreatitis, Alzheimer's disease, asthma,
 CC cancer, fever, inflammatory bowel disease, ischemia, multiple
 CC sclerosis, osteoporosis, Parkinson's disease or psoriasis. Numerous
 CC examples of other diseases are given in the specification.
 CC The AFTI nucleic acids are useful as hybridization probes in diagnostic
 CC assays to test for the presence of an AFTI or Apo-A-I DNA in mammalian
 CC tissue or bodily fluid samples.
 CC
 SO Sequence 267 AA;

Query Match 100.0%; Score 556; DB 22; length 267;
 Best Local Similarity 100.0%; Pred. No. 1,1e-48;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKLHELOEKLSPLGEMRRARAHVDALRTHLAPYSDCLRORLAARLEALKENGARLAE 60
 DB 156 qkLheqeklsplgeemrdrarahvdalrthlapydelrqlraarleaalkengarlae 215
 QY 61 YHAKATEHLSTSEKAPALDELROGLLPVLESFKVSFSALEEYTKKINTQ 112
 DB 216 yHakatehltstsekakpaledlrqglpvlsefkvsfisaaleeytkkintq 267

RESULT 9
 AAP80668
 ID AAP80668 standard; protein; 268 AA.
 XX
 AC AAP80668;
 XX
 DT 24-OCT-1990 (first entry)
 XX
 DE Recombinant human preproapoprotein A1.
 XX
 KW human preproapoprotein A1; high density lipoprotein deficiency; ss.
 OS synthetic.
 XX
 FH Key location/Qualifiers
 FT Peptide 1..18
 FT Peptide /label=precursor
 FT Peptide 19..25
 FT /label=protein
 FT 26..268

FT /label=mature apoprotein A1
 XX EP293357-A.
 PN 30-NOV-1988.
 XX
 PD 24-MAY-1988; 88EP-0870095.
 XX
 PR 28-MAY-1987; 87GB-0012540.
 XX
 PA (UNIO) UCB SA.
 XX
 PI Bollen A, Gobert J, Wulfert E;
 DR WPI; 1988-339891/48.
 DR N-PSDB; AAN81258.
 XX
 PT New DNA encoding human preproapoprotein A1 -
 PT modified to eliminate hairpin structures
 PS Claim 1; Page 12; 25pp; French.
 XX
 CC Met at posn 19 is inserted as an extra amino acid c.f. wild-type
 CC protein.
 CC The DNA fragment used to replace the wild-type sequence encoding
 CC amino acids -6 to +14 (= Arg 20 to Leu 39) modifies codons
 CC corresponding to wild-type amino acids -1, 1, 3, 4, 5, 6, 7,
 CC 10, 11 and 14. The changed codons still encode the same amino acids
 CC as in the wild-type protein but reduce formation of secondary
 CC structures in mRNA.
 CC See also AAN82064.
 CC
 SQ Sequence 268 AA;
 Query Match 100.0%; Score 556; DB 9; Length 268;
 Best Local Similarity 100.0%; Pred. No. 1.le-48;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 QKHLQEKLSPLGEMDRARAHVDALRTHLAPYSDELRORLAARLEALKENGARLAE 60
 DB 157 qklhelqeklsplgsemrdarahvdalrthlapysdelrqlraarleaalkengarlae 216
 OY 61 YHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKVSFLSALEEYTKKINTQ 112
 DB 217 yhakatehlstlsekakpaledlrglilpvlesfkvsflsaleeytkkintq 268
 RESULT 10
 ID AAM08602
 AC AAM08602 standard; Protein; 267 AA.
 XX
 AC AAM08602;
 XX
 DT 04-SEP-1997 (first entry)
 XX
 DE Human apolipoprotein A-1 variant "Paris" protein sequence.
 XX
 KW Human; apolipoprotein A-1; variant; mutation; serum lipid; cholesterol;
 KW high density lipoprotein; triglyceride; symptom; cardiovascular disease;
 KW atherosclerosis; restenosis; myocardial infarct; angina; death; stroke;
 KW cardiac decompensation; metabolic deficit.
 XX
 OS Homo sapiens.
 XX
 FH key Location/Qualifiers
 FH Peptide 1..24
 FT /note= "prepro peptide"
 FT Region 172..178
 FT /note= "this sequence which contains the mutated amino
 FT acid residue is claimed - claim 2"
 FT Misc-difference 175
 FT /note= "changed from Arg residue in wild type protein,"

FT due to a C to T transition mutation"
 XX W09637608-A1.
 PN 28-NOV-1996.
 XX
 PD 20-MAY-1996; 96WO-FR00747.
 XX
 PR 22-MAY-1995; 95FR-0006061.
 XX
 PA (INSP) INST PASTEUR LILLE.
 PA (RHON) RHONE-POULENC RORER SA.
 PA (UYPA-) UNIV CURIE PARIS VI P & M.
 XX
 PI Benoit P, Bruckert E, Deneffe P, Duverger N, Fruchart J;
 PI Luc G, Turping, Assmann G, Funke H;
 DR WPI; 1997-021218/02.
 DR N-PSDB; AAT43691.
 XX
 PT New variant of human apoA-1 with Cys at position 151 - has
 PT anti-atherogenic activity for treatment and prevention of
 PT cardiovascular disease
 PS Claim 2; Page -: 58pp; French.
 XX
 CC This is the amino acid sequence of a human apolipoprotein A-1 variant
 CC designated the "Paris" variant which has a Cys replacing the Arg residue
 CC at position 151. The substitution is generated by a mutation of
 CC the C nucleotide at position 523 in the wild type gene to a T residue,
 CC changing the encoded residue from an Arg to a Cys. The gene was isolated
 CC from a patient with an unusual pattern of serum lipids i.e. low levels of
 CC apoA-1 and high density lipoprotein (HDL)-cholesterol and high
 CC triglycerides, but showing symptoms of atherosclerosis. The new variant
 CC protein has anti-atherogenic activity so is useful for treatment and
 CC prevention of cardiovascular diseases such as atherosclerosis,
 CC restenosis, myocardial infarct, angina, sudden death, stroke and cardiac
 CC decompensation, or more generally any condition involving genetic or
 CC metabolic deficit of apoA-1.
 CC Note: this sequence is not given in the specification but is generated
 CC from the wild type apoA-1 gene disclosed in the specification and has
 CC the appropriate amino acid changed.
 CC
 SQ Sequence 267 AA;
 Query Match 98.6%; Score 548; DB 18; Length 267;
 Best Local Similarity 99.1%; Pred. No. 7.le-48;
 Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 QKHLQEKLSPLGEMDRARAHVDALRTHLAPYSDELRORLAARLEALKENGARLAE 60
 DB 156 qklhelqeklsplgsemrdarahvdalrthlapysdelrqlraarleaalkengarlae 215
 OY 61 YHAKATEHLSTLSEKAKPALEDLROGLLPVLESFKVSFLSALEEYTKKINTQ 112
 DB 216 yhakatehlstlsekakpaledlrglilpvlesfkvsflsaleeytkkintq 267
 RESULT 11
 ID AAR56863
 AC AAR56863 standard; Protein; 264 AA.
 XX
 AC AAR56863;
 XX
 DT 26-JAN-1995 (first entry)
 XX
 DE Apo-lipoprotein AI-M.
 XX
 KW Apo-lipoprotein AI-M; Apo AI-M; Escherichia coli; plasmid pKF683;
 KW vector; atherosclerosis; cardiovascular disease.
 XX
 OS Homo sapiens.

XX WO9413819-A.
 XX 23-JUN-1994.
 PD
 XX 09-DEC-1993; 93WO-SE01061.
 PF
 XX 11-DEC-1992; 92SE-0003753.
 PR
 XX (KABI) KABI PHARMACIA AB.
 PA
 XX Abrahmsen L, Holmgren E, Kalderen C, Lake M, Mikaelsson A;
 PI Sejlitz T;
 PI
 DR WPI; 1994-217892/26.
 DR N-PSDB; AA068357.
 XX
 PT Expression vector for extracellular prodn of apo-lipoprotein AI-M
 PT in E. coli - includes inducible promoter and signal peptide
 PT sequences providing improved yield, useful in treating
 PT atherosclerosis and cardiovascular disease.
 PT
 PS Disclosure; Fig. 3; 33pp; English.
 XX
 CC Plasmid pKP683 encodes human apo-lipoprotein AI-M in E. coli. The
 CC NotI-HindIII segment of pKP683 and the deduced amino acid sequence
 CC of the translated Apo AI-M protein were determined. The plasmid
 CC provides high yields of extracellular Apo AI-M.
 CC
 SQ Sequence 264 AA;

Query Match 98.0%; Score 545; DB 15; Length 264;
 Best Local Similarity 98.2%; Pred. No. 1,4e-47;
 Matches 110; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDLRQRLAARLEALKENGARLAE 60
 DB 153 qklhelqeklsplgeemdrarahvdalrtlhlapysdelrqclaaalkengarlarlae 212
 QY 61 YHAKATEHLSTLSEKAKPALEDLRQGLPVLSEFKVSFLSALDEYTKKLTNQ 112
 DB 213 yhakatehlstlsekakpaledlrqglpvlsefkvsflsalseeytkkltntq 264

RESULT 12

AAR56864
 ID AAR56864 standard; Protein: 264 AA.
 AC
 XX AAR56864;

DT 26-JAN-1995 (first entry)
 XX
 DE Apo-lipoprotein AI-M.
 XX
 KW Apo-lipoprotein AI-M; Apo AI-M; Escherichia coli; plasmid pKP764;
 KW vector; atherosclerosis; cardiovascular disease.
 XX
 OS Homo sapiens.
 OS
 PN WO9413819-A.
 PN
 PD 23-JUN-1994.
 PD
 PF 09-DEC-1993; 93WO-SE01061.
 PF
 PR 11-DEC-1992; 92SE-0003753.
 PR
 XX (KABI) KABI PHARMACIA AB.
 PA
 XX Abrahmsen L, Holmgren E, Kalderen C, Lake M, Mikaelsson A;
 PI Sejlitz T;
 PI
 XX

DR WPI; 1994-217892/26.
 DR N-PSDB; AA068358.
 DR
 XX
 PT Expression vector for extracellular prodn of apo-lipoprotein AI-M
 PT in E. coli - includes inducible promoter and signal peptide
 PT sequences providing improved yield, useful in treating
 PT atherosclerosis and cardiovascular disease.
 PT
 PS Disclosure; Fig. 4; 33pp; English.
 XX
 CC Plasmid pKP764 encodes human apo-lipoprotein AI-M in E. coli. The
 CC NotI-HindIII segment of pKP764 and the deduced amino acid sequence
 CC of the translated Apo AI-M protein were determined. The plasmid
 CC provides high yields of extracellular Apo AI-M.
 CC
 SQ Sequence 264 AA;

Query Match 98.0%; Score 545; DB 15; Length 264;
 Best Local Similarity 98.2%; Pred. No. 1,4e-47;
 Matches 110; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OKLHELQEKLSPLGEEMDRARAHVDALRTHLAPYSDLRQRLAARLEALKENGARLAE 60
 DB 153 qklhelqeklsplgeemdrarahvdalrtlhlapysdelrqclaaalkengarlarlae 212
 QY 61 YHAKATEHLSTLSEKAKPALEDLRQGLPVLSEFKVSFLSALDEYTKKLTNQ 112
 DB 213 yhakatehlstlsekakpaledlrqglpvlsefkvsflsalseeytkkltntq 264

RESULT 13

AAU33170
 ID AAU33170 standard; Protein: 299 AA.
 AC
 XX AAU33170;

DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #3661.

XX Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 OS
 PN WO200179449-A2.
 PN
 PD 25-OCT-2001.
 PD
 PF 16-APR-2001; 2001WO-US08656.
 PF
 PR 18-APR-2000; 2000US-0552929.
 PR
 XX 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT;
 PI
 DR WPI; 2001-611725/70.
 DR
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 PT
 PS Claim 20; Page 718; 765pp; English.
 PS
 XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.

XX Sequence 299 AA;

Query Match 93.9%; Score 522; DB 22; Length 299;

Best Local Similarity 92.9%; Pred. No. 3.6e-45;

Matches 104; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 OKHLELQKLSPLGEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAE 60

DB 188 qklhelqeklsplgeemdrarahvdalrthlapysdelqrlgarlgaltengarmg 247

OY 61 YHAKATEHLSTLSEKAKPALEDLROGLLPVSEFVSFLSALEETKRLNTQ 112

DB 248 yhaqatehstlsekakpaledlrqglpvlsefvsflsaaleeytkklnltq 299

RESULT 14

AAU30470

ID AAU30470 standard; Protein: 359 AA.

AC AAU30470;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #961.

XX Human; vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-611725/70.

XX Nucleic acids encoding a range of human polypeptides, useful in genetic

PT vaccination, testing and therapy -

PS Claim 20; Page 297; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically

CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.

XX Sequence 359 AA;

Query Match 89.3%; Score 496.5; DB 22; Length 359;

Best Local Similarity 88.5%; Pred. No. 1.8e-42;

Matches 100; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

OY 1 OKHLELQKLSPLGEEMDRARAHVDALRTHLAPYSDELQRLAARLEALKENGARLAE 59

DB 247 eslhelarlsplgeemdrarahvdalrthlapysdelqrlgarlgaltengarmg 306

OY 60 YHAKATEHLSTLSEKAKPALEDLROGLLPVSEFVSFLSALEETKRLNTQ 112

DB 307 yhaqatehstlsekakpaledlrqglpvlsefvsflsaaleeytkklnltq 359

RESULT 15

AAU30268

ID AAU30268 standard; Protein: 318 AA.

AC AAU30268;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #759.

XX Human; vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-611725/70.

XX Nucleic acids encoding a range of human polypeptides, useful in genetic

PT vaccination, testing and therapy -

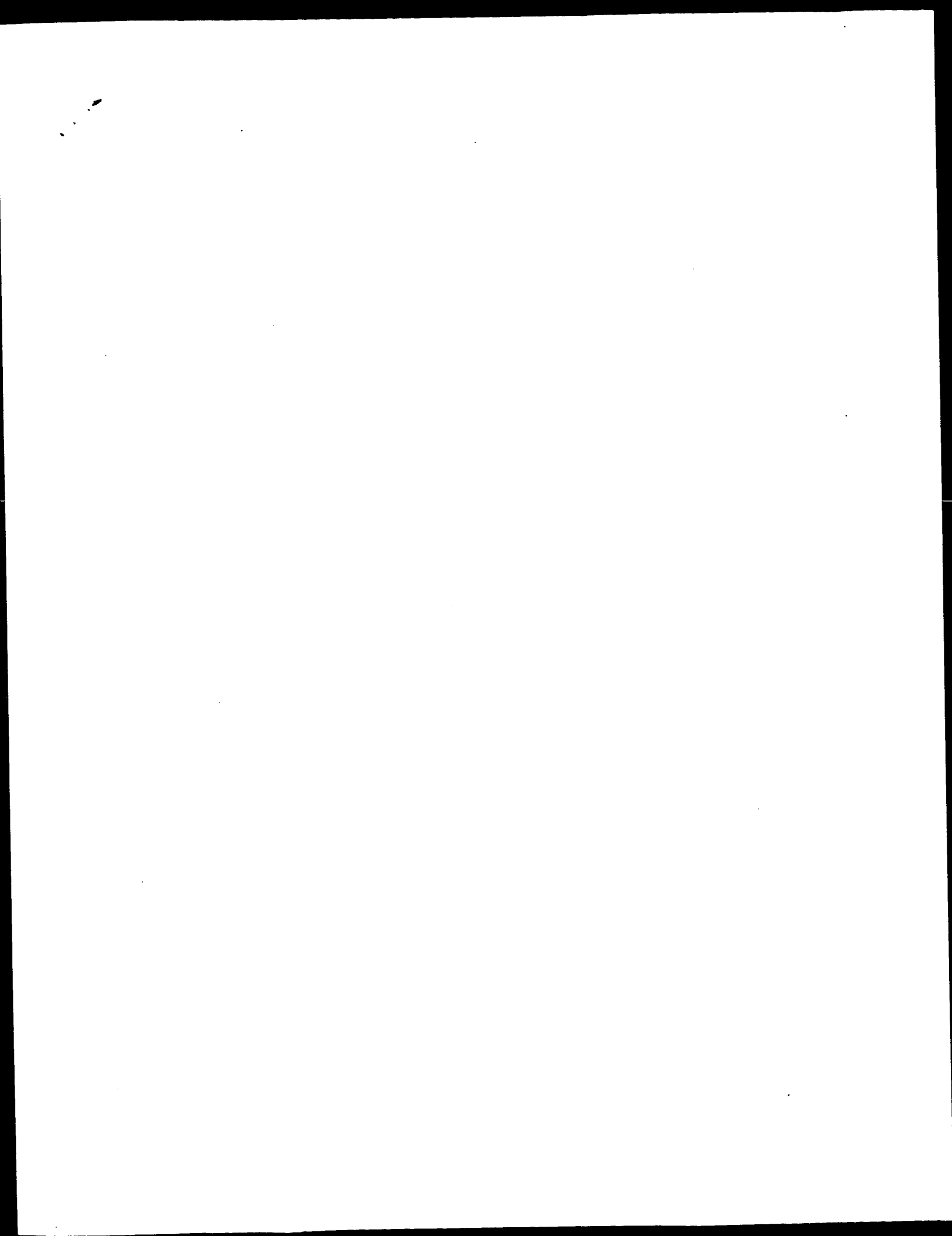
PS Claim 20; Page 270; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to

CC increase stem cell proliferation, to regulate haematopoiesis, and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukemias. AA029510-AA033304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX
Sequence 318 AA:
50

Query Match	73.7%	Score 409.5;	DB 22;	Length 318;
Best Local Similarity	77.4%;	Pred. No. 1,1.e-33;		
Matches	89;	Conservative	8;	Mismatches 15; Indels 3; Gaps 3;
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Db	179	eslhelatrrslplpgavsrprtrpmwdalrthlapiysdempalgrapgalrengar	238	
QY	58	LAENHAKATHTLSTLSEKAKPALDEDROGLLPVLESFKVSTLSALEYTKRLNTQ	112	
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Db	239	mgqyhaqathtstlsekakpaledlrgllprvlesfxfvslsleeytkkintq	293	

Search completed: September 22, 2002, 12:05:16
Job time: 291 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:02:51 : Search time 51.49 Seconds

(without alignments)
53.130 Million cell updates/sec

Title: US-09-803-918a-2_COPY_156_267

Perfect score: 556
Sequence: 1 QKHELOEKLSPGEMRDR.....SPKVSFLSALEYTKKLNQ 112

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	100.0	267	1	US-07-959-946-3
2	556	100.0	267	1	US-08-333-577-3
3	556	100.0	267	4	US-08-952-796-2
4	556	100.0	267	5	PCT-US92-08634-3
5	548	98.6	200	4	US-08-952-796-15
6	548	98.6	264	1	US-08-448-606-6
7	92	16.5	317	1	US-07-709-949-2
8	90	16.2	317	4	US-08-949-155-6
9	86	15.5	64	2	US-08-292-870-1
10	83	14.9	1184	4	US-09-541-782-2
11	80.5	14.5	110	1	US-07-849-389-7
12	80.5	14.5	220	2	US-08-726-306A-29
13	75.5	13.6	878	3	US-08-941-936-2
14	75.5	13.6	1939	4	US-09-310-187A-1
15	73.5	13.2	1886	4	US-08-938-105-3
16	73	13.1	1618	1	US-07-853-913-4
17	72.5	13.0	618	3	US-08-834-306-65
18	72.5	13.0	618	4	US-08-993-674A-65
19	72	12.9	1561	3	US-08-894-017-23
20	72	12.9	1565	6	5352450-2
21	71.5	12.9	955	1	US-08-006-676B-1
22	71.5	12.9	955	1	US-08-282-845-2
23	71.5	12.9	955	2	US-08-428-414A-3
24	71.5	12.9	955	5	PCT-US94-00324-1
25	69.5	12.5	2101	1	US-08-466-390-4
26	69.5	12.5	2101	1	US-08-470-950-4
27	69.5	12.5	2101	1	US-08-467-781-4

28	69.5	12.5	2101	1	US-08-195-487-4	Sequence 4, Appli
29	69.5	12.5	2101	2	US-08-483-924-4	Sequence 4, Appli
30	69.5	12.5	2101	4	US-09-452-294-1	Sequence 1, Appli
31	69.5	12.5	2101	5	PCT-US93-06160-4	Sequence 4, Appli
32	69	12.4	566	2	US-08-533-669A-8	Sequence 8, Appli
33	69	12.4	566	2	US-08-511-872-2	Sequence 2, Appli
34	68.5	12.3	337	1	US-08-445-135-4	Sequence 4, Appli
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36	68.5	12.3	339	1	US-08-174-745A-4	Sequence 4, Appli
37	68.5	12.3	339	2	US-08-195-947-4	Sequence 4, Appli
38	68.5	12.3	339	2	US-08-433-885-4	Sequence 4, Appli
39	68.5	12.3	339	2	US-08-433-908B-4	Sequence 4, Appli
40	68.5	12.3	339	4	US-08-410-614-4	Sequence 4, Appli
41	68	12.2	180	1	US-08-328-254-7	Sequence 7, Appli
42	68	12.2	184	2	US-08-715-204-5	Sequence 5, Appli
43	68	12.2	184	2	US-08-691-814B-50	Sequence 50, Appli
44	68	12.2	184	3	US-09-162-597-5	Sequence 5, Appli
45	68	12.2	337	1	US-08-317-223-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-07-959-946-3
Sequence 3, Application US/07959946
Patent No. 5408038
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Witzium, Joseph L.
APPLICANT: Cutliss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dresler, Goldsmith, Shore, Sutker &
ADDRESSEE: Milnamow, Ltd.
STREET: 180 No. 5408038th Stetson, Suite 4700
STATE: Illinois
CITY: Chicago
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,946
FILING DATE: 19921008
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-959-946-3
Query Match 100.0%; Score 556; DB 1; Length 267;

Best Local Similarity 100.0%; Pred. No. 2.4e-53;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DQ 1 QKHLQEKLSPGEMDRARAHVDALRTHLPYSDQLRQLARLEALKENGANLAELAE 60
|||
DQ 156 QKHLQEKLSPGEMDRARAHVDALRTHLPYSDQLRQLARLEALKENGANLAELAE 215

[illegible]

RESULT 2
US-08-333-577-3

; Sequence 3, Application US/08333577
: Patent No. 5786206

GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Wiltzium, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:

```

? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/333,577

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; amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-333-577-3

QY 1 QKHELEQEKSP LGEEMDRARAHVDALRTHLAPYSDELQRLARLEALKENGARIAE 60
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Dp 156 QKHLEQEKSP LGEEMDRARAHVDALRTHLAPYSDELQRLARLEALKENGARIAE 215

OY	61 YAKATEHLSTSEKAKPALEDIROGLLPVLESFVKVSFLSALAEYYTKKLNTQ	112
Dd	216 YAKATEHLSTSEKAKPALIEDIROGLLPVLEEFKVSFLSALAEYYTKKLNTQ	267

RESULT
US-08-952--796-2

- ; Sequence 2, Application US/08952796
- ; Patent No. 6258596

```

? GENERAL INFORMATION:
? APPLICANT: BENOTT, Patrick
? APPLICANT: BRUCKERT, Eric
? APPLICANT: DENEFLE, Patrice
? APPLICANT: DUBERGER, Nicolas
? APPLICANT: FRUCHART, Jean-Charles
? APPLICANT: LUC, Gerald
? APPLICANT: TURPIN, Gerrard
? APPLICANT: ASSMANN, Gerd
? APPLICANT: FUNKE, Harald
? TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPROTEIN A-I
? NUMBER OF SEQUENCES: 19
? CORRESPONDENCE ADDRESS:
?

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,796
FILING DATE: 1998-08-10

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;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-952-796-2

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QY	61	YAAKATHEHLSLSEKARALDEDLNOGLLPVLSBFKVSFLSALBEYTKKILNQ	112
Db	216	YAAKATHEHLSLSEKARALDEDLNOGLLPVLSBFKVSFLSALBEYTKKILNQ	267

RESULT 4
PCT-US92-08634-3
; Sequence 3, Application PC/TUS9208634

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RESULT 4
PCT-US92-08634-3
; Sequence 3, Application PC/TUS9208634
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Wiltum, Joseph L.

```

APPLICANT: Curtiss, Linda K.
 TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
 TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Goldsmith, Shore, Suter &
 ADDRESSEE: Milanow, Ltd.
 STREET: 180 North Stetson, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/08634
 FILING DATE: 19921009
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,706
 FILING DATE: 18-JUN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Gamsen, Edward P.
 REGISTRATION NUMBER: 29, 381
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312)616-5400
 TELEFAX: (312)616-5460
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 267 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US92-08634-3

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STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,796
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/06061
FILING DATE: 22-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/00747
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fehner Esq., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: ST95031-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-952-796-15

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Query Match	100.0%	Score 556;	DB 5;	Length 267;
Best Local Similarity	100.0%	Pred. No. 2,4e-53;		
Matches 112;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
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Db	156	QKHELOEKISPGGEEMDRARAHVNLTHLAPYSDELRRIARLRLEAKENGARTAE	215	
Qy	61	YHAATEHLSTLSKAKPALEDLROGLTLYLSEFVYSELSALEEYTKKLNQ	112	
Db	216	YHAATEHLSTLSKAKPALEDLROGLTLYLSEFVYSELSALEEYTKKLNQ	267	

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1 RESULT 5
2 US-08-952-796-15
3 : Sequence 15, Application US/08952796
4 : Patent No. 6258596
5 :
6 : GENERAL INFORMATION:
7 :
8 : APPLICANT: BENOTT, Patrick
9 :
10 : APPLICANT: BROCKERT, Eric
11 :
12 : APPLICANT: DENEFLE, Patrice
13 :
14 : APPLICANT: DUEBERGER, Nicolas
15 :
16 : APPLICANT: FRUCHART, Jean-Charles
17 :
18 : APPLICANT: LUC, Gerald
19 :
20 : APPLICANT: TURPIN, Gerard
21 :
22 : APPLICANT: ASSMANN, Gerd
23 :
24 : APPLICANT: FUNKE, Harald
25 :
26 : TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPOPROTEIN A-I
27 :
28 : NUMBER OF SEQUENCES: 19
29 :
30 : CORRESPONDENCE ADDRESS:
31 :
32 : ADDRESSEE: Rhone-Poulenc Rorer Inc.
33 :
34 : STREET: 500 Arcola Road, Mailstop 3C43
35 :
36 : CITY: Collegeville
37 :

```

		98.6%;	Score	548;	DB	4;	Length	200;	
		Best Local Similarity	99.1%;	Pred.	No.	1.2e-52;			
	Matches	111;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps
Oy	1	QKLEHLOEKISPGGEEMDRARAHVDALTLHPAPSDCLRRLAARLAEALKENGARGLAE							60
Dd	89	QKLEHLOEKISPGEEMDRCARAHVDAETHLPASDELRLRLARLBALKENGGARLAE							148
Oy	61	YHAATEHTLSISEKANPALEDIROGLLPVLESFVFYSLSIALEYTKKLNTQ							112
Dd	149	YHAATHTSLTSSEKAKPALEDIRQGCLLVLSFVSFVSTLSALEETTKKLNTQ							200

RESULT 6
 US-08-448-606-6
 : Sequence 6, Application US/08448606
 : Patent No. 5721114
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Abrahams n, Lars
 : APPLICANT: Holmgren, Erik
 : APPLICANT: Kalder n, Christina
 : APPLICANT: Lake, Mats
 : APPLICANT: Mikaelsson, sa
 : APPLICANT: Sejlitz, Torsten
 :
 : TITLE OF INVENTION: Expression System For Producing
 : TITLE OF INVENTION: Apolipoprotein AI-M
 :
 : NUMBER OF SEQUENCES: 7
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Pollock, Vande Sande & Priddy
 : STREET: 1990 M Street, N.W., Suite 800
 : CITY: Washington
 :
 : STATE: D.C.
 :
 : COUNTRY: U.S.
 :
 : ZIP: 20036
 :
 : COMPUTER READABLE FORM:
 :
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448, 606
FILING DATE: 25-AUG-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE93/01061
FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9203753-0
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Amernick, Burton A.
REGISTRATION NUMBER: 24,852
REFERENCE/DOCKET NUMBER: 0151/00121
TELEPHONE: (202) 331-7111
TELEFAX: (202) 293-6229
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-448-606-6

```

```

Query Match          98.6%; Score 548; DB 1; Length 264;
Best Local Similarity 99.1%; Pred. No. 1.8e-52;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 1 OKLHLOKLSPLGEMDRARAHVDALRTHLAPYSDELRLRLAELKENGARLAE 60
DB 153 OKLHLOKLSPLGEMDRARAHVDALRTHLAPYSDELRLRLAELKENGARLAE 212
OY 61 YHAKTEHSTLSEKAPALDELROGLIPVLESFVSFLSLEYTKKLNQ 112
DB 213 YHAKTEHSTLSEKAPALDELROGLIPVLESFVSFLSLEYTKKLNQ 264

```

```

RESULT 7
US-07-709-949-2
Sequence 2, Application US/07709949
Patent No. 5472858
GENERAL INFORMATION:
APPLICANT: Attie, Alan D
APPLICANT: Gretch, Daniel G
APPLICANT: Sturley, Stephen L
APPLICANT: Beckage, Nancy E
TITLE OF INVENTION: Production of Recombinant Proteins in
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: P.O. Box 2113
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/709, 949
FILING DATE: 19910604
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 9629691801
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000

```

```

TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-709-949-2

```

```

Query Match          16.5%; Score 92; DB 1; Length 317;
Best Local Similarity 28.9%; Pred. No. 0.02;
Matches 35; Conservative 20; Mismatches 30; Indels 36; Gaps 4;

```

```

OY 5 ELQKLSPLGEMDR-----ARAHVA-----LRTHLAPYSDELRL 42
DB 95 ELQKLSPLGEMDRARAHVDALRTHLAPYSDELRLRLAELKENGARLAE 154
OY 43 LAARLEALK-----ENGARLAEYHAKTEHSTLSEKAPALDELROGLIPVLESFK 95
DB 155 LASHLRLKRLRLRDPDDLQKRLAVYQAGA-----REGARGLSATRERLGPVLEQGR 207
OY 96 V 96
DB 208 V 208

```

```

RESULT 8
US-08-949-155-6
Sequence 6, Application US/08949155
Patent No. 6271436
GENERAL INFORMATION:
APPLICANT: Piedrahita, Jorge A
APPLICANT: Bazer, Fuller W
TITLE OF INVENTION: Compositions and Methods for the
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE AND DURKEE
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949, 155
FILING DATE: Concurrently Herewith
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027, 338
FILING DATE: 11-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046, 094
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-949-155-6

```

Query Match	16.2%;	Score 90;	DB 4;	Length 317;
Best Local Similarity	23.8%;	Pred. No. 0.033;		
Matches 25; Conservative	22;	Mismatches 58;	Indels 0;	Gaps 0;

[illegible]

RESULT 9
US-08-292-870-1
; Sequence 1, Application US/08292870
; Patent No. 5814467

```

? APPLICANT: Curtiss, Linda K
? APPLICANT: Banka, Carole L
? APPLICANT: Bonnet, David J
? APPLICANT: Smith, Richard S
? TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
? TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
? TITLE OF INVENTION: METHODS
? NUMBER OF SEQUENCES: 4
? ADDRESS:

```

ADDRESS: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 NO. 5814/67th Torrey Pines Road., TPC 8
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/292,870
 FILING DATE: 17-AUG-1994
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/534,761
 FILING DATE: 07-JUN-1990
 PRIOR APPLICATION NUMBER: US 07/711,333
 APPLICATION DATE: 06-JUN-1991

APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pitting Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRT 210.1 DI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

```

; INFORMATION FOR SEQ ID NO: 1:
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 64 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
;   FRAGMENT TYPE: internal
US-08-292-870-1

```

```
Query Match      15.58; Score 86; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.011;
```

Matches	17;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	QKRLHEQKRLSPGDEM	17						
Db	48	QKRLHEQKRLSPGDEM	64						

RESULT 10
US-09-541-782-2

```

? APPLICANT: Nislow, Corey
? APPLICANT: Sakowicz, Roman
? APPLICANT: Betraud, Christophe
? TITLE OF INVENTION: Antifungal Assay
? FILE REFERENCE: 1015
? CURRENT APPLICATION NUMBER: US/09/541,782
? CURRENT FILING DATE: 2000-04-03
? NUMBER OF SEQ ID NOS: 10
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 2
? LENGTH: 1184
? TYPE: PRT
? ORGANISM: A. nidulans
? US-09-541-782-2

```

Query Match	14.9%	Score 83;	DB 4;	Length 1184;
Best Local Similarity	30.1%	Pred. No. 1.1;		
Matches 25; Conservative	13;	Mismatches 37;	Indels 8;	Gaps 2

QY 23 AHVDALKRHLAPYDELRQRLAARLALKENGARLAEKHAKATSHLSTSEKAPALD 82
||: | | | : | | | : : | | | : | | |
Db 926 AHIALDLTIATGYRDSY-----SSIEGRVENTLGRMNFQOEAYHHHATLEESIAPLSND 980C

```

          :|: | : || : |||
Db 981 VRKPLTDLSSSFQ--NRSLEEX 1000

```

RESULT 11
US-07-849-389-7
: Sequence 7, Application US/07849389
: Patent No. 5525493

CONTACT: CONNOR, BING
 APPLICANT: HORNES, ERIK
 TITLE: CLONING
 TITLE OF INVENTION: CLONING METHOD AND KIT
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500

COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/849,389
FILING DATE: 19920519
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109

TELEX: 899149
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-849-389-7

Query Match 14.5%; Score 80.5; DB 1; Length 110;
Best Local Similarity 30.4%; Pred. No. 0.089;
Matches 28; Conservative 13; Mismatches 22; Indels 29; Gaps 3;

QY 5 ELEQKLSPLGEMDRAR-----AHVDLRTHLAPY-----SDELRR 42
DB 9 ELEQKLPVAEETRARLSKEIQAAEAPLADMEVRCGLVQYRGVQAMLGOSTEELRVR 68
QY 43 LAARLEALK-----ENGARLAETHAKATE 67
DB 69 LASHLRKRLRLRDADDLQKRLAVYQAGARE 100

RESULT 12
US-08-726-306A-29
Sequence 29, Application US/08726306A
Patent No. 5958684
GENERAL INFORMATION:
APPLICANT: Van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-726-306A-29

Query Match 14.5%; Score 80.5; DB 2; Length 220;
Best Local Similarity 29.8%; Pred. No. 0.22;

Matches 31; Conservative 16; Mismatches 24; Indels 33; Gaps 4;
QY 5 ELEQKLSPLGEMDR-----ARAHYDA-----LRTHLAPYSDELRR 42
DB 115 ELEQKLPVAEETRARLSKEIQAAEAPLADMEVRCGLVQYRGVQAMLGOSTEELRVR 174
QY 43 LAARLEALK-----ENGARLAETHAKATE-----HLSTLSEK 75
DB 175 LASHLRKRLRLRDADDLQKRLAVYQAGAREGARGISAIRR 218

RESULT 13
US-08-941-936-2
Sequence 2, Application US/08941936
Patent No. 6054305
GENERAL INFORMATION:
APPLICANT: Tatsumi, Hiroki
APPLICANT: Etsaki, Naoki
APPLICANT: Horiuchi, Tatsuo
APPLICANT: Nagahara, Ayumu
TITLE OF INVENTION: Pyruvate Orthophosphate Dikinase Gene,
Title of Invention: Recombinant DNA, and Process for Producing Pyruvate
TITLE OF INVENTION: Orthophosphate Dikinase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,936
FILING DATE: 01-Oct-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: HIRAKI-03009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-705-8410
TELEFAX: 415-397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 878 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-941-936-2

Query Match 13.6%; Score 75.5; DB 3; Length 878;
Best Local Similarity 30.3%; Pred. No. 4.8;
Matches 37; Conservative 13; Mismatches 41; Indels 31; Gaps 8;

QY 3 LHEQKLSPL-----GEEMDRARAHVDALRTHLAPYSDELRRRLAARLEALKENGAR 57
DB 501 LGEVPTASVPAKRYFEGEPDELVAVDRIMH-----ADSVR-RLAVANANDTEEDAR 555
QY 58 LAETHAKA-----TEHLSTLSEKAKPALEDL-----RQGLPYLSEFKVSFLSALE 104
DB 556 ARRYGAGGIGLCRETH-FLGERRR-LVEDLLAATPERQALDALDEPLQT-----ED 607
QY 105 YR 106
DB 608 FT 609

```

RESULT 14
US-09-310-187A-1
; Sequence 1, Application US/09310187A
; Patent No. 6358751
; GENERAL INFORMATION:
; APPLICANT: Benichou, Gilles
; APPLICANT: Fedoseyeva, Eugenia
; TITLE OF INVENTION: Involvement of Autoantigens in Cardiac
; FILE REFERENCE: UCSF-090
; CURRENT APPLICATION NUMBER: US/09/310,187A
; CURRENT FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1939
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-310-187A-1

```

```

Query Match          13.6%; Score 75.5; DB 4; Length 1939;
Best Local Similarity 27.0%; Pred. No. 14;
Matches 37; Conservative 21; Mismatches 44; Indels 35; Gaps 6;

QY 1 OKLHEIQEKLSPGEMRDR--ARAHVDALRTHLAPYSDELRORLARLEALKENGGA-- 56
   :||| | : : : ||| : ||| : : : : ||| : ||| : : : : ||| : |||
Db 1108 KKLKENQARIIELEELAEERTAKVEKIRSDLRLEIISER-----LEBAGGATS 1160
      :||| | : : : ||| : ||| : : : : ||| : ||| : : : : ||| : |||

QY 57 -----RLAEYH-----AKAT-EHLSTSEKAKPALE-----DRQGLLPVLE 92
   :||| | : : : ||| : ||| : : : : ||| : ||| : : : : ||| : |||
Db 1161 VOIEMNKKREAEFOKKRRDLAEATLQHEHTAALRKKHADSVAEIGQIDNLRVKOKLE 1220
      :||| | : : : ||| : ||| : : : : ||| : ||| : : : : ||| : |||

QY 93 SFRVSPFLSALEEYTKL 109
Db 1221 KEKSEFKLELDVTSNM 1237

```

```

RESULT 15
US-08-938-105-3
; Sequence 3, Application US/08938105
; Patent No. 6353151
; GENERAL INFORMATION:
; APPLICANT: Leinwand, Leslie A.
; APPLICANT: Vikstrom, Karen L.
; TITLE OF INVENTION: TRANSGENIC MODEL FOR HEART FAILURE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,105
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Crook, Wanneil M.
; REGISTRATION NUMBER: 31,071
; REFERENCE/DOCKET NUMBER: 3595-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1886 amino acids

```

```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-938-105-3

```

```

Query Match          13.2%; Score 73.5; DB 4; Length 1886;
Best Local Similarity 27.0%; Pred. No. 22;
Matches 37; Conservative 20; Mismatches 45; Indels 35; Gaps 6;

QY 1 OKLHEIQEKLSPGEMRDR--ARAHVDALRTHLAPYSDELRORLARLEALKENGGA-- 56
   :||| | : : : ||| : ||| : : : : ||| : ||| : : : : ||| : |||
Db 1055 KKLKENQARIIELEELAEERTAKVEKIRSDLRLEIISER-----LEBAGGATS 1107
      :||| | : : : ||| : ||| : : : : ||| : ||| : : : : ||| : |||

QY 57 -----RLAEYH-----AKAT-EHLSTSEKAKPALE-----DRQGLLPVLE 92
   :||| | : : : ||| : ||| : : : : ||| : ||| : : : : ||| : |||
Db 1108 VOIEMNKKREAEFOKKRRDLAEATLQHEHTAALRKKHADSVAEIGQIDNLRVKOKLE 1167
      :||| | : : : ||| : ||| : : : : ||| : ||| : : : : ||| : |||

QY 93 SFRVSPFLSALEEYTKL 109
Db 1168 KEKSEFKLELDVTSNM 1184

```

Search completed: September 22, 2002, 12:02:52
Job time: 252 sec

Sun Sep 22 12:10:09 2002

us-09-803-918a-2_copy_156_267.ra1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:02:50 : Search time 51.49 Seconds

(without alignments)
56.925 Million cell updates/sec

Title: US-09-803-918a-2_COPY_25_144

Perfect score: 631
Sequence: 1 DEPPQSPMDRKYDIAIVYVD.....LDDPQKKQWQEMELRYQKVE 120Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	631	100.0	264	1	US-08-448-606-6 Sequence 6, Appli
2	631	100.0	267	1	US-07-959-946-3 Sequence 3, Appli
3	631	100.0	267	1	US-08-333-577-3 Sequence 3, Appli
4	631	100.0	267	4	US-08-952-796-2 Sequence 2, Appli
5	631	100.0	267	5	PCT-US92-08634-3 Sequence 3, Appli
6	404	64.0	200	4	US-08-952-796-15 Sequence 15, Appli
7	198	31.4	44	2	US-08-292-870-2 Sequence 2, Appli
8	188	29.8	64	2	US-08-292-870-1 Sequence 1, Appli
9	138	21.9	32	2	US-08-292-870-3 Sequence 3, Appli
10	124	19.7	25	2	US-08-292-870-4 Sequence 4, Appli
11	91	14.4	16	1	US-07-959-946-5 Sequence 5, Appli
12	91	14.4	16	1	US-08-333-577-5 Sequence 5, Appli
13	91	14.4	16	5	PCT-US92-08634-5 Sequence 5, Appli
14	87.5	13.9	317	4	US-08-949-155-6 Sequence 6, Appli
15	82.5	13.1	515	2	US-08-705-660-4 Sequence 46, Appli
16	82.5	13.1	515	3	US-08-989-045-46 Sequence 46, Appli
17	79	12.5	230	1	US-08-726-306A-29 Sequence 29, Appli
18	79	12.5	230	1	US-08-118-469A-3 Sequence 3, Appli
19	79	12.5	230	1	US-08-909-119-3 Sequence 3, Appli
20	79	12.5	317	1	US-07-709-949-2 Sequence 2, Appli
21	78	12.4	110	1	US-07-849-389-7 Sequence 7, Appli
22	78	12.4	900	2	US-08-630-822A-62 Sequence 62, Appli
23	78	12.4	900	2	US-09-005-069-62 Sequence 62, Appli
24	77	12.2	1786	4	US-08-973-462-8 Sequence 8, Appli
25	76	12.0	107	1	US-08-182-175A-105 Sequence 105, Appli
26	76	12.0	107	1	US-08-474-633A-92 Sequence 92, Appli
27	76	12.0	107	5	PCT-US92-06412-105 Sequence 105, Appli

28	75.5	12.0	203	1	US-08-216-593-5 Sequence 5, Appli
29	75.5	12.0	203	5	PCT-US93-12380-5 Sequence 5, Appli
30	75.5	12.0	205	1	US-07-992-827D-5 Sequence 5, Appli
31	75.5	12.0	393	2	US-08-904-031-3 Sequence 3, Appli
32	74.5	11.8	897	1	US-08-095-737-4 Sequence 4, Appli
33	74.5	11.8	897	1	US-08-480-145-4 Sequence 4, Appli
34	74.5	11.8	897	2	US-08-477-389-4 Sequence 4, Appli
35	73.5	11.6	386	4	US-09-085-199B-2 Sequence 2, Appli
36	73.5	11.6	896	1	US-08-095-737-2 Sequence 2, Appli
37	73.5	11.6	896	1	US-08-480-145-2 Sequence 2, Appli
38	73.5	11.6	896	2	US-08-477-389-2 Sequence 2, Appli
39	73.5	11.6	914	4	US-09-085-199B-4 Sequence 4, Appli
40	73.5	11.6	1090	4	US-09-085-199B-5 Sequence 5, Appli
41	73.5	11.6	1093	4	US-09-315-793-52 Sequence 52, Appli
42	73	11.6	707	2	US-08-949-941B-2 Sequence 2, Appli
43	72.5	11.5	392	2	US-08-904-031-1 Sequence 1, Appli
44	72.5	11.5	984	1	US-08-242-932-2 Sequence 2, Appli
45	72.5	11.5	984	1	US-08-714-481-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-448-606-6
; Sequence 6, Application US/08448606
; Patent No. 5721114
; GENERAL INFORMATION:
; APPLICANT: Adrahams n, Lars
; APPLICANT: Holmgren, Erik
; APPLICANT: Kalder n, Christina
; APPLICANT: Lake, Mats
; APPLICANT: Mikaelsson, sa
; APPLICANT: Sejlitz, Torsten
; TITLE OF INVENTION: Expression System For Producing
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pollock, Vande Sande & Priddy
; STREET: 1990 M Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,606
; FILING DATE: 25-AUG-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SE93/01061
; FILING DATE: 09-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9203753-0
; FILING DATE: 11-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Amerinick, Burton A.
; REGISTRATION NUMBER: 24,852
; REFERENCE/DOCKET NUMBER: 0151/00121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)331-7111
; TELEFAX: (202) 293-6229
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-448-606-6

Query Match 100.0%; Score 631; DB 1; Length 264;
 Best Local Similarity 100.0%; Pred. No. 2.7e-54;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DEPPSPMDRVKDLATVYVDVVKDSGRDYSQFEGSALGKQLNLKLDNDMSVSTFSKL 60
 |||
 Db 22 DEPPSPMDRVKDLATVYVDVVKDSGRDYSQFEGSALGKQLNLKLDNDMSVSTFSKL 81
 |||
 Oy 61 RQGLPVYQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFOKKQOEEMELYRQKVE 120
 |||
 Db 82 RQGLPVYQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFOKKQOEEMELYRQKVE 141
 |||

RESULT 2

US-07-959-946-3
 ; Sequence 3, Application US/07959946
 ; Patent No. 5408038

GENERAL INFORMATION:
 APPLICANT: Smith, Richard K.
 APPLICANT: Koduri, Raju
 APPLICANT: Young, Stephen G.
 APPLICANT: Wiltum, Joseph L.
 APPLICANT: Curtiss, Linda K.
 TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
 TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
 ADDRESSEE: Milnamow, Ltd.
 STREET: 180 No. 5408038th Stetson, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/959,946
 FILING DATE: 19921008

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,706

FILING DATE: 18-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)616-5400

TELEFAX: (312)616-5460

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-959-946-3

Query Match 100.0%; Score 631; DB 1; Length 267;

Best Local Similarity 100.0%; Pred. No. 2.7e-54;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DEPPSPMDRVKDLATVYVDVVKDSGRDYSQFEGSALGKQLNLKLDNDMSVSTFSKL 60

|||

Db 25 DEPPSPMDRVKDLATVYVDVVKDSGRDYSQFEGSALGKQLNLKLDNDMSVSTFSKL 84

|||

Oy 61 RQGLPVYQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFOKKQOEEMELYRQKVE 120

|||

Db 82 RQGLPVYQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFOKKQOEEMELYRQKVE 141

|||

Oy 1 DEPPSPMDRVKDLATVYVDVVKDSGRDYSQFEGSALGKQLNLKLDNDMSVSTFSKL 60

|||

Db 85 RQGLPVYQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFOKKQOEEMELYRQKVE 144
 |||

RESULT 3

US-08-333-577-3
 ; Sequence 3, Application US/08333577
 ; Patent No. 5786206

GENERAL INFORMATION:

APPLICANT: Smith, Richard K.

APPLICANT: Koduri, Raju

APPLICANT: Young, Stephen G.

APPLICANT: Wiltum, Joseph L.

APPLICANT: Curtiss, Linda K.

TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a

TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &

ADDRESSEE: Milnamow, Ltd.

STREET: 180 No. 5786206th Stetson, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/333,577

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: SCRF 234.0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)616-5400

TELEFAX: (312)616-5460

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-333-577-3

Query Match 100.0%; Score 631; DB 1; Length 267;

Best Local Similarity 100.0%; Pred. No. 2.7e-54;

Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DEPPSPMDRVKDLATVYVDVVKDSGRDYSQFEGSALGKQLNLKLDNDMSVSTFSKL 60

|||

Db 25 DEPPSPMDRVKDLATVYVDVVKDSGRDYSQFEGSALGKQLNLKLDNDMSVSTFSKL 84

|||

Oy 61 RQGLPVYQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFOKKQOEEMELYRQKVE 120

|||

Db 85 RQGLPVYQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFOKKQOEEMELYRQKVE 144

|||

Oy 1 DEPPSPMDRVKDLATVYVDVVKDSGRDYSQFEGSALGKQLNLKLDNDMSVSTFSKL 60

|||

Db 25 DEPPSPMDRVKDLATVYVDVVKDSGRDYSQFEGSALGKQLNLKLDNDMSVSTFSKL 84

|||

Oy 61 RQGLPVYQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFOKKQOEEMELYRQKVE 120

|||

Db 85 RQGLPVYQEFWDLNLEKETEGLRQEMSKDLEEVKAKVQPYLDDFOKKQOEEMELYRQKVE 144

|||

Oy 1 DEPPSPMDRVKDLATVYVDVVKDSGRDYSQFEGSALGKQLNLKLDNDMSVSTFSKL 60

|||

Db 25 DEPPSPMDRVKDLATVYVDVVKDSGRDYSQFEGSALGKQLNLKLDNDMSVSTFSKL 84

|||

APPLICANT: LUC, Gerald
APPLICANT: TURPIN, Gerard
APPLICANT: ASSMANN, Gerd
APPLICANT: FUNKE, Harald
TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPOPROTEIN A-I
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,796
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/06061
FILING DATE: 22-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/00747
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fehlner Esq., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: ST95031-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-952-796-2

Query Match 100.0%; Score 631; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 2,7e-54;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPMDRVKDLATVYVDVKDSGRDYSQFEGSALGKQLNLKLDNMDSVTSTFSKL 60
DB 25 DEPPQSPMDRVKDLATVYVDVKDSGRDYSQFEGSALGKQLNLKLDNMDSVTSTFSKL 84
QY 61 REQLGPVTOEFMDNLEKETEGRLQEMSKDLEVKAKVQPYLDDFOKKMOEEMELRYKVE 120
DB 85 REQLGPVTOEFMDNLEKETEGRLQEMSKDLEVKAKVQPYLDDFOKKMOEEMELRYKVE 144

RESULT 5
PCT-US92-08634-3
Sequence 3, Application PC/TUS9208634
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Witzum, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Suter &
ADDRESSEE: Milanow, Ltd.
STREET: 180 North Stetson, Suite 4700

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08634
FILING DATE: 19921009
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5400
TELEFAX: (312) 616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-08634-3

Query Match 100.0%; Score 631; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 2,7e-54;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPMDRVKDLATVYVDVKDSGRDYSQFEGSALGKQLNLKLDNMDSVTSTFSKL 60
DB 25 DEPPQSPMDRVKDLATVYVDVKDSGRDYSQFEGSALGKQLNLKLDNMDSVTSTFSKL 84
QY 61 REQLGPVTOEFMDNLEKETEGRLQEMSKDLEVKAKVQPYLDDFOKKMOEEMELRYKVE 120
DB 85 REQLGPVTOEFMDNLEKETEGRLQEMSKDLEVKAKVQPYLDDFOKKMOEEMELRYKVE 144

RESULT 6
US-08-952-796-15
Sequence 15, Application US/08952796
Patent No. 6258596
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: BRUCKERT, Eric
APPLICANT: DENEFFE, Patrice
APPLICANT: FRUCHART, Jean-Charles
APPLICANT: LUC, Gerald
APPLICANT: TURPIN, Gerard
APPLICANT: ASSMANN, Gerd
APPLICANT: FUNKE, Harald
TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPOPROTEIN A-I
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,796
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/06061
FILING DATE: 22-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/00747
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Reinher Esq., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: S795031-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-952-796-15

Query Match 64.0%; Score 404; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 2,9e-32;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 44 LKLDNDSTSTSKRLRQGLGPTOEFWNLKETEGLRQMSKDLLEVKAKVOPYLD 103
|||||
Db 1 LKLDNDSTSTSKRLRQGLGPTOEFWNLKETEGLRQMSKDLLEVKAKVOPYLD 60
|||||
OY 104 FOKKQEMELYRQKVE 120
|||||
Db 61 FOKKQEMELYRQKVE 77
|||||

RESULT 7
US-08-292-870-2
Sequence 2, Application US/08292870
Patent No. 5814467
GENERAL INFORMATION:
APPLICANT: Curtiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Bonnet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,761
FILING DATE: 07-JUN-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/711,333
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-292-870-2

Query Match 31.4%; Score 198; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 5,7e-13;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 ROEMSKDLEEVKAKVOPYLDFOKKQEMELYRQKVE 120
|||||
Db 1 ROEMSKDLEEVKAKVOPYLDFOKKQEMELYRQKVE 38
|||||

RESULT 8
US-08-292-870-1
Sequence 1, Application US/08292870
Patent No. 5814467
GENERAL INFORMATION:
APPLICANT: Curtiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Bonnet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,761
FILING DATE: 07-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,333
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-292-870-1

Query Match
Best Local Similarity 100.0%; Pred. No. 8.7e-12;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 85 EMSKDLSEVKKAKVQPYLDDFOKKWOEMELVROKVE 120
|||||
Db 1 EMSKDLSEVKKAKVQPYLDDFOKKWOEMELVROKVE 36

RESULT 9
US-08-292-870-3
Sequence 3, Application US/08292870
Patent No. 5814467
GENERAL INFORMATION:
APPLICANT: Curtiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Bonnet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,761
FILING DATE: 07-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,333
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal

TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Region
LOCATION: 11
OTHER INFORMATION: /note="Xaa can be either E (Glu)
or F (Phe)"
US-08-292-870-3

Query Match
Best Local Similarity 96.3%; Pred. No. 2.8e-07;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 94 KAKVQPYLDDFOKKWOEMELVROKVE 120
|||||
Db 1 KAKVQPYLDDFOKKWOEMELVROKVE 27

RESULT 10
US-08-292-870-4
Sequence 4, Application US/08292870
Patent No. 5814467
GENERAL INFORMATION:
APPLICANT: Curtiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Bonnet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,761
FILING DATE: 07-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,333
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal

US-08-292-870-4

Query Match 19.7%; Score 124; DB 2; Length 25;
Best Local Similarity 96.0%; Pred. No. 4,8e-06;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 87 SKDLEEVKAKVQPYLDDFOKKMOEE 111
|||||
DB 1 SKDLEEVKAKVQPYLDDFOKKMOEE 25

RESULT 11

US-07-959-946-5
; Sequence 5, Application US/07959946
; Patent No. 5408038
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Wiltzium, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 No. 5408038th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,946
; FILING DATE: 19921008
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,706
; FILING DATE: 18-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamsom, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-959-946-5

Query Match 14.4%; Score 91; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 96 KVQPYLDDFOKKMOEE 111
|||||
DB 1 KVQPYLDDFOKKMOEE 16

RESULT 12
US-08-333-577-5
; Sequence 5, Application US/08333577

; Patent No. 5786206
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Wiltzium, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 No. 5786206th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,577
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamsom, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: SCRF 234.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-333-577-5

Query Match 14.4%; Score 91; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 96 KVQPYLDDFOKKMOEE 111
|||||
DB 1 KVQPYLDDFOKKMOEE 16

RESULT 13
PCT-US92-08634-5
; Sequence 5, Application PC/TUS9208634
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Wiltzium, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 North Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08634
FILING DATE: 19921009
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-08634-5

Query Match 14.4%; Score 91; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 96 KVQPYLDPFQKKQOE 111
Db 1 KVQPYLDPFQKKQOE 16

RESULT 14
US-08-949-155-6
Sequence 6, Application US/08949155
Patent No. 6271436
GENERAL INFORMATION:
APPLICANT: Pledrabita, Jorge A
APPLICANT: Bazer, Fuller W
TITLE OF INVENTION: Compositions and Methods for the
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE AND DUNKEE
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,155
FILING DATE: Concurrently Herewith
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,338
FILING DATE: 11-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,094
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TARK:177
TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-949-155-6

Query Match 13.9%; Score 87.5; DB 4; Length 317;
Best Local Similarity 20.5%; Pred. No. 0.42;
Matches 25; Conservative 28; Mismatches 66; Indels 3; Gaps 1;
QY 1 DEPP---QSPMDRYKDLATVYVDVLDGSDRYVQFEGSALGKOLKLDWDSVSTF 57
Db 33 EEPKMGSSQPEQALGRFWDYLRWQSLSDQVQEEILSTKVTQELTLEESMKVKAIR 92
QY 58 SKLRDGLPYTOEFMDNLEKTEGRLQEMSKDLEVKAKVOPYLDDPFQKKQOELEYRQ 117
Db 93 EELEAQDGPYTOETQARLSKELQAAQARVGADEVDYRNRLVLYRSEVHNMUGTTEILRS 152
QY 118 KV 119
Db 153 RL 154

RESULT 15
US-08-705-660-46
Sequence 46, Application US/08705660
Patent No. 5858683
GENERAL INFORMATION:
APPLICANT: KESSEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,660
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GREENHALGH, DUNCAN A
REGISTRATION NUMBER: 38,678
REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 515 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-705-660-46

Query Match

13.1%; Score 82.5; DB 2; Length 515;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:05:15 : Search time 139.03 Seconds
(without alignments)
95.870 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_144

Perfect score: 631

Sequence: 1 DEPPQSPMDRVKDLATVYVD.....LDDPQKKWQEMELYRQKE 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: A_Geneseq_032802.*
2: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT.*
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22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT.*
23: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	100.0	243	9 AAP81082	Sequence of mature Apo-1 lipoprotein AI
2	631	100.0	264	15 AAR56863	Assumed human apol
3	631	100.0	264	15 AAR56864	Entire human prepr
4	631	100.0	267	7 AAP61079	Sequence of apo AI
5	631	100.0	267	9 AAP82128	Human apo A-I incl
6	631	100.0	267	14 AAR34032	Human apolipoprote
7	631	100.0	267	16 AAR72705	Human apolipoprote
8	631	100.0	267	18 AAW08602	Human apolipoprote
9	631	100.0	267	20 AAY18675	Full length Apo-A1
10	631	100.0	267	22 AAB47620	Recombinant human
11	631	100.0	268	9 AAP80668	

Result No.	Score	Query Match	Length	ID	Description
12	631	100.0	299	22 AAU33170	Novel human secret
13	500	79.2	154	22 AA012095	Human polypeptide
14	489	77.5	151	22 AA022278	Human polypeptide
15	485.5	76.9	166	22 AAU28372	Novel human secret
16	485.5	76.9	244	22 AAU28184	Novel human secret
17	476.5	75.5	120	22 AAU30267	Novel human secret
18	476.5	75.5	120	22 AAU30469	Novel human secret
19	458	72.6	221	22 AAU29835	Novel human secret
20	410	65.0	119	22 AAU30468	Novel human secret
21	381.5	60.5	318	22 AAU30268	Novel human secret
22	247.5	39.2	359	22 AAU30470	Novel human secret
23	193	30.6	42	13 AAR20164	Apo AI polypeptide
24	142.5	22.6	377	14 AAR39502	Human apolipoprote
25	139	22.0	183	14 AAR39482	Human apolipoprote
26	139	22.0	333	14 AAR39481	Human apolipoprote
27	139	22.0	333	14 AAR39488	Human apolipoprote
28	139	22.0	333	14 AAR39490	Human apolipoprote
29	139	22.0	333	14 AAR39495	Human apolipoprote
30	139	22.0	333	14 AAR39497	Human apolipoprote
31	139	22.0	337	14 AAR39492	Human apolipoprote
32	139	22.0	342	14 AAR39489	Human apolipoprote
33	139	22.0	342	14 AAR39491	Human apolipoprote
34	139	22.0	342	14 AAR39496	Human apolipoprote
35	139	22.0	342	14 AAR39498	Human apolipoprote
36	139	22.0	346	14 AAR39493	Human apolipoprote
37	139	22.0	377	14 AAR39443	Human apolipoprote
38	139	22.0	377	14 AAR45242	Human apolipoprote
39	139	22.0	377	14 AAR45243	Human apolipoprote
40	139	22.0	377	14 AAR45244	Human apolipoprote
41	139	22.0	377	14 AAR45244	Human apolipoprote
42	139	22.0	396	22 AAB90664	Human secreted pro
43	138	21.9	32	13 AAR20165	Apo AI polypeptide
44	138	21.9	377	14 AAR39501	Human apolipoprote
45	137	21.7	337	14 AAR39494	Human apolipoprote

ALIGNMENTS

RESULT 1
AAP81082 standard; protein; 243 AA.
ID AAP81082 standard; protein; 243 AA.
XX
AC AAP81082;
XX
DE 14-JAN-1991 (first entry)
XX
XX Sequence of mature human apolipoprotein AI (apoAI).
XX
XX Atherosclerosis; therapy; cardiovascular disease.
XX
XX Homo sapiens.
XX
XX WO8803166-A.
XX
XX 05-MAY-1988.
XX
XX 21-OCT-1987; 87WO-EP00621.
XX
XX 23-OCT-1986; 86GB-0025435.
XX
XX (FARM) FARMITALIA C ERBA SPA.
XX
XX Lorenzetti R, Monaco L, Soria M, Palomba R, Isacchi A, Sarmientos P;
XX
XX WPI; 1988-133240/19.
XX
XX N-PSDB; AAN80243.
XX
XX Recombinant human apo-1 lipoprotein AI -
XX
XX used to lower plasma cholesterol and/or tri glyceride levels and
XX
XX to combat atherosclerosis and cardiovascular diseases
XX
XX Disclosure; Fig 1; 51pp; English.

XX The protein comprising apo AI genetic variants may be used to lower
 CC plasma cholesterol and/or triglyceride levels. They may also be used to
 CC combat atherosclerosis and cardiovascular diseases such as coronary
 CC heart disease. Prefd. proteins are Met-apo AI, Met-apo AI-T6, Met-apo
 CC AI-MI and Met-apo AI-T6/MI.
 XX
 SQ Sequence 243 AA;

Query Match 100.0%; Score 631; DB 9; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1.2e-50;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPMDRVKDLATVYVDVLDKSGRDYVSQFEGSALGKQNLKLDNMDSVTSFESKL 60
 DB 1 deppqspmdrvkdlatvyyvdvldksgrdyvsqfegsalsgkqnlkldnmdsvtsfesk 60
 QY 61 REQLGCVTQEFWMDNLEKETEGLRQEMSKDLEEVKAKVQPYLDLDFQKKWOEMELYROKVE 120
 DB 61 reqlgcvtqefwmdnleketeglrqemskdleevkakvqpyldldfqqkwgeemelyrqkve 120

RESULT 2

AAR56863
 ID AAR56863 standard; Protein; 264 AA.

AC AAR56863;

DT 26-JUN-1995 (first entry)

DE Apo-1ipoprotein AI-M.

KM Apo-1ipoprotein AI-M; Apo AI-M; Escherichia coli; plasmid PKP63;
 KM vector; atherosclerosis; cardiovascular disease.

OS Homo sapiens.

PN WO9413819-A.

PD 23-JUN-1994.

PE 09-DEC-1993; 93WO-SE01061.

PR 11-DEC-1992; 92SE-0003753.

PS (KABI) KABI PHARMACIA AB.

PI Abrahamson L, Holmgren E, Kalderen C, Lake M, Mikaelsson A;
 PI Sejlitz T;

DR WPI; 1994-217892/26.

DR N-PSDB; AAQ68357.

PT Expression vector for extracellular prodn of apo-1ipoprotein AI-M
 PT in E. coli - includes inducible promoter and signal peptide
 PT sequences providing improved yield, useful in treating
 PT atherosclerosis and cardiovascular disease.

PS Disclosure; Fig. 3; 33pp; English.

CC Plasmid PKP63 encodes human apo-1ipoprotein AI-M in E. coli. The
 CC NotI-HindIII segment of PKP63 and the deduced amino acid sequence
 CC of the translated Apo AI-M protein were determined. The plasmid
 CC provides high yields of extracellular Apo AI-M.

XX Sequence 264 AA;

Query Match 100.0%; Score 631; DB 15; Length 264;
 Best Local Similarity 100.0%; Pred. No. 1.3e-50;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPMDRVKDLATVYVDVLDKSGRDYVSQFEGSALGKQNLKLDNMDSVTSFESKL 60
 DB 22 deppqspmdrvkdlatvyyvdvldksgrdyvsqfegsalsgkqnlkldnmdsvtsfesk 81
 QY 61 REQLGCVTQEFWMDNLEKETEGLRQEMSKDLEEVKAKVQPYLDLDFQKKWOEMELYROKVE 120
 DB 82 reqlgcvtqefwmdnleketeglrqemskdleevkakvqpyldldfqqkwgeemelyrqkve 141

RESULT 3

AAR56864
 ID AAR56864 standard; Protein; 264 AA.

AC AAR56864;

DT 26-JUN-1995 (first entry)

DE Apo-1ipoprotein AI-M.

KM Apo-1ipoprotein AI-M; Apo AI-M; Escherichia coli; plasmid PKP64;
 KM vector; atherosclerosis; cardiovascular disease.

OS Homo sapiens.

PN WO9413819-A.

PD 23-JUN-1994.

PE 09-DEC-1993; 93WO-SE01061.

PR 11-DEC-1992; 92SE-0003753.

PS (KABI) KABI PHARMACIA AB.

PI Abrahamson L, Holmgren E, Kalderen C, Lake M, Mikaelsson A;
 PI Sejlitz T;

DR WPI; 1994-217892/26.

DR N-PSDB; AAQ68358.

PT Expression vector for extracellular prodn of apo-1ipoprotein AI-M
 PT in E. coli - includes inducible promoter and signal peptide
 PT sequences providing improved yield, useful in treating
 PT atherosclerosis and cardiovascular disease.

PS Disclosure; Fig. 4; 33pp; English.

CC Plasmid PKP64 encodes human apo-1ipoprotein AI-M in E. coli. The
 CC NotI-HindIII segment of PKP64 and the deduced amino acid sequence
 CC of the translated Apo AI-M protein were determined. The plasmid
 CC provides high yields of extracellular Apo AI-M.

XX Sequence 264 AA;

Query Match 100.0%; Score 631; DB 15; Length 264;
 Best Local Similarity 100.0%; Pred. No. 1.3e-50;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPMDRVKDLATVYVDVLDKSGRDYVSQFEGSALGKQNLKLDNMDSVTSFESKL 60
 DB 22 deppqspmdrvkdlatvyyvdvldksgrdyvsqfegsalsgkqnlkldnmdsvtsfesk 81
 QY 61 REQLGCVTQEFWMDNLEKETEGLRQEMSKDLEEVKAKVQPYLDLDFQKKWOEMELYROKVE 120
 DB 82 reqlgcvtqefwmdnleketeglrqemskdleevkakvqpyldldfqqkwgeemelyrqkve 141

RESULT 4

AAP61079
 ID AAP61079 standard; Protein; 267 AA.

AC AAP61079;

XX 07-OCT-1991 (first entry)
 XX
 XX Assumed human apolipoprotein A-1 derivative gene product.
 DE
 XX Hyperlipaemia; arteriosclerosis.
 XX
 XX Homo sapiens.
 OS
 XX JP61096998-A.
 PN
 XX
 PD 15-MAY-1986.
 XX
 XX 16-OCT-1984; 84JP-0216988.
 PF
 XX 16-OCT-1984; 84JP-0216988.
 PR
 XX (MITU) MITSUBISHI CHEM IND KK.
 PA
 XX WPI; 1986-165025/26.
 DR
 XX N-PSDB; AAN60886.
 XX
 PT Human apo:lipoprotein A-1 (deriv.) prepn. - by providing DNA
 PT fragment in cloning site downstream of expression vector promoter
 PT and introducing into host microorganism.
 PS
 XX Disclosure; Fig 2; 9pp; Japanese.
 XX
 XX The human apolipoprotein may be produced by a suitable transformed
 CC host, it is effective in treating hyperlipaemia and arteriosclerosis.
 CC
 XX Sequence 267 AA:
 SQ

Query Match 100.0%; Score 631; DB 7; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.4e-50;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPWDKVDLATVYVDVILKDSGRDYVSQFEGSALGKOLNKLDDNMDSVTSTPSKL 60
 DB 25 deppqspwdkvdlatvvydvilkdsgdyvsqfegsaiqkqnlklldnwdsvtstfslk 84
 QY 61 REQLGPVTOEFWMDNLEKETEGRLROEMSKDLEEVKAKVQPYLDPOKKQOEMELYRQKVE 120
 DB 85 reqlgpvtgefwdnlakeeteglrgemskdleevkavqpylddfqkqgemelyrqkve 144

RESULT 5
 AAP82128
 ID AAP82128 standard; protein; 267 AA.
 XX
 AC AAP82128;
 XX
 DT 24-OCT-1990 (first entry)
 XX
 DE Entire human preproapoprotein A1.
 XX
 KM human preproapoprotein A1; high density lipoprotein deficiency; ss.
 OS
 XX synthetic.
 XX
 FH key
 FT Peptide 1..18 Location/Qualifiers
 FT /label=precursor 19..24
 FT Peptide /label=propeptide 25..267
 FT Protein /label=mature apoprotein
 FT
 XX EP293357-A.
 XX
 PD 30-NOV-1988.
 XX

PF 24-MAY-1988; 88EP-0870095.
 XX
 PR 28-MAY-1987; 87GB-0012540.
 XX
 XX (UNIO) UCB SA.
 PA
 XX
 PI Bollen A, Gobert J, Wulfert E;
 PI
 XX WPI; 1988-339891/48.
 DR
 XX N-PSDB; AAN82064.
 DR
 XX
 PT New DNA encoding human preproapoprotein A1 -
 PT modified to eliminate hairpin structures
 PS
 XX Disclosure; P; French.
 XX
 XX The cDNA 878bp fragment encoding preproapoprotein A1 was detected
 CC in clone PULB1609 derived from human liver cells.
 CC See also AAN81258.
 CC
 XX Sequence 267 AA:
 SQ

Query Match 100.0%; Score 631; DB 9; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.4e-50;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPWDKVDLATVYVDVILKDSGRDYVSQFEGSALGKOLNKLDDNMDSVTSTPSKL 60
 DB 25 deppqspwdkvdlatvvydvilkdsgdyvsqfegsaiqkqnlklldnwdsvtstfslk 84
 QY 61 REQLGPVTOEFWMDNLEKETEGRLROEMSKDLEEVKAKVQPYLDPOKKQOEMELYRQKVE 120
 DB 85 reqlgpvtgefwdnlakeeteglrgemskdleevkavqpylddfqkqgemelyrqkve 144

RESULT 6
 AAR34032
 ID AAR34032 standard; Protein; 267 AA.
 XX
 AC AAR34032;
 XX
 DT 13-AUG-1993 (first entry)
 XX
 DE Sequence of apo A1.
 XX
 KM Lipoprotein; apoprotein; B-100; A-1; LDL; HDL; assay.
 OS
 XX Homo sapiens.
 OS
 XX W09307165-A.
 PN
 XX 15-APR-1993.
 PD
 XX 09-OCT-1992; 92WO-US08634.
 PF
 XX 09-OCT-1991; 91US-0774633.
 PR 08-OCT-1992; 92US-055555.
 PR 28-JUN-1992; 92US-0901706.
 PR
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX
 XX Curtiss LK, Koduri KR, Smith RS, Wirtzium JL, Young SG;
 PI
 XX WPI; 1993-134378/16.
 DR
 XX N-PSDB; AAO40030.
 DR
 XX Polypeptide mimic of native apo B-100 and native apo A-I - useful
 PT in assays for LDL and HDL in plasma samples
 PT
 XX Claim 19; Pages 105-106; 137pp; English.
 PS
 XX
 CC The inventors claim a portion of the polypeptide contg. apo B-100

CC that immunoreacts with antibodies secreted by the hybridoma MB47
 CC having ATCC Accession No. 8746. Polypeptides specifically claimed
 CC include residues 217-297, 216-310, 216-331, 216-377, 1-377,
 CC 205-297, 173-297, 140-297. DNA sequences encoding the polypeptides
 CC are also claimed. Also claimed are a fusion polypeptide that
 CC contains: (a) a first amino acid residue sequence up to 250 residues
 CC in length that includes residues 120-135 of apo A-I, (b) a second
 CC amino acid residue sequence up to 375 residues in length that
 CC includes residues 217-297 of apo B-100 and DNA encoding it.

XX Sequence 267 AA;

Query Match 100.0%; Score 631; DB 14; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.4e-50;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DEPPQSPMDRKVDLATVYVDLKSGRDVVSQFEGSALGKQLNLKLDNWDSTSTFESKL 60
 |||||||
 Db 25 deppqspmdrvkdlatvvdvdkdsgdyvsqfegsalgkqnlkldnwdsvstfsl 84
 |||||||
 OY 61 REQLGPTVQEFMNLKETEGLRQEMSKDLEVKAKVQPYLDPOKKQEMELYRQKVE 120
 |||||||
 Db 85 reqlgpvtqefwlnleketeglrqemskdleevkakvqpylddfqkkwqeemelyrqkve 144

RESULT 7

AAR72705
 ID AAR72705 standard; Protein: 267 AA.

AC AAR72705;

DT 31-OCT-1995 (first entry)

DE Human apo A-I including signal and propeptide sequences.

KM Apo A-I; LDL cholesterol; low density lipoprotein; lipid.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Peptide 1..18 /label= presignal

FT Peptide 19..24 /label= propeptide

FT Peptide 120..135 /label= claimed

FT Peptide /note= "as part of fusion polypeptide"

FT Peptide 19..240 /label= claimed

FT Peptide /note= "as part of fusion polypeptide"

XX US5408038-A.

XX 18-APR-1995.

XX 09-OCT-1991; 91US-0774633.

XX 09-OCT-1991; 91US-0774633.

XX 18-OCT-1992; 92US-0901706.

XX 08-OCT-1992; 92US-0959946.

XX (SCRI) SCRIPPS RES INST.

XX Curliiss LK, Koduri KR, Smith RS, Witzlum JL, Young SG;

XX WPI: 1995-161146/21.

XX N-PSDB; AAQ89634.

XX New Apo-11ipoprotein B-100 peptide(s) and fusion peptide(s) - used
 PT in assay systems for detecting LDL and HDL cholesterol levels in
 PT body fluids.
 XX

PS Claim 10; Fig 2; 41pp; English.

XX AA89634 and AAR72705 depict the AA sequence of human apo A-I and its

CC corresp. cDNA, including presignal residues and propeptide

CC residues, according to Seilhamer et al., DNA 3(4):309 (1984).

CC A dispersible apo A-I/B-100 fusion polypeptide is claimed which

CC contains a first AA sequence of apo A-I and that includes at

CC least AA sequence positions 120-135 (see AAR72606) and which reacts

CC with pan anti-apo A-I antibodies such as: At-4 ATCC HB8744; At-7

CC ATCC HB 8745; At-9 ATCC HB 8741; At-10 ATCC HB 9200; At-11 ATCC

CC HB 9201; At-12 ATCC HB 9202; At-13 ATCC HB 9203; At-14 ATCC HB

CC 9204; At-18 ATCC HB 9507.

XX Sequence 267 AA;

Query Match 100.0%; Score 631; DB 16; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.4e-50;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DEPPQSPMDRKVDLATVYVDLKSGRDVVSQFEGSALGKQLNLKLDNWDSTSTFESKL 60
 |||||||
 Db 25 deppqspmdrvkdlatvvdvdkdsgdyvsqfegsalgkqnlkldnwdsvstfsl 84
 |||||||
 OY 61 REQLGPTVQEFMNLKETEGLRQEMSKDLEVKAKVQPYLDPOKKQEMELYRQKVE 120
 |||||||
 Db 85 reqlgpvtqefwlnleketeglrqemskdleevkakvqpylddfqkkwqeemelyrqkve 144

RESULT 8

AAM08602
 ID AAM08602 standard; Protein: 267 AA.

AC AAM08602;

DT 04-SEP-1997 (first entry)

DE Human apolipoprotein A-1 variant "Paris" protein sequence.

XX Human; apolipoprotein A-1; variant; mutation; serum lipid; cholesterol;

KM high density lipoprotein; triglyceride; symptom; cardiovascular disease;

KW atherosclerosis; restenosis; myocardial infarct; angina; death; stroke;

KW cardiac decompensation; metabolic deficit.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Peptide 1..24 /note= "prepro peptide"

FT Region 172..178 /note= "this sequence which contains the mutated amino
 acid residue is claimed - claim 2"

FT Misc-difference 175 /note= "changed from Arg residue in wild type protein,
 due to a C to T transition mutation"

XX WO9637608-A1.

XX 28-NOV-1996.

XX 20-MAY-1996; 96MO-FR00747.

XX 22-MAY-1995; 95FR-0006061.

XX (INSP) INST PASTEUR LILLE.

XX (RHON) RHONE-POULENC ROBER SA.

XX (UYPA-) UNIV CURIE PARIS VI P & M.

XX Benoit P, Bruckert E, Deneffe P, Duverger N, Fruchart J;

XX Luc G, Turpin, Assmann G, Funke H;

XX WPI: 1997-021218/02.

XX N-PSDB; AAT43691.

XX New variant of human apoA-I with Cys at position 151 - has
PT anti-atherogenic activity for treatment and prevention of
PT cardiovascular disease
XX

PS Claim 2; Page -; 58pp; French.

XX This is the amino acid sequence of a human apolipoprotein A-I variant
CC designated the "Paris" variant which has a Cys replacing the Arg residue
CC at position 151. The substitution is generated by a mutation of
CC the C nucleotide at position 523 in the wild type gene to a T residue,
CC changing the encoded residue from an Arg to a Cys. The gene was isolated
CC from a patient with an unusual pattern of serum lipids i.e. low levels of
CC apoA-I and high density lipoprotein (HDL)-cholesterol and high
CC triglycerides, but showing symptoms of atherosclerosis. The new variant
CC protein has anti-atherogenic activity so is useful for treatment and
CC prevention of cardiovascular diseases such as atherosclerosis,
CC restenosis, myocardial infarct, angina, sudden death, stroke and cardiac
CC decompensation, or more generally any condition involving genetic or
CC metabolic deficit of apoA-I.
CC Note: this sequence is not given in the specification but is generated
CC from the wild type apoA-I gene disclosed in the specification and has
CC the appropriate amino acid changed.
XX

SQ Sequence 267 AA;

Query Match 100.0%; Score 631; DB 18; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.4e-50;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPSPMDRVKDLATVYVDVILKDSGRDYSQFEGSALGKQLNLKLDNMDSVTSFESKL 60
DB 25 DEPPSPMDRVKDLATVYVDVILKDSGRDYSQFEGSALGKQLNLKLDNMDSVTSFESKL 84
QY 61 REQLGPTVTOEFMDNLEKETEGRLROEMSKDLEEVKAKVQPYLDDPOKKQOEMELYROKVE 120
DB 85 REQLGPTVTOEFMDNLEKETEGRLROEMSKDLEEVKAKVQPYLDDPOKKQOEMELYROKVE 144

RESULT 9

AAV18675 ID AAV18675 standard; Protein: 267 AA.

AC AAV18675;

DT 09-JUL-1999 (first entry)

DE Human apolipoprotein AI protein sequence.

XX Gene therapy: apolipoprotein A-I; agonist: dyslipidemic disorder;
KW ApoA-I; cardiovascular disease; atherosclerosis; restenosis; LCAT;
KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.
XX

OS Homo sapiens.

OS WO9916409-A2.

PN 08-APR-1999.

PF 28-SEP-1998; 98WO-US20329.

PR 29-SEP-1997; 97US-0940136.

PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (DASS/) DASSERUX J.
PA (DUFO/) DUFOURCO J.
PA (METZ/) METZ G.
PA (SEKUL/) SEKUL R.

XX Butner K, Cornut I, Dasseux J, Dufourcq J, Metz G;
PI Sekul R;

XX WPI: 1999-254921/21.
DR N-PSDB: AAX55971.

PT Nucleic acid encoding apolipoprotein A-I agonist peptides

PS Example: Fig 1; 232pp; English.

XX The present invention describes a nucleic acid (A) encoding an
CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,
CC which forms an amphipathic alpha-helix in presence of lipids. (A),
CC optionally as a complex with lipids, and host cells that contain (A),
CC are useful for gene therapy, or prevention, of diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I
CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat
CC endotoxemia (septic shock). Host cells containing (A) can also be used
CC to study the role of apoA-I in lipid metabolism. (B) can be used
CC diagnostically, e.g. to measure serum HDL (particularly its
CC subpopulation involved in retrograde cholesterol transport) and for
CC imaging the circulatory system or HDL accumulations at fatty streaks.
CC The present sequence represents human apoA-I.
XX

SQ Sequence 267 AA;

Query Match 100.0%; Score 631; DB 20; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.4e-50;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPSPMDRVKDLATVYVDVILKDSGRDYSQFEGSALGKQLNLKLDNMDSVTSFESKL 60
DB 25 DEPPSPMDRVKDLATVYVDVILKDSGRDYSQFEGSALGKQLNLKLDNMDSVTSFESKL 84
QY 61 REQLGPTVTOEFMDNLEKETEGRLROEMSKDLEEVKAKVQPYLDDPOKKQOEMELYROKVE 120
DB 85 REQLGPTVTOEFMDNLEKETEGRLROEMSKDLEEVKAKVQPYLDDPOKKQOEMELYROKVE 144

RESULT 10

ABA47620 ID ABA47620 standard; Protein: 267 AA.

AC ABA47620;

DT 21-JAN-2002 (first entry)

DE Full length Apo-AI.

XX Apolipoprotein; Apo-AI; Apo-A-I fragment T-cell activation inhibitor;
KW APTI; monocyte; IL-1; interleukin 1; TNF; tumour necrosis factor;
KW acute pancreatitis; Alzheimer's disease; asthma; cancer; fever;
KW inflammatory bowel disease; ischemia; multiple sclerosis; osteoporosis;
KW Parkinson's disease; psoriasis; probe.
XX

OS Homo sapiens.

OS Key Location/Qualifiers

FT Binding-site 44..65

FT Binding-site 220..241

FT Binding-site 74..111

FT Binding-site 149..219

FT Binding-site 99..120

FT Binding-site 99..143

FT Binding-site 66..120

FT Binding-site 149..219

FT Binding-site 99..120

FT Binding-site 99..143

FT Binding-site 66..120

FT Binding-site 149..219

Query Match	Best Local Similarity	Score	DB	Length	267;
Matches	120%	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;

QY 1 DEPPDSMPDRVADATATVYVDYLKDCGRPYVSOFPESALGRJONTLKLDDNDSVWSTFSKL 60
Db 25 deppgsmpdrvxdtatlyvdvrlksgsgrdyvsqfegsalsgklnlklldnndsvstfsskl 84
QY 61 RROGLSPVIOEFMDNLFEKTEEGELRQMSDLEEVYAKNOPYLDDPOKKWQEMELIYRKVE 120
Db 85 rrglspvqgelrdmleeketeglrgemsdyleevayaknopyliddtqkvwqeemelyrkvve 144

RESULT	11
AAP80668	
ID	AAP80668 standard; 268 AA
XX	
AC	AAP80668;
XX	

DT	24-OCT-1990 (first entry)
XX	
DE	Recombinant human preproapoprotein AI
YY	

KM	human preproapoprotein A1; high density lipoprotein deficiency; ss
XX	
OS	synthetic.
xx	

Key	Location/Qualifiers
Peptide	1..18
Peptide	/label=precursor
Peptide	19..25
Protein	/label=proprotein
Protein	26..268
Protein	/label=immature apoprotein A1

PN	EP293357-A.	
XX	30-NOV-1988.	
PD		
XX	24-MAY-1988;	88EP-0870095.
PF		
XX	28-MAY-1987;	87GB-0012540.
PR		

PA (UNIO) UCB SA.
XX
PI Bollen A, Gobert J, Wulfert E,
XX
DR WPI; 1988-339891/48.
DR N-PsDB; AAN1258.

PT New DNA encoding human preproapoptin A1
PT modified to eliminate hairpin structures
XX
PS Claim 1; Page 12; 25pp; French.

CC Met at pposn 19 is inserted as an extra amino acid c.f. wild-type
CC protein.
CC The DNA fragment used to replace the wild-type sequence encoding
CC amino acids -6 to +14 (= Arg 20 to Leu 39) modifies codons
CC corresponding to wild-type amino acids -6, -1, 1, 3, 4, 5, 6, 7,
CC 10, 11 and 14. The changed codons still encode the same amino acids
CC as in the wild-type protein but reduce formation of secondary
CC structures in mRNA.
CC See also AAN82064.

SQ Sequence 268 AA;

Query Match	100.0%	Score 631;	DB 9;	Length 268;
Best Local Similarity	100.0%	Pred. No. 1.4e-50;		
Matches 120;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

```
QY      1 DEPOSPWMDRYKDLATVYVDVLKDSGRDYVSQFEGSALGQLNLKLDDNWDSVTSTFSKLL 600
         |||
Db    26 deppspwdrkdlatvyvdvlkdsgrdyvsqfegsalgqlnlklldnwdsvstfskl 855
```

QY 61 REQLGPTVTOEFWMDLKEKETEGRLQEMSKDLEEVAKAVQPYLDDFOKKMOEEMELYRQKVE 120
 |||
 Db 86 reqlgpvtgctgwndlkeketegllrqemskdleevakavqpylddfqkkgwgemelyrqkve 145

RESULT 12

AAU33170
 ID AAU33170 standard; Protein; 299 AA.

AC AAU33170;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #3661.

KW Human; Vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

PA (HYSEQ-) HYSEQ INC.

PI Tang YT, Liu C, Dormanac RT;

DR WPI; 2001-611725/70.

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -

PS Claim 20; Page 718; 765pp; English.

CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptide and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemia. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.

XX Sequence 299 AA;

Query Match 100.0%; Score 631; DB 22; Length 299;
 Best Local Similarity 100.0%; Pred. No. 1.6e-50;
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPOSPWDRVKDLATVYVDVLDKSGRDVVSQFEGSALGKQLNLKLDNDMSVTSFSKL 60
 |||
 Db 57 deppspwdrvkdlatvyvdvldksgrdvvsqfegsalgkqlnlkldndmsvtsfskl 116
 |||
 QY 61 REQLGPTVTOEFWMDLKEKETEGRLQEMSKDLEEVAKAVQPYLDDFOKKMOEEMELYRQKVE 120
 |||
 Db 117 reqlgpvtgctgwndlkeketegllrqemskdleevakavqpylddfqkkgwgemelyrqkve 176

RESULT 13

AAO12095
 ID AAO12095 standard; Protein; 154 AA.

AC AAO12095;

DT 06-NOV-2001 (first entry)

DE Human polypeptide SEQ ID NO 25987.

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

OS Homo sapiens.

PN WO200164835-A2.

PD 07-SEP-2001.

PF 26-FEB-2001; 2001WO-US04927.

PR 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

PA (HYSEQ-) HYSEQ INC.

PI Tang YT, Liu C, Dormanac RT;

DR WPI; 2001-514838/56.

DR N-PSDB; AA192026.

PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

PS Claim 20; SEQ ID NO 25987; 1399pp + Sequence Listing; English.

CC The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibit activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WPI
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 154 AA;

Query Match 79.2%; Score 500; DB 22; Length 154;
 Best Local Similarity 84.8%; Pred. No. 9.3e-39;
 Matches 95; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 DEPOSPWDRVKDLATVYVDVLDKSGRDVVSQFEGSALGKQLNLKLDNDMSVTSFSKL 60
 |||
 Db 33 deppspwdrvkdlatvyvdvldksgrdvvsqfegsalgkqlnlkldndmsvtsfskl 92
 |||
 QY 61 REQLGPTVTOEFWMDLKEKETEGRLQEMSKDLEEVAKAVQPYLDDFOKKMOEEMELYRQKVE 120
 |||
 Db 93 reqlgpvtgctgwndlkeketegllrqemskdleevakavqpylddfqkkgwgemelyrqkve 144

RESULT 14

AA002278
 ID AA002278 standard; Protein: 151 AA.
 XX
 AC AA002278;
 XX
 DT 06-NOV-2001 (first entry)
 DE Human polypeptide SEQ ID NO 16170.
 XX
 DE Human polypeptide SEQ ID NO 16170.
 XX
 DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PF 26-FEB-2001; 2001WO-US04927.
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 PA (HYSE-) HYSBO INC.
 PI Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-514838/56.
 DR N-PSDB; AA182209.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 PS
 PS Claim 20; SEQ ID NO 16170; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 XX
 SO Sequence 151 AA;
 Query Match 77.5%; Score 489; DB 22; Length 151;
 Best Local Similarity 94.9%; Pred. No. 9.5e-38;
 Matches 94; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 22 LKDSGRDYVSQFEGSALCKQLNKLNDWSDVTSFSLRQQLPVPQEFMDNLEKELEG 81
 DB 1 lkdsgdyvsqfegsalcqlnklndwdsdvtstfslrqqlpvpqetwlnlekdteq 60
 QY 82 LRQESKDLSEYKAKVOPYLDPFOKKQOEEMELYRQKYE 120
 DB 61 lrqeskdleekakvvpylldpfokkqoeemelyrqkce 99

AAU28372;
 XX
 DT 18-DEC-2001 (first entry)
 DE Novel human secretory protein, Seq ID No 729.
 XX
 DE Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; parkinson's disease; burn;
 KW anyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.
 XX
 OS Homo sapiens.
 PN WO200166689-A2.
 PD 13-SEP-2001.
 PF 05-MAR-2001; 2001WO-US04942.
 PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 PA (HYSE-) HYSBO INC.
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX WPI; 2001-589934/66.
 DR N-PSDB; AAS45272.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 PS
 PS Example 2; SEQ ID NO 729; 107pp; English.
 XX
 CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of

CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention.
 XX

SQ Sequence 166 AA:

Query Match 76.9%: Score 485.5; DB 22; Length 166;
 Best Local Similarity 80.0%; Pred. No. 2.2e-37;
 Matches 96; Conservative 1; Mismatches 0; Indels 23; Gaps 1;

QY 1 DEPPQSPWDRVKDLATYVYVDVLDKSGRDYVVSQFEGSALGKQLNLKLDNDSYTSFSKL 60
 |||||||
 Db 34 deppspwdrvkdlatyvdvldksgk-----dsytslfskl 70
 |||||||
 QY 61 REQLGPVTQEFWDLKETEGLRQEMSKDLEVKAKVQPYLDDFORKKWOEMELYRQKYE 120
 |||||||
 Db 71 reqlgpvtqefwldlketegllrqemskdleevkakvqpylddfqkkwqemelyrqkve 130
 |||||||

Search completed: September 22, 2002, 12:05:15
 Job time: 290 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:22:55 ; Search time 26.49 Seconds
(without alignments)
1743.663 Million cell updates/sec

Title: US-09-803-918a-2
Perfect score: 267
Sequence: 1 MKAALVTLAVLFTGSGARH.....SFKVSPLSALEYTKKLNTQ 267

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 segs, 172994929 residues

Word size : 0
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	12.7	67	4 Q9Y355	Q9Y355 homo sapien
2	26	9.7	26	4 Q9UCR8	Q9UCR8 homo sapien
3	19	7.1	36	6 Q02762	Q02762 ovls aries
4	19	7.1	264	11 Q9Z2L4	Q9Z2L4 mesocricetu
5	13	4.9	82	6 Q29248	Q29248 sus scrofa
6	12	4.5	258	11 Q09054	Q09054 rattus norv
7	12	4.5	258	11 Q08877	Q08877 rattus norv
8	12	4.5	263	11 Q08855	Q08855 mus musculu
9	12	4.5	263	11 Q08855	Q08855 mus musculu
10	10	3.7	132	16 Q9HWR9	Q9HWR9 mus musculu
11	8	3.0	69	11 Q99JY9	Q99JY9 mus musculu
12	8	3.0	72	5 Q9UAA7	Q9UAA7 conus livid
13	8	3.0	300	16 Q9HW34	Q9HW34 pseudomonas
14	8	3.0	387	16 Q9PDM0	Q9PDM0 xyliella fas
15	8	3.0	395	11 Q9DBN0	Q9DBN0 mus musculu
16	8	3.0	395	11 Q9IXF8	Q9IXF8 mus musculu

17	8	3.0	413	15 Q11556	Q11556 human immun
18	8	3.0	435	11 Q01488	Q01488 mus musculu
19	8	3.0	691	5 Q9VZE7	Q9VZE7 drosophila
20	8	3.0	714	2 Q9Z3F4	Q9Z3F4 xanthomonas
21	8	3.0	770	5 Q9GPD3	Q9GPD3 drosophila
22	8	3.0	771	5 Q9GPD5	Q9GPD5 drosophila
23	8	3.0	772	5 Q9GPD4	Q9GPD4 drosophila
24	8	3.0	773	5 Q9GPD8	Q9GPD8 drosophila
25	8	3.0	3562	2 Q9F829	Q9F829 microonosp
26	8	3.0	5050	2 Q9KSM1	Q9KSM1 arabidopsis
27	7	2.6	9	4 Q9UCS8	Q9UCS8 homo sapien
28	7	2.6	41	4 Q13587	Q13587 homo sapien
29	7	2.6	63	15 Q37693	Q37693 human immun
30	7	2.6	67	10 Q81764	Q81764 arabidopsis
31	7	2.6	72	4 Q14970	Q14970 homo sapien
32	7	2.6	73	4 Q75702	Q75702 homo sapien
33	7	2.6	78	12 Q9DKW9	Q9DKW9 spodoptera
34	7	2.6	83	10 Q942Y3	Q942Y3 oryza sativ
35	7	2.6	87	15 Q9DXP2	Q9DXP2 human immun
36	7	2.6	88	15 Q9EAP6	Q9EAP6 human immun
37	7	2.6	88	15 Q9RAM4	Q9RAM4 human immun
38	7	2.6	88	15 Q9ORW4	Q9ORW4 human immun
39	7	2.6	89	4 Q9BR82	Q9BR82 homo sapien
40	7	2.6	89	15 Q9ID03	Q9ID03 human immun
41	7	2.6	90	15 Q78841	Q78841 human immun
42	7	2.6	91	15 Q9W9A0	Q9W9A0 human immun
43	7	2.6	91	15 Q9DK41	Q9DK41 human immun
44	7	2.6	92	15 Q9DK65	Q9DK65 human immun
45	7	2.6	92	15 Q77305	Q77305 human immun
46	7	2.6	94	15 Q9WNU8	Q9WNU8 human immun
47	7	2.6	95	15 Q91JUS	Q91JUS human immun
48	7	2.6	95	15 Q75278	Q75278 human immun
49	7	2.6	96	15 Q9WL10	Q9WL10 human immun
50	7	2.6	100	15 Q9YDT9	Q9YDT9 human immun
51	7	2.6	101	15 Q72382	Q72382 human immun
52	7	2.6	101	15 Q72383	Q72383 human immun
53	7	2.6	101	16 Q50067	Q50067 mycobacteri
54	7	2.6	102	13 Q98TJ9	Q98TJ9 platichtys
55	7	2.6	113	15 Q71020	Q71020 human immun
56	7	2.6	113	15 Q71022	Q71022 human immun
57	7	2.6	113	15 Q71024	Q71024 human immun
58	7	2.6	114	15 Q78358	Q78358 human immun
59	7	2.6	114	15 Q74742	Q74742 human immun
60	7	2.6	114	15 Q71017	Q71017 human immun
61	7	2.6	120	15 Q71376	Q71376 human immun
62	7	2.6	121	15 Q9Q727	Q9Q727 human immun
63	7	2.6	122	8 Q03686	Q03686 actinastrium
64	7	2.6	129	4 Q00245	Q00245 homo sapien
65	7	2.6	134	5 Q46206	Q46206 ascaris lum
66	7	2.6	134	5 Q46208	Q46208 ascaris lum
67	7	2.6	130	5 Q9TYJ8	Q9TYJ8 caenorhabdt
68	7	2.6	150	16 Q9CHN5	Q9CHN5 lactococcus
69	7	2.6	155	2 Q9LEP0	Q9LEP0 salmonella
70	7	2.6	163	4 Q9HBK0	Q9HBK0 homo sapien
71	7	2.6	170	15 Q901E4	Q901E4 human immun
72	7	2.6	170	15 Q901E3	Q901E3 human immun
73	7	2.6	181	4 Q9BUC7	Q9BUC7 homo sapien
74	7	2.6	181	4 Q9H674	Q9H674 homo sapien
75	7	2.6	185	15 Q90LW2	Q90LW2 human immun

ALIGNMENTS

RESULT 1
Q9Y355 PRELIMINARY; PRT; 67 AA.
AC Q9Y355; ID Q9Y355;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE APOLOPROTEIN A1 (FRAGMENT).
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99216322; PubMed=10198255;
 RA Hamid Asl K., Liepnieks J.J., Nakamura M., Parker F., Benson M.D.;
 RT "A novel apolipoprotein A-1 variant, Arg173Pro, associated with
 RT cardiac and cutaneous amyloidosis.";
 RL Biochem. Biophys. Res. Commun. 257:584-588(1999).
 DR EMBL: AE148963; AAD34604.1; -;
 DR HSSP: P02647; IAV1.
 KM Lipoprotein.
 FT NON_TER 1 1
 FT NON_TER 67 67
 SQ SEQUENCE 67 AA; 7433 MW; 525E1FE7BDD5AFB CRC64;

Query Match 12.7%; Score 34; DB 4; Length 67;
 Best Local Similarity 100.0%; Pred. No. 5e-26;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 198 LAARLEALKENGARLAERHAKATEHLSTSEKA 231
 DB 34 LAARLEALKENGARLAERHAKATEHLSTSEKA 67
 ||||||||||||||||||||||||||||||||
 ||||||||||||||||||||||||||||||||

RESULT 2
 O9UCT8 PRELIMINARY; PRT; 26 AA.
 AC 09UCT8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE SPERM ACTIVATING PROTEIN SUBUNIT I, SPAP SUBUNIT I.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91369902; PubMed=1909886;
 RA Akerlof E., Jorcnvall H., Slotte H., Pousette A.;
 RT "Identification of apolipoprotein A1 and immunoglobulin as components
 RT of a serum complex that mediates activation of human sperm motility.";
 RL Biochemistry 30:8986-8990(1991).
 DR HSSP: P02647; IAV1.
 DR InterPro: IPR000074; Apolipoprotein.
 KW Pfam: PF01442; Apolipoprotein; 1.
 SQ SEQUENCE 26 AA; 2930 MW; 64921A333E768D7 CRC64;

Query Match 9.7%; Score 26; DB 4; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2e-18;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 DEPOSMDRVKDLATVYVYLKDSG 50
 DB 1 DEPOSMDRVKDLATVYVYLKDSG 26
 ||||||||||||||||||||||||||||
 ||||||||||||||||||||||||||||

RESULT 3
 O02762 PRELIMINARY; PRT; 56 AA.
 AC 002762;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE APOLIPROTEIN A1 (FRAGMENT).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=99098454; PubMed=9883985;
 RA Robertson J.A., Bhattacharya S., Ing N.H.;
 RT "Tamoxifen up-regulates oestrogen receptor-alpha, c-fos and
 RT glyceroldehyde 3-phosphate-dehydrogenase mRNAs in ovine endometrium.";
 RL J. Steroid Biochem. Mol. Biol. 67:285-292(1998).
 DR EMBL: U94720; AAB57840.1; -;
 DR HSSP: P02647; IAV1.
 KM Lipoprotein.
 FT NON_TER 1 1
 FT NON_TER 56 56
 SQ SEQUENCE 56 AA; 6617 MW; 2AB38E08F1E8F1BC CRC64;

Query Match 7.1%; Score 19; DB 6; Length 56;
 Best Local Similarity 100.0%; Pred. No. 4.1e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 85 REQLGPTQEFMDNLEKET 103
 DB 15 REQLGPTQEFMDNLEKET 33
 ||||||||||||||||||||||||
 ||||||||||||||||||||||||

RESULT 4
 O922L4 PRELIMINARY; PRT; 264 AA.
 AC 0922L4;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE APOLIPROTEIN A-1.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GOLDEN SYRIAN; TISSUE=INTESTINE;
 RX MEDLINE=99061559; PubMed=9843713;
 RA Wu J.Y.J., Reeves S.K., Wang Y.R., Wu Y., Lei P.P., Lei K.Y.;
 RT "Zinc deficiency decreases plasma level and hepatic mRNA abundance of
 RT apolipoprotein A-I in rats and hamsters.";
 RL Am. J. Physiol. 275:G1516-G1525(1998).
 DR EMBL: AF046919; AAC98484.1; -;
 DR HSSP: P02647; IAV1.
 DR InterPro: IPR000074; Apolipoprotein.
 KW Pfam: PF01442; Apolipoprotein; 1.
 SQ SEQUENCE 264 AA; 30739 MW; 280B22FAC0F0B129 CRC64;

Query Match 7.1%; Score 19; DB 11; Length 264;
 Best Local Similarity 100.0%; Pred. No. 1.7e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86 EQLGPTQEFMDNLEKET 104
 DB 85 EQLGPTQEFMDNLEKET 103
 ||||||||||||||||||||||||
 ||||||||||||||||||||||||

RESULT 5
 O29248 PRELIMINARY; PRT; 82 AA.
 AC 029248;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE APOLIPROTEIN A-1 (FRAGMENT).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9823;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SMALL INTESTINE;
 RX MEDLINE=96327607; PubMed=8672129;
 RA Wintere A.K., Fredholm M., Davies W.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 RT library.";
 RL Mamm. Genome 7:509-517(1996).
 DR EMBL, F14858; CAA23298.1; -;
 KW Lipoprotein.
 FT NON_TER
 SQ SEQUENCE 82 AA; 9168 MW; 24625C65CBFFEDD8 CRC64;

Query Match 4.9%; Score 13; DB 6; Length 82;
 Best Local Similarity 100.0%; Pred. No. 5.8e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AVFLTGSQARHF 21
 DB 9 AVFLTGSQARHF 21

RESULT 6
 ID 009054 PRELIMINARY; PRT; 258 AA.
 AC 009054;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE APOLIPROTEIN A-I.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WKY, AND SHRS; TISSUE=SPLEEN;
 RA Chang A.N., Fan K.C., Shaw G.C., Yang U.C.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U79578; AAB58430.1; -;
 DR EMBL; U79577; AAB58429.1; -;
 DR HSSP; P02647; IAV1.
 DR InterPro; IPR000074; Apolipoprotein.
 DR Pfam; PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 SQ SEQUENCE 258 AA; 29918 MW; 093E6FE2E629CD08 CRC64;

Query Match 4.5%; Score 12; DB 11; Length 258;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 KDSGRDYVSQFE 58
 DB 45 KDSGRDYVSQFE 56

RESULT 7
 ID 008877 PRELIMINARY; PRT; 258 AA.
 AC 008877;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE APOLIPROTEIN A-I.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SHR; TISSUE=SPLEEN;

RX MEDLINE=98077648; PubMed=9415807;
 RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
 RT "Repetitive elements in the third intron of murine apolipoprotein A-I
 RT gene.";
 RL Biochem. Mol. Biol. Int. 43:989-996(1997).
 DR EMBL; U79576; AAB58428.1; -;
 DR HSSP; P02647; IAV1.
 DR InterPro; IPR000074; Apolipoprotein.
 DR Pfam; PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 SQ SEQUENCE 258 AA; 29831 MW; 093FB582E629CD08 CRC64;

Query Match 4.5%; Score 12; DB 11; Length 258;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 KDSGRDYVSQFE 58
 DB 45 KDSGRDYVSQFE 56

RESULT 8
 ID 009042 PRELIMINARY; PRT; 263 AA.
 AC 009042;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE APOLIPROTEIN A-I.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR AND BALB/C; AND C3H; TISSUE=SPLEEN;
 RA Chang A.N., Fan K.C., Shaw G.C., Yang U.C.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U79575; AAB58427.1; -;
 DR EMBL; U79572; AAB58424.1; -;
 DR EMBL; U79573; AAB58425.1; -;
 DR HSSP; P02647; IAV1.
 DR InterPro; IPR000074; Apolipoprotein.
 DR Pfam; PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 SQ SEQUENCE 263 AA; 30516 MW; E245DF7483A5A0DD CRC64;

Query Match 4.5%; Score 12; DB 11; Length 263;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 KDSGRDYVSQFE 58
 DB 46 KDSGRDYVSQFE 57

RESULT 9
 ID 008855 PRELIMINARY; PRT; 263 AA.
 AC 008855;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE APOLIPROTEIN A-I.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=SPLEEN;

RX MEDLINE=98077648; PubMed=9415807;
 RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
 RT "Repetitive elements in the third intron of murine apolipoprotein A-I
 gene."
 RL Biochem. Mol. Biol. Int. 43:989-996(1997).
 DR EMBL: U79574; AAB58426.1; -;
 DR HSSP: P02647; IAV1.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 SQ SEQUENCE 263 AA; 30544 MW; 7825DF7483A5B24A CRC64;

Query Match 4.5%; Score 12; DB 11; Length 263;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 KDSGRDYVSQFE 58
 DB 46 KDSGRDYVSQFE 57

RESULT 10
 ID 09HWR9 PRELIMINARY; PRT; 132 AA.
 AC 09HWR9:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL PROTEIN PA4111.
 GN PA4111.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou M.,
 Garber R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 Brody L.A., Coulter D.H., Folger K.R., Kas A., Latdige K., Lim R.M.,
 Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen."
 RT Nature 406:959-964(2000).
 RL EMBL: AE004827; AAG07498.1; -;
 DR InterPro: IPR001109; HupF_HypC.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 132 AA; 15113 MW; A56B0BB1D9E3BA0 CRC64;

Query Match 3.7%; Score 10; DB 16; Length 132;
 Best Local Similarity 100.0%; Pred. No. 0.09;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 QRLARLEAL 205
 DB 41 QRLARLEAL 50

RESULT 11
 ID 099JY9 PRELIMINARY; PRT; 69 AA.
 AC 099JY9:
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 7.9 KDA PROTEIN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC005635; AA005635.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 69 AA; 7862 MW; 5996C0B406CA5F4 CRC64;

Query Match 3.0%; Score 8; DB 11; Length 69;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 ALGKQLNL 68
 DB 47 ALGKQLNL 54

RESULT 12
 ID 09UAA7 PRELIMINARY; PRT; 72 AA.
 AC 09UAA7:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE FOUR-LOOP CONOTOXIN LVIA (FRAGMENT).
 OS Conus lividus.
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=89426;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2;
 RX MEDLINE=99289555; PubMed=10359796;
 RA Duda T.F. Jr., Palumbi S.R.;
 RT "Molecular genetics of ecological diversification: duplication and
 rapid evolution of toxin genes of the venomous gastropod Conus."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).
 DR EMBL: AF089912; AAD48167.1; -;
 DR InterPro: IPR004214; Conotoxin.
 DR Pfam: PF02950; Conotoxin; 1.
 FT NON_TIR 1
 SQ SEQUENCE 72 AA; 7970 MW; B7A0DDC87533D8D CRC64;

Query Match 3.0%; Score 8; DB 5; Length 72;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AVLFLTGS 16
 DB 5 AVLFLTGS 12

RESULT 13
 ID 09HW34 PRELIMINARY; PRT; 300 AA.
 AC 09HW34:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE HYPOTHETICAL PROTEIN PA4368.
 GN PA4368.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;

RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong K.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 DR EMBL: AE004852; AAC07756.1; -
 DR InterPro: IPR002048; EF-hand.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 300 AA; 33580 MW; 7D9ED17502137BA7 CRC64;

Query Match 3.0%; Score 8; DB 16; Length 300;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 197 RLAARLEA 204
 |||||||
 Db 228 RLAARLEA 235

RESULT 14
 O9PDMO PRELIMINARY; PRT; 387 AA.
 AC O9PDMO.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHEICAL PROTEIN XF1359.
 GN XF1359.
 OS *Xylella fastidiosa*.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC *Xylella*.
 OX NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-9A5C;
 RX MEDLINE-20365717; PubMed=10910347;
 RA Simpson A.J.G., Reilach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.R., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carer H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Faciniani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hohelsel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madalena A.M.B.N., Madalena H.M.F., Matsukuma A.Y.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorillo C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A.J., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E.Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsunako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*,";
 RT Nature 406:151-159(2000).
 DR EMBL: AE003967; AAF84168.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 387 AA; 42872 MW; 82C09EC7EC7B7027 CRC64;

Query Match 3.0%; Score 8; DB 16; Length 387;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 AAVLTILAV 10
 |||||||
 Db 161 AAVLTILAV 168

RESULT 15
 O9DBNO PRELIMINARY; PRT; 395 AA.
 AC O9DBNO.
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ADULT MALE LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
 DE CLONE:1300002K10, FULL INSERT SEQUENCE.
 GN APOA4.
 OS *Mus musculus* (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE=LIVER;
 RX MEDLINE-21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi Y., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Koehl P., Lewis S., Matsuo T., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki K., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection,";
 RL Nature 409:685-690(2001).
 DR EMBL: AK004856; BAB23620.1; -
 DR MGD: MGI:88051; APOA4.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein.1.
 SQ SEQUENCE 395 AA; 45044 MW; 4102D84ACH0D182A CRC64;

Query Match 3.0%; Score 8; DB 11; Length 395;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KAAVLTILAV 9
 |||||||
 Db 4 KAAVLTILAV 11

RESULT 16
 O9IXF8 PRELIMINARY; PRT; 395 AA.
 AC O9IXF8.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE UNKNOWN (PROTEIN FOR MGC:18592).

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strassberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC010769; AAH10769.1;
SQ SEQUENCE 395 AA; 45029 MW; C48BE32ED441F71 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 11; Length 395;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KAAVTLA 9
DB 4 KAAVTLA 11

RESULT 17
O11556 PRELIMINARY; PRT; 413 AA.
AC O11556;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Balotta C., Riva C., Violin M., Colombo C., Galli M., Moroni M.;
RT "Analysis of the VI-V5 env region in Long-Term Non Progressor and in
RT rapid progressor HIV-1 infected individuals."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U95459; AAB52806.1;
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT 413
SQ SEQUENCE 413 AA; 45471 MW; 893560C04CE12295 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 15; Length 413;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 SKREOLG 89
DB 238 SKREOLG 245

RESULT 18
O01488 PRELIMINARY; PRT; 435 AA.
AC O01488;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE VARIANT APOLOPROTEIN A-IV PRECURSOR (APOA-IV).
GN APOA-4.
OS Mus musculus castaneus (southeastern Asian house mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10091;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=91286309; PubMed=1648102;
RA Reue K., Lee T.H.;
RT "Genetic variation in mouse apolipoprotein A-IV due to insertion and
RT deletion in a region of tandem repeats."
RL J. Biol. Chem. 266:12715-12721(1991).
CC -I- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
CC LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
CC COMPONENT OF HDL AND CHYLOMICRONS. IT MAY PLAY A ROLE IN THE
CC INTRAVASCULAR METABOLISM OF HDL. POTENTIAL ROLE IN CELLULAR
CC CHOLESTEROL EFFLUX.
CC -I- TISSUE SPECIFICITY: INTESTINE, LIVER, AND PLASMA.
CC -I- MISCELLANEOUS: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS
CC (EACH 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A & B, RELATED 11-
CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
CC HELICAL, & MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH
CC LECITHIN:CHOLESTEROL ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
CC -I- MISCELLANEOUS: THE APOA-IV POLYMORPHISMS ARE CLASSIFIED BASED ON
CC THE OCCURENCE OF THREE, FOUR, OR FIVE E-Q-A-Q/ E-Q-Q-Q/ E-Q-V-Q
CC REPEAT UNITS.
DR EMBL: M64250; AAA37216.1;
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein; 1.
DR Lipid transport; HDL; VLDL; Chylomicron; Repeat; Signal; Liver;
RW Plasma; Multigene family; Polymorphism; Cholesterol metabolism.
FT SIGNAL 1
FT CHAIN 21 435 POTENTIAL.
FT DOMAIN 374 393 VARIANT APOLOPROTEIN A-IV.
FT REPEAT 374 377 TANDEM REPEATS.
FT REPEAT 378 381 1.
FT REPEAT 382 385 2.
FT REPEAT 386 389 3.
FT REPEAT 390 393 4.
FT REPEAT 390 393 5.
SQ SEQUENCE 435 AA; 49254 MW; B2AF55E8A8E456B2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 11; Length 435;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KAAVTLA 9
DB 4 KAAVTLA 11

RESULT 19
O9VZE7 PRELIMINARY; PRT; 691 AA.
AC O9VZE7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG1311 PROTEIN.
GN CG1311.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BERKELEY;
RC STRAIN=BERKELEY;
RX Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Evans, D., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris K.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibbegam C.,
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spletter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003480; AAF47876.1;
 DR FlyBase: FBgn0035523; CG1311.
 SQ SEQUENCE 691 AA; 76840 MW; 73309ED51C733208 CRC64;

Query Match 3.0%; Score 8; DB 5; Length 691;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AVTLAVL 11
 |||||
 DB 281 AVTLAVL 288

RESULT 20
 Q923F4 PRELIMINARY; PRT; 714 AA.
 AC Q923F4;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE AVIRULENCE PROTEIN AVRS2.
 GN AVRS2.
 OS *Xanthomonas campestris* (pv. *vesicatoria*).
 OC Bacteria; Proteobacteria; gamma subdivision; *Xanthomonas* group;
 CC *Xanthomonas*.
 OX NCBI_TaxID=341;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96345635; PubMed=8755898;
 RA Swords K.M., Dahlbeck D., Kearney B., Roy M., Staskawicz B.J.;
 RT "Spontaneous and induced mutations in a single open reading frame
 RT alter both virulence and avirulence in *Xanthomonas campestris* pv.
 RT *vesicatoria* avrBs2.";
 RL J. Bacteriol. 178:4661-4669(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Swords K.M., Dahlbeck D., Kearney B., Roy M., Staskawicz B.J.;
 RL Submitted (DDB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF114720; AAD1434.1; -;
 DR InterPro: IPR004129; GPPD.
 DR Pfam: PF03009; GPPD; 1.
 FT VARIANT 231 231 F -> S (IN REF. 1).
 SQ SEQUENCE 714 AA; 78487 MW; 79C034E286FDC145 CRC64;

Query Match 3.0%; Score 8; DB 2; Length 714;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 ALGKQLNL 68
 |||||
 DB 180 ALGKQLNL 187

RESULT 21
 Q9GPD3 PRELIMINARY; PRT; 770 AA.
 AC Q9GPD3;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ACP36DE (FRAGMENT).
 GN ACP36DE.
 OS *Drosophila simulans* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7240;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SIM8.
 RA Begun D., Whitley P., Todd B., Waldrup H., Clark A.;
 RT "Molecular population genetics of male accessory gland proteins in
 RT *Drosophila*.";
 RL Genetics 0:0-0(2001).
 DR EMBL: AY010674; AAC37418.1; -;
 DR FlyBase: FBgn0041931; Dsim\Acp36DE.
 FT NON_TER 1 1
 FT NON_TER 770 770
 SQ SEQUENCE 770 AA; 86139 MW; 640DFA51AB2B340B CRC64;

Query Match 3.0%; Score 8; DB 5; Length 770;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 KQLNKKLL 71
 |||||
 DB 216 KQLNKKLL 223

RESULT 22
 Q9GPD5 PRELIMINARY; PRT; 771 AA.
 AC Q9GPD5;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ACP36DE (FRAGMENT).
 GN ACP36DE.
 OS *Drosophila simulans* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7240;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SIM4.
 RA Begun D., Whitley P., Todd B., Waldrup H., Clark A.;
 RT "Molecular population genetics of male accessory gland proteins in
 RT *Drosophila*.";
 RL Genetics 0:0-0(2001).
 DR EMBL: AY010672; AAC37416.1; -;
 DR FlyBase: FBgn0041931; Dsim\Acp36DE.
 FT NON_TER 1 1
 FT NON_TER 771 771

SEQ SEQUENCE 771 AA; 86183 MW; ED3D1D945898CA16 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 5; Length 771;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 KQNLKLL 71
| | | | | | | |
DB 214 KQNLKLL 221

RESULT 23

Q9GPD4 PRELIMINARY; PRT; 772 AA.
AC 09GPD4;
DT 01-MAR-2001 (TREMBLREL. 16, Created)
DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE ACP36DE (FRAGMENT).
GN ACP36DE.
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SIM7;
RA Begun D., Whitely P., Todd B., Waldrip H., Clark A.;
RT "Molecular population genetics of male accessory gland proteins in Drosophila."
RL Genetics 0:0-0(2001).
DR EMBL: AY010673; AAG37417.1; -;
DR Flybase: FBgn0041931; Dsim\Acp36DE.
FT NON_TER 1 772 1
FT NON_TER 772 772
SQ SEQUENCE 772 AA; 86317 MW; 6EA11326DA49B0C7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 5; Length 772;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 KQNLKLL 71
| | | | | | | |
DB 216 KQNLKLL 223

RESULT 24

Q9GPD8 PRELIMINARY; PRT; 773 AA.
AC 09GPD8;
DT 01-MAR-2001 (TREMBLREL. 16, Created)
DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE ACP36DE (FRAGMENT).
GN ACP36DE.
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SIM1;
RA Begun D., Whitely P., Todd B., Waldrip H., Clark A.;
RT "Molecular population genetics of male accessory gland proteins in Drosophila."
RL Genetics 0:0-0(2001).
DR EMBL: AY010669; AAG37413.1; -;
DR Flybase: FBgn0041931; Dsim\Acp36DE.
FT NON_TER 1 773 1

FT NON_TER 773 773
SQ SEQUENCE 773 AA; 86429 MW; F059CA84C0267A10 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 5; Length 773;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 KQNLKLL 71
| | | | | | | |
DB 216 KQNLKLL 223

RESULT 25

Q9F829 PRELIMINARY; PRT; 3562 AA.
AC 09F829;
DT 01-MAR-2001 (TREMBLREL. 16, Created)
DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
DE MEGALOMICIN 6-DEOXYERYTHRONOLIDE B SYNTHASE 2.
GN MEGAL.
OS Micromonospora megalomica subsp. nigra.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Micromonosporinae; Micromonosporaceae;
OC Micromonospora.
OX NCBI_TaxID=136926;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL3275;
RX MEDLINE=20430101; PubMed=10972798;
RA Volchegursky Y., Hu Z., Katz L., McDaniel R.;
RT "Biosynthesis of the anti-parasitic agent megalomicin: transformation of erythromycin to megalomicin in Saccharopolyspora erythraea."
RL Mol. Microbiol. 37:752-762(2000).
DR EMBL: AF263245; AAG13918.1; -;
DR HSSP: P25715; 1MLA.
DR InterPro: IPR001227; Acyltransferase domain.
DR InterPro: IPR002085; Adh_zn_family.
DR InterPro: IPR000794; Ketoacyl-synth.
DR InterPro: IPR003880; Phosphopant_attach.
DR Pfam: PF00698; Acyl_transf. 2.
DR Pfam: PF00107; adh_zincf. 1.
DR Pfam: PF00109; ketoacyl-synth. 2.
DR Pfam: PF02801; ketoacyl-synth. 2.
DR PROSITE: PSS0075; ACP_DOMAIN. 2.
DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
KW Phosphopantetheine.
SQ SEQUENCE 3562 AA; 373617 MW; 4810786A14EC540B CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 3562;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 LRORLAR 201
| | | | | | | |
DB 1430 LRORLAR 1437

RESULT 26

Q9K5M1 PRELIMINARY; PRT; 5060 AA.
AC 09K5M1;
DT 01-OCT-2000 (TREMBLREL. 15, Created)
DT 01-OCT-2000 (TREMBLREL. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
DE PEPTIDE SYNTHETASE.
GN ADP.
OS Anabaena sp. 90.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=46234;
RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=90;
 RX MEDLINE=20392447; PubMed=10931313;
 RA Rouhainen L., Paulin L., Suomalainen S., Hyttinen H., Buikema W.,
 RA Haasikorn R., Sivonen K.;
 RT "Genes encoding synthetases of cyclic depsipeptides,
 RT anabaenopeptilides, in Anabaena strain 90.";
 RL Mol. Microbiol. 37:156-167(2000).
 DR EMBL: AJ269505; CAC01604.1; -
 DR HSSP: P14687; 1AMU
 DR InterPro: IPR000873; AMP-bind.
 DR InterPro: IPR001242; DUF4.
 DR InterPro: IPR001601; Meth.transf.
 DR InterPro: IPR003880; Phosphopant_attach.
 DR InterPro: IPR000051; SAM bind.
 DR Pfam: PF00501; AMP-binding; 4.
 DR Pfam: PF00668; Condensation; 4.
 DR PRINTS: PR00154; AMPBINDING.
 DR PROSITE: PS50075; ACP_DOMAIN; 4.
 DR PROSITE: PS00455; AMP_BINDING; 4.
 DR PROSITE: PS00012; PHOSPHOPANTHEINE; UNKNOWN_2.
 KW Phosphopantetheine.
 SQ SEQUENCE 5060 AA; 565934 MW; 0A6D498ABC69093E CRC64;

Query Match 3.0%; Score 8; DB 2; Length 5060;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 193 EURORLAA 200
 DB 4821 EURORLAA 4828

RESULT 27
 ID 09UCS8 PRELIMINARY; PRT; 9 AA.
 AC 09UCS8;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE APOLIPOPROTEIN A-I.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92075698; PubMed=1742316;
 RA Ehnholm C., Bozas S.E., Tenkanen H., Kirsbaum L., Metso J.,
 RA Murphy B., Walker I.D.;
 RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40
 RT protein of human blood are different proteins which both bind to
 RT apolipoprotein A-I.";
 RL Biochim. Biophys. Acta 1086:255-260(1991).
 SQ SEQUENCE 9 AA; 981 MW; 7EE37775A6C7776B CRC64;

Query Match 2.6%; Score 7; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5.6e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 DEPOSP 31
 DB 1 DEPOSP 7

RESULT 28
 ID Q13587 PRELIMINARY; PRT; 41 AA.
 AC Q13587;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE FATTY ACID SYNTHASE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96278786; PubMed=8662758;
 RA Hsu M.H., Chirala S.S., Wakil S.J.;
 RT "Human fatty-acid synthase gene. Evidence for the presence of two
 RT promoters and their functional interaction.";
 RL J. Biol. Chem. 271:13584-13592(1996).
 DR EMBL: U52428; AAC50536.1; -
 FT NON_TER
 SQ SEQUENCE 41 AA; 4668 MW; ECA60F116AB6E729 CRC64;

Query Match 2.6%; Score 7; DB 4; Length 41;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 93 QEFWDNL 99
 DB 20 QEFWDNL 26

RESULT 29
 ID 037693 PRELIMINARY; PRT; 63 AA.
 AC 037693;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DKID;
 RX MEDLINE=98080439; PubMed=9420250;
 RA van't Mont A.B., Ran L.J., Kuiken C.L., Kootstra N.A., Pals S.T.,
 RA Schuitemaker H.;
 RT "Analysis of the temporal relationship between human immunodeficiency
 RT virus type 1 quasispecies in sequential blood samples and various
 RT organs obtained at autopsy.";
 RL J. Virol. 72:488-496(1998).
 DR EMBL: AF021606; AAC04060.1; -
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 63 AA; 7341 MW; 53991BE85AD01767 CRC64;

Query Match 2.6%; Score 7; DB 15; Length 63;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KLRDOLG 89
 DB 52 KLRDOLG 58

RESULT 30
 ID 081764 PRELIMINARY; PRT; 67 AA.
 AC 081764;
 DT 01-NOV-1998 (Tremblrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE HYPOHETICAL 7.6 KDA PROTEIN.
 GN F1715.150 OR ATAG33960
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vitale D., Liguori R., Argitoni A., De Simone V., Hohnsels J.,
 RA Jesse T., Heijnen L., Vos P., Mewes H.W., Mayer K.F.X., Schueller C.,
 RA Bevan M.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Vitale D., Liguori R., Argitoni A., De Simone V., Mewes H.W.,
 RA Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031032; CAI19878.1; -;
 DR EMBL; AL161584; CAB80113.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 67 AA; 7600 MW; 241f65ffed8b65cf CRC64;

Query Match 2.6%; Score 7; DB 10; Length 67;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 LRGLIP 244
 DB 46 LRGLIP 52

RESULT 31
 ID 014970 PRELIMINARY; PRT; 72 AA.
 AC 014970;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE INTEGRAL MEMBRANE PROTEIN (FRAGMENT).
 GN NRAMP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95053705; PubMed=7964458;
 RA Cellier M.F., Govoni G., Vidal N., Kwan T., Groulx N., Liu J.,
 RA Sanchez F., Skamene E., Schurr E., Gros P.;
 RT "Human natural resistance-associated macrophage protein: cDNA cloning,
 RT chromosomal mapping, genomic organization and tissue-specific
 RT expression.";
 RL J. Exp. Med. 180:1741-1752(1994).
 DR EMBL; L38593; AAA57556.1; -;
 DR EMBL; L38592; AAA57556.1; JOINED.
 DR InterPro: IPR001046; Ntamp.
 DR Pfam: PF01566; Ntamp; 1.
 DR ProDom: PD001861; Ntamp; 1.
 FT NON_TER 1
 SQ SEQUENCE 72 AA; 7778 MW; 4b5e8d1a67d8498 CRC64;

Query Match 2.6%; Score 7; DB 4; Length 72;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 QRLAARL 202
 DB 16 QRLAARL 22

RESULT 32
 ID 075702 PRELIMINARY; PRT; 73 AA.
 AC 075702;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE PROTEIN-TYROSINE-PROSPHATASE, ISOFORM 3 (EC 3.1.3.48).
 GN ACP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Modesti A., Marzocchini R., Raugei G., Chiti A., Sereni A.,
 RA Magherini F., Ramponi G.;
 RT "Cloning, expression and characterisation of a new human low Mr
 RT phosphotyrosine protein phosphatase originating by alternative
 RT splicing.";
 RL FEBS Lett. 0:0-0(0).
 DR EMBL; Y16846; CA76416.1; -;
 DR HSSP; P24666; SPNT.
 DR InterPro: IPR00106; Low_mwt_PTPase.
 DR SMART; SM00226; LMPpc; 1.
 KW Hydrolase.
 SQ SEQUENCE 73 AA; 7660 MW; D261205427CBECF3 CRC64;

Query Match 2.6%; Score 7; DB 4; Length 73;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AVLFLTG 15
 DB 54 AVLFLTG 60

RESULT 33
 ID 09DKM9 PRELIMINARY; PRT; 78 AA.
 AC 09DKM9;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE HYPOHETICAL 9.0 KDA PROTEIN.
 OS Spodoptera frugiperda ascovirus 1.
 OC Viruses; dsDNA viruses, no RNA stage; Ascoviridae; Ascovirus.
 OX NCBI_TaxID=113374;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20540044; PubMed=11086137;
 RA Stasiak K., Demattè M.V., Federici B.A., Bigot Y.;
 RT "Phylogenetic position of the Diadromus pulchellus ascovirus DNA
 RT polymerase among viruses with large double-stranded DNA genomes.";
 RL J. Gen. Virol. 81:3059-3072(2000).
 DR EMBL; AJ279828; CAC19164.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 78 AA; 9012 MW; D3A91C1186502AE2 CRC64;

Query Match 2.6%; Score 7; DB 12; Length 78;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 76 SVSTFS 82

Db 35 SVSTSES 41
|||||

RESULT 34
Q942Y3 PRELIMINARY; PRT; 83 AA.
AC Q942Y3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE P0492G09.14 PROTEIN.
GN P0492G09.14.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriobotryaceae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone: P0492G09.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003266; BAB64192.1; -
SQ SEQUENCE 83 AA; 8687 MW; B06A60DB1CD1814C CRC64;

Query Match 2.6%; Score 7; DB 10; Length 83;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 174 DRARAHV 180
|||||
DB 19 DRARAHV 25

RESULT 35
Q9DXP2 PRELIMINARY; PRT; 87 AA.
AC Q9DXP2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=91CAS23750;
RA Op de Coul E.L.M., Prins M., Cornelissen M., van der Schoot A.,
RA Boufassa F., Brettle R., Hernandez-Aguado I., Schiffer V.,
RA McKenman J., Retza G., Robertson R., Goudsmit J., Coutinho R.,
RA Lukashov V.;
RT "Using Phylogenetic analysis to trace HIV-1 migration among western
European IDUs seroconverting from 1984 to 1997";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307254; AAG32422.1; -
FT NON_TER 1
FT 87
SQ SEQUENCE 87 AA; 9949 MW; 2103B8706FF2D927 CRC64;

Query Match 2.6%; Score 7; DB 15; Length 87;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KUREOLG 89
|||||
DB 77 KUREOLG 83

RESULT 36
Q9EAM6 PRELIMINARY; PRT; 88 AA.
AC Q9EAM6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GP120 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAB178R;
RA Machuca R.A.R., Bogh M., Gerstoft J., Kvinesdal B., Pedersen C.,
RA Obel N., Nielsen H., Nielsen C.;
RT "HIV-1 subtypes in Denmark";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=JAB178R;
RA Bogh M., Machuca R.A.R., Nielsen C.;
RT "Subtype specific problems with Roche PCR";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ289516; CAC06500.1; -
DR InterPro; IPR000777; GP120.
KW Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
FT 88
SQ SEQUENCE 88 AA; 9966 MW; 9059197BD2C09D9A CRC64;

Query Match 2.6%; Score 7; DB 15; Length 88;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KUREOLG 89
|||||
DB 79 KUREOLG 85

RESULT 37
Q9EAM4 PRELIMINARY; PRT; 88 AA.
AC Q9EAM4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GP120 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PR527;
RA Machuca R.A.R., Bogh M., Gerstoft J., Kvinesdal B., Pedersen C.,
RA Obel N., Nielsen H., Nielsen C.;
RT "HIV-1 subtypes in Denmark";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PR527;
RA Bogh M., Machuca R.A.R., Nielsen C.;
RT "Subtype specific problems with Roche PCR";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ289592; CAC06572.1; -
DR InterPro; IPR000777; GP120.
KW Pfam; PF00516; GP120; 1.

KM AIDS: Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 88
 SQ SEQUENCE 88 AA; 9908 MW; 46C7E92C65B6BAAC CRC64;

Query Match 2.6%; Score 7; DB 15; Length 88;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KIREOLG 89
 ID 111111
 DB 78 KIREOLG 84

RESULT 38
 Q90RM4 PRELIMINARY; PRT; 88 AA.
 AC Q90RM4:
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD_206V3;
 RA Machado D.M., Delwart E.L., Diaz R.S., Oliveira C.F., Rawal B.D.,
 RA Sullivan M., Gwin M., Clark K.A., Busch M.P.;
 RT "Use of the Dual Sensitive/Less-Sensitive (Detuned) EIA Strategy for
 RT Targeting Genetic Analysis of HIV-1 to Recently Infected U.S. Blood
 RT Donors."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF373756; AAK55377.1;
 FT NON_TER 1
 FT NON_TER 88
 SQ SEQUENCE 88 AA; 10037 MW; 575937C83EC5D42E CRC64;

Query Match 2.6%; Score 7; DB 15; Length 88;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KIREOLG 89
 ID 111111
 DB 81 KIREOLG 87

RESULT 39
 Q9BR82 PRELIMINARY; PRT; 89 AA.
 AC Q9BR82:
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOHEMICAL 9.6 KDA PROTEIN.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE, RHABDOMYOSARCOMA;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006438; AAO6438.1;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 89 AA; 9567 MW; 8908855FF350C3C2 CRC64;

Query Match 2.6%; Score 7; DB 4; Length 89;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VLIPLAVL 11
 ID 111111
 DB 26 VLIPLAVL 32

RESULT 40
 Q9ID03 PRELIMINARY; PRT; 89 AA.
 AC Q9ID03:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ENVELOPE PROTEIN (FRAGMENT).
 GN ENV OR GP120.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COL684;
 RC MEDLINE=99388930; PubMed=10461834;
 RX Navas M.C., Letourneur E., Gomas E., Boshell J., Saragosti S.;
 RA "Analysis of the V3 loop sequences from 12 HIV type-1 infected
 RT patients from Colombia, South America."
 RL AIDS Res. Hum. Retroviruses 15:1141-1144(1999).
 DR EMBL; Y10366; CAA71395.1;
 DR InterPro: IPR00777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS: Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 89
 SQ SEQUENCE 89 AA; 9858 MW; 688C7D9A96FEE10F CRC64;

Query Match 2.6%; Score 7; DB 15; Length 89;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KIREOLG 89
 ID 111111
 DB 70 KIREOLG 76

RESULT 41
 Q78841 PRELIMINARY; PRT; 90 AA.
 AC Q78841:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ENVELOPE PROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HOMOSEXUAL_136, SEROCONVERSION SAMPLE 1991;
 RA Kuiken C.L., Lukashov V., Baan E., Dekker J., Leunissen J.A.M.,
 RA Goudsmit J.;
 RT "Evidence for limited intra-subject evolution of the V3 domain of the
 RT HIV-1 envelope in the Amsterdam population."
 RL AIDS 0:0-0(1996).
 DR EMBL; Z68059; CAA92075.1;
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS: Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 90

SO SEQUENCE 90 AA; 10132 MW; 98A3444C0855B45B CRC64;

Query Match
Best Local Similarity 2.6%; Score 7; DB 15; Length 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KLRQGLG 89
|||||
DB 78 KLRQGLG 84

RESULT 42

O9W9A0

ID O9W9A0 PRELIMINARY; PRT; 91 AA.

AC O9W9A0;

DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)

DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BALD3, AND BALD1;

RX MEDLINE=99252178; PubMed=10233948;

RA Naif H.M., Ili S., Alali M., Chang J., Wayne C., Sullivan J.,

Cunningham A.L.;

RT "Definition of the stage of host cell genetic restriction of

RT replication of human immunodeficiency virus type 1 in monocytes and

RL J. Virol. 73:4866-4881(1999).

DR EMBL: AF133376; AAD37200.1; -

DR EMBL: AF133366; AAD37190.1; -

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

KW AIDS; Coat protein; Envelope protein; Glycoprotein.

FT NON_TER 1 91

FT SEQUENCE 91 AA; 10346 MW; 147AAEFAFA162D CRC64;

Query Match
Best Local Similarity 2.6%; Score 7; DB 15; Length 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KLRQGLG 89
|||||

DB 81 KLRQGLG 87

RESULT 43

O9DK41

ID O9DK41 PRELIMINARY; PRT; 91 AA.

AC O9DK41;

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-3B-V31;

RX MEDLINE=20539347; PubMed=11089615;

RA Haddad D.N., Birch C., Middleton T., Dwyer D.E., Cunningham A.L.,

Saksena N.K.;

RT "Evidence for late stage compartmentalization of HIV-1 resistance

RT mutations between lymph node and peripheral blood mononuclear cells.;"

RL AIDS 14:2273-2281(2000).

DR EMBL: AY011090; AAG41039.1; -

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

KW AIDS; Coat protein; Glycoprotein.

FT NON_TER 1 91

FT SEQUENCE 91 AA; 9950 MW; 2356715882E06FF5 CRC64;

Query Match
Best Local Similarity 2.6%; Score 7; DB 15; Length 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KLRQGLG 89
|||||

DB 60 KLRQGLG 66

RESULT 44

O9DK65

ID O9DK65 PRELIMINARY; PRT; 92 AA.

AC O9DK65;

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-2L-V33;

RX MEDLINE=20539347; PubMed=11089615;

RA Haddad D.N., Birch C., Middleton T., Dwyer D.E., Cunningham A.L.,

Saksena N.K.;

RT "Evidence for late stage compartmentalization of HIV-1 resistance

RT mutations between lymph node and peripheral blood mononuclear cells.;"

DR EMBL: AY011062; AAG41026.1; -

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

KW AIDS; Coat protein; Glycoprotein.

FT NON_TER 1 92

FT SEQUENCE 92 AA; 10113 MW; BCF9F1D04014371 CRC64;

Query Match
Best Local Similarity 2.6%; Score 7; DB 15; Length 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KLRQGLG 89
|||||

DB 60 KLRQGLG 66

RESULT 45

O77305

ID O77305 PRELIMINARY; PRT; 92 AA.

AC O77305;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE (A08-12) PARTIAL CDS (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92295544; PubMed=1376536;

RA Wofls T.F., Zwart G., Bakker M., Goudsmit J.;
 RT "HIV-1 genomic RNA diversification following sexual and parenteral
 virus transmission."
 RL Virology 189:103-110(1992).
 DR EMBL: M81878; AAA73294.1;
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 SO SEQUENCE 92 AA; 10351 MW; 99219A30601C373C CRC64;

Query Match 2.6%; Score 7; DB 15; Length 92;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KLRQLG 89
 Db 77 KLRQLG 83

RESULT 46

O9WN08 PRELIMINARY; PRT; 94 AA.
 AC O9WN08;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN GP120 (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M7;
 RX MEDLINE=20072106; PubMed=10606090;
 RA Zacher V., Zacharova V., Fink T., Thomas R.A., King B.R., Ebbesen P.,
 RA Jones T.B., Goustin A.S.;
 RT "Genetic analysis reveals ongoing HIV type 1 evolution in infected
 human placental trophoblast."
 RL AIDS Res. Hum. Retroviruses 15:1673-1683(1999).
 DR EMBL: AF150066; AAD43683.1;
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 94
 SO SEQUENCE 94 AA; 10731 MW; D92889598023B0DC CRC64;

Query Match 2.6%; Score 7; DB 15; Length 94;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KLRQLG 89
 Db 79 KLRQLG 85

RESULT 47

O91J05 PRELIMINARY; PRT; 95 AA.
 AC O91J05;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RA Wang B., Wu H., Fang R.;
 RT "The nucleotide sequence analysis on the C2-V3 region of HIV1 strains
 in Shandong area."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF220239; AAF74416.1;
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 95
 SO SEQUENCE 95 AA; 10557 MW; EADBFB08BC0BD7D2 CRC64;

Query Match 2.6%; Score 7; DB 15; Length 95;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KLRQLG 89
 Db 74 KLRQLG 80

RESULT 48

O75278 PRELIMINARY; PRT; 95 AA.
 AC O75278;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ENVELOPE GP120 V3 REGION (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95191036; PubMed=7884906;
 RA Soya P., van Ranst M., Gupta P., Balachandran R., Chao W., Itescu S.,
 RA McKinley G., Volsky D.J.;
 RT "Conservation of an intact human immunodeficiency virus type 1 vif
 gene in vitro and in vivo."
 RL J. Virol. 69:2557-2564(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Foley B.T.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U50621; AAA96040.1;
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 95
 SO SEQUENCE 95 AA; 10524 MW; 2114CB712DBA49C2 CRC64;

Query Match 2.6%; Score 7; DB 15; Length 95;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KLRQLG 89
 Db 77 KLRQLG 83

RESULT 49

O9WL10 PRELIMINARY; PRT; 96 AA.
 AC O9WL10;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SI4V3-3;
 RX MEDLINE=98445411; PubMed=9770526;
 RA Markham R.B., Wang W.C., Weisstein A.E., Wang Z., Munoz A.,
 RA Templeton A., Margolick J., Vlahov D., Quinn T., Farzadegan H.,
 RA Yu X.F.;
 RT "Patterns of HIV-1 evolution in individuals with differing rates of
 RT CD4 T cell decline."
 RL Proc. Natl. Acad. Sci. U.S.A. 95:12568-12573(1998).
 DR EMBL: AF089606; AAC70633.1; -;
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT 96
 SQ SEQUENCE 96 AA; 10931 MW; C6F38880B04CAB28 CRC64;

Query Match 2.6%; Score 7; DB 15; Length 96;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KIREOLG 89
 |||||
 DB 79 KIREOLG 85

RESULT 50
 O9IDT9
 ID O9IDT9 PRELIMINARY; PRT; 100 AA.
 AC O9IDT9;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN GP120 (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20556821; PubMed=11103039;
 RA Machuca R.A.R., Schonning K., Fomsgaard A., Nielsen C.;
 RT "No association of HIV-1 envelope (C2-V3-C3) sequence pattern with
 RT long-term nonprogression."
 RL J. Acquir. Immune Defic. Syndr. 25:103-108(2000).
 DR EMBL: AJ278207; CAB96355.1; -;
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT 100
 SQ SEQUENCE 100 AA; 11347 MW; 29412D312341BD8C CRC64;

Query Match 2.6%; Score 7; DB 15; Length 100;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83 KIREOLG 89
 |||||
 DB 85 KIREOLG 91

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:06:35 ; Search time 29.35 Seconds
(without alignments)
1010.450 Million cell updates/sec

Title: US-09-803-918a-2
Perfect score: 267
Sequence: 1 MKAVALTLAVFLITGSOARH.....SFVSEFLSALEYTKKLNTQ 267

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size: 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database:

A_Geneseq.032802.*
1: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1981.DAT:*
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4: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1983.DAT:*
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12: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1991.DAT:*
13: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1992.DAT:*
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15: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1994.DAT:*
16: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1995.DAT:*
17: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1996.DAT:*
18: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1997.DAT:*
19: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	267	100.0	267	7 AAP61079	Assumed human apol
2	267	100.0	267	9 AAP82128	Entire human prepr
3	267	100.0	267	14 AAR34032	Sequence of apo AI
4	267	100.0	267	16 AAR72705	Human apo A-I Incl
5	267	100.0	267	20 AAY18675	Human apolipoprote
6	267	100.0	267	22 AAB47620	Full length Apo-AI
7	249	93.3	268	9 AAP80668	Recombinant human
8	243	91.0	243	9 AAP81082	Sequence of mature
9	193	72.3	244	22 AAU28184	Novel human secret
10	191	71.5	299	22 AAU33170	Novel human secret
11	174	65.2	267	18 AAM08602	Human apolipoprote

ALIGNMENTS

Result ID	Score	Query Match	Length	ID	Description
1	267	100.0	267	7 AAP61079	Assumed human apol
2	267	100.0	267	9 AAP82128	Entire human prepr
3	267	100.0	267	14 AAR34032	Sequence of apo AI
4	267	100.0	267	16 AAR72705	Human apo A-I Incl
5	267	100.0	267	20 AAY18675	Human apolipoprote
6	267	100.0	267	22 AAB47620	Full length Apo-AI
7	249	93.3	268	9 AAP80668	Recombinant human
8	243	91.0	243	9 AAP81082	Sequence of mature
9	193	72.3	244	22 AAU28184	Novel human secret
10	191	71.5	299	22 AAU33170	Novel human secret
11	174	65.2	267	18 AAM08602	Human apolipoprote


```

OS Homo sapiens.
XX WO9307165-A.
XX
XX 15-APR-1993.
XX
XX 09-OCT-1992; 92WO-US08634.
XX
XX 09-OCT-1991; 91US-0774633.
XX 08-OCT-1992; 92US-055555.
XX 28-JUN-1992; 92US-0901706.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Curtiss LK, Koduri KR, Smith RS, Wiltzium JL, Young SG;
XX
XX WPI: 1993-134378/16.
XX N-PSDB; AA040030.
XX
XX Polypeptide mimic of native apo B-100 and native apo A-I - useful
XX in assays for LDL and HDL in plasma samples
XX
XX Claim 19; Pages 105-106; 137pp; English.
XX
XX The inventors claim a portion of the polypeptide contg. apo B-100
XX that immunoreacts with antibodies secreted by the hybridoma MB47
XX having ATCC Accession No. 8746. Polypeptides specifically claimed
XX include residues 217-297, 216-310, 216-331, 216-352, 216-377, 1-377,
XX 205-297, 173-297, 140-297. DNA sequences encoding the polypeptides
XX are also claimed. Also claimed are a fusion polypeptide that
XX contains: (a) a first amino acid residue sequence up to 250 residues
XX in length that includes residues 120-135 of apo A-I, (b) a second
XX amino acid residue sequence up to 375 residues in length that
XX includes residues 217-297 of apo B-100 and DNA encoding it.
XX
XX Sequence 267 AA:
XX
Query Match 100.0%; Score 267; DB 14; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.2e-241;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKAAYTLAVLFLTSGARHFWQDEPPQSPMDRVKDLATVYVDVLDKSGRDYVSQFEGS 60
DB 1 mkaavtlavllflltsgarhfwqdeppqspmdrvkdlatvyvdvldksgrdyvsqfegs 60
QY 61 ALGKOLNLKLDNMDSVTFSKLRKQVQFQFMDNLEKTEGLRQEMSKDLEEVKAK 120
DB 61 alkgolnlkldnmwsvstfsklrqlgqvqfmdnlekteglrqemskdleevkak 120
QY 121 VQPYLDDFQKKWQEMELYQKVEPLRAELQEGAROKLHELQEKSLPGEEMRDRARAHV 180
DB 121 vqpylddfqkkwqemelyrqvkeplraelqegargklhelqekslpgeemdrarahv 180
QY 181 DALRTHLAPYSDELROGLARLEALKENGARLAETAAKATHEHLSLSEKAKPALEDLRO 240
DB 181 dalrthlapysdelrqlarleaalkengarlaetaaakathehlslsekakpaledlro 240
QY 241 GLPYLESFQVSLSALEETKTLNTO 267
DB 241 glpylesfqsflsaleeytkklnltq 267
XX
RESULT 4
ID AAR72705 standard; Protein: 267 AA.
XX
XX AAR72705;
XX
XX 31-OCT-1995 (first entry)
XX
XX Human apo A-I including signal and propeptide sequences.
XX

```

```

KW Apo A-I; LDL cholesterol; low density lipoprotein; lipid.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Peptide 1..18
XX FT Peptide /label= presignal
XX FT Peptide 19..24
XX FT Peptide /label= propeptide
XX FT Peptide 120..135
XX FT Peptide /label= claimed
XX FT Peptide /note= "as part of fusion polypeptide"
XX FT Peptide 19..240
XX FT Peptide /label= claimed
XX FT Peptide /note= "as part of fusion polypeptide"
XX
XX US5408038-A.
XX
XX 18-APR-1995.
XX
XX 09-OCT-1991; 91US-0774633.
XX
XX 09-OCT-1991; 91US-0774633.
XX 18-JUN-1992; 92US-0901706.
XX 08-OCT-1992; 92US-0959946.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Curtiss LK, Koduri KR, Smith RS, Wiltzium JL, Young SG;
XX
XX WPI: 1995-161146/21.
XX N-PSDB; AA089634.
XX
XX New apo.lipoprotein B-100 peptide(s) and fusion peptide(s) - used
XX in assay systems for detecting LDL and HDL cholesterol levels in
XX body fluids.
XX
XX Claim 10; Fig 2; 41pp; English.
XX
XX AAA89634 and AAR72705 depict the AA sequence of human apo A-I and its
XX corresp. cDNA, including presignal residues and propeptide
XX residues, according to Sellhammer et al., DNA 3(4):309 (1984).
XX A dispersible apo A-I/B-100 fusion polypeptide is claimed which
XX contains a first AA sequence of apo A-I and that includes at
XX least AA sequence positions 120-135 (see AAR72606) and which reacts
XX with pan anti-apo AI antibodies such as: AI-4 ATCC HB8/44; AI-7
XX ATCC HB 8745; AI-9 ATCC HB 8741; AI-10 ATCC HB 9200; AI-11 ATCC
XX HB 9201; AI-12 ATCC HB 9202; AI-13 ATCC HB 9203; AI-14 ATCC HB
XX 9204; AI-18 ATCC HB 9507.
XX
XX Sequence 267 AA:
XX
Query Match 100.0%; Score 267; DB 16; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.2e-241;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKAAYTLAVLFLTSGARHFWQDEPPQSPMDRVKDLATVYVDVLDKSGRDYVSQFEGS 60
DB 1 mkaavtlavllflltsgarhfwqdeppqspmdrvkdlatvyvdvldksgrdyvsqfegs 60
QY 61 ALGKOLNLKLDNMDSVTFSKLRKQVQFQFMDNLEKTEGLRQEMSKDLEEVKAK 120
DB 61 alkgolnlkldnmwsvstfsklrqlgqvqfmdnlekteglrqemskdleevkak 120
QY 121 VQPYLDDFQKKWQEMELYQKVEPLRAELQEGAROKLHELQEKSLPGEEMRDRARAHV 180
DB 121 vqpylddfqkkwqemelyrqvkeplraelqegargklhelqekslpgeemdrarahv 180
QY 181 DALRTHLAPYSDELROGLARLEALKENGARLAETAAKATHEHLSLSEKAKPALEDLRO 240
DB 181 dalrthlapysdelrqlarleaalkengarlaetaaakathehlslsekakpaledlro 240

```

QY 241 GILPVLESFVKVSLALEEYTKKLNQ 267
 Db 241 gllpvlesfkvsflsaleeytkklnq 267

RESULT 5

AA18675
 ID AAY18675 standard; Protein; 267 AA.

XX AAY18675;

DT 09-JUL-1999 (first entry)

DE Human apolipoprotein AI protein sequence.

XX Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder;
 KW ApoA-I; cardiovascular disease; atherosclerosis; restenosis; LCAT;
 KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.

OS Homo sapiens.

XX W0916409-A2.

PD 08-APR-1999.

PF 28-SEP-1998: 98WO-US20329.

PR 29-SEP-1997: 97US-0940136.

XX (BUTT/) BUTTNER K.

PA (CORN/) CORNUT I.

PA (DASS/) DASSEUX J.

PA (DUFQ/) DUFOURCQ J.

PA (METZ/) METZ G.

PA (SEKU/) SEKUL R.

PI Butner K, Cornut I, Dasseux J, Dufourcq J, Metz G;

PI Sekul R;

XX WPI: 1999-254921/21.

DR N-PSDB; AAX55971.

XX Nucleic acid encoding apolipoprotein A-I agonist peptides

XX Example; Fig 1; 232pp; English.

CC The present invention describes a nucleic acid (A) encoding an
 CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,
 CC which forms an amphipathic alpha-helix in presence of lipids. (A),
 CC optionally as a complex with lipids, and host cells that contain (A),
 CC are useful for gene therapy, or prevention, of diseases associated with
 CC dyslipidemia, specifically hypercholesterolemia, cardiovascular disease,
 CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I
 CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat
 CC endotoxemia (septic shock). Host cells containing (A) can also be used
 CC to study the role of apoA-I in lipid metabolism. (B) can be used
 CC diagnostically, e.g. to measure serum HDL (particularly its
 CC subpopulation involved in retrograde cholesterol transport) and for
 CC imaging the circulatory system or HDL accumulations at fatty streaks.
 CC The present sequence represents human apoA-I.

XX Sequence 267 AA;

Query Match 100.0%; Score 267; DB 20; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.2e-241;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAAVLTAVLTGSGARHFWQDEPPSPMDRVKDLATVYVDLKDGRDVSQFESS 60
 Db 1 mkaavltavltgsgarhfwqdeppspmdrvkdlatvyvdldkdsgrdyvsqfegs 60
 QY 61 ALGKOLNKLIDMWDVSTFISKLRBQLGPFVDFEFDNLEKTEGILRQEKSKDLEEVKAK 120

Db 61 algyqnlklidmwdsvstfisklrqglpvtqefwlnlekeleglrqemskdleevkak 120
 QY 121 VQPYLDDPQKKWQEBEMELRYQKVEPLRAELQEGAROKLHLOKSLPLGEMDRARAY 180
 Db 121 vqpylddfqkkwqemelmryqkveplraelqegarklhelgelsplgemdraray 180
 QY 181 DALRTHLAPYSDELRORLARLEALKENGARLAEYAKATEHLSTSEKAPALDLNQ 240
 Db 181 dalrthlapydsdelrqlaarlalealkengarilaeyhakatehlstsekakpaledlrg 240
 QY 241 GILPVLESFVKVSLALEEYTKKLNQ 267
 Db 241 gllpvlesfkvsflsaleeytkklnq 267

RESULT 6

AA18675
 ID AAB47620 standard; Protein; 267 AA.

XX AAB47620;

DT 21-JAN-2002 (first entry)

DE Full length Apo-A1.

XX Apolipoprotein; Apo-A1; Apo-A-I fragment T-cell activation inhibitor;
 KW APT1; monocyte; IL-1; interleukin 1; TNF; tumour necrosis factor;
 KW acute pancreatitis; Alzheimer's disease; asthma; cancer; fever;
 KW inflammatory bowel disease; ischemia; multiple sclerosis; osteoporosis;
 KW Parkinson's disease; psoriasis; probe.

OS Homo sapiens.

XX Location/Qualifiers

FT Binding-site 44..65 Helical lipid binding domain

FT Binding-site 220..241 Helical lipid binding domain

FT Domain 74..111 Helical lipid binding domain

FT Binding-site 149..219 Helical lipid binding domain

FT Domain 99..120 Helical lipid binding domain

FT Domain 99..143 Helical lipid binding domain

FT Domain 66..120 Helical lipid binding domain

FT Domain 90..111 Helical lipid binding domain

FT Domain 44..65 Helical lipid binding domain

FT Domain 66..98 Helical lipid binding domain

FT Domain 99..120 Helical lipid binding domain

FT Domain 121..142 Helical lipid binding domain

FT Domain 143..164 Helical lipid binding domain

FT Domain 165..208 Helical lipid binding domain

FT Domain 209..219 Helical lipid binding domain

FT Domain 220..241 Helical lipid binding domain

FT Domain 25..194 Helical lipid binding domain

FT Peptide 25..144 Helical lipid binding domain

FT Peptide 25..144 Helical lipid binding domain

199 AAKLEALKRENGGARLAEYHAKATEHLSLSEKAKPALEDLRQGLLPVLESEKVSFLSALE 25

OY 259 EYTKLNTQ 267
 |||||
 DB 260 eytkkintq 268

RESULT 8
 AAP81082
 ID AAP81082 standard; protein; 243 AA.

AC AAP81082;

DT 14-JAN-1991 (first entry)

DE Sequence of mature human apolipoprotein AI (apoAI).

XX Atherosclerosis; therapy; cardiovascular disease.

XX Homo sapiens.

XX W08803166-A.

XX PD 05-MAY-1988.

XX PF 21-OCT-1987; 87WO-EP00621.

XX PR 23-OCT-1986; 86GB-0025435.

XX (FARM) FARMITALIA C ERBA SPA.

XX PI Lorenzetti R, Monaco L, Soria M, Palomba R, Isacchi A, Sarmientos P;

XX DR WPI: 1988-133240/19.

XX DR N-PSDB; AAN80243.

XX PT Recombinant human apo:lipoprotein AI -

XX PT used to lower plasma cholesterol and/or tri glyceride levels and

XX PS to combat atherosclerosis and cardiovascular diseases

XX XX Disclosure: Fig 1; 51pp; English.

XX The protein comprising apo AI genetic variants may be used to lower

XX CC plasma cholesterol and/or triglyceride levels. They may also be used to

XX CC combat atherosclerosis and cardiovascular diseases such as coronary

XX CC heart disease. Prefd. proteins are Met-apo AI, Met-apo AI-T6, Met-apo

XX CC AI-M1 and Met-apo AI-T6/M1.

XX SQ Sequence 243 AA;

XX Query Match 91.0%; Score 243; DB 9; Length 243;

XX Best Local Similarity 100.0%; Pred. No. 3.2e-219;

XX Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 DEPPQFWDRKDLATVYVVDVILKDSGRDYSQPSGALGKQNLKLDNMDSYSTFEKTL 84

DB 1 deppqswdrvklalatyvdvildsgdyvsqfegsalsgkqnlkldnmdsvstlsk1 60

OY 85 REGUGPTTQGFNNLEKTEGTLGKQEMSKDLEEKAKVQPYLDPOKMOEELTRQKVE 144

DB 61 reglqptqgfwnleketegtlrqemskdleeekavqpylddtkkqgemelytrqkve 120

OY 145 PLRRLDEGAROKLHELOEKLSPDGEMDRARAHVADLRTHLAPYSDELRLQRLARLEA 204

DB 121 plrreldegarqrkheleklspdgemdrarahvdalrthlapydelrlqrlaaria 180

OY 205 LKENGARLAEYHAKKATEHSTSEKAKPALDELRLGGLPVLESFVSLSALEYTKKL 264

DB 181 lkengarlaeeyhakatehstlsekakpaledrlgglpvlesfvsfslsaieytkkl 240

OY 265 NTO 267

DB 241 ntq 243

RESULT 9
 AAU28184
 ID AAU28184 standard; Protein; 244 AA.

AC AAU28184;

DT 18-DEC-2001 (first entry)

DE Novel human secretory protein, Seq ID No 353.

XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;

XX transhaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;

XX ischaemic animal; Alzheimer's disease; Parkinson's disease; burn;

XX amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;

XX ulcer; osteoporosis; bone degenerative disorder; periodontal disease;

XX gut protection; lung; liver fibrosis; immune deficiency; infection;

XX severe combined immunodeficiency; SCID; autoimmune disorder; allergy;

XX multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;

XX fertility; analgesic; pain; antigen.

XX OS Homo sapiens.

XX PN W0200166689-A2.

XX PD 13-SEP-2001.

XX PF 05-MAR-2001; 2001WO-US04942.

XX PR 07-MAR-2000; 2000US-0519705.

XX PR 19-MAY-2000; 2000US-0574454.

XX PR 17-JUN-2000; 2000US-0596193.

XX PR 14-JUL-2000; 2000US-0616847.

XX PR 19-SEP-2000; 2000US-0665363.

XX PR 20-OCT-2000; 2000US-0693267.

XX PA (HSE-) HXSEQ INC.

XX Tang YN, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

XX PI Zhao QN, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

XX DR WPI: 2001-589934/66.

XX N-PSDB; AAS45084.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries

XX prepared from various human tissues, for diagnosis and treatment of

XX cancer, neurological, inflammatory, and autoimmune disorders -

XX Example 5; SEQ ID No 353; 107pp; English.

XX The invention relates to novel isolated human secreted polypeptides (I)

XX and polynucleotides (II). (I) and (II) are useful for treating

XX inflammatory conditions such as arthritis, nephritis, Crohn's disease,

XX ischaemia-reperfusion injury, shock, sepsis, immune responses, and is

XX involved in increasing haematopoiesis, stem cell survival, bone growth

XX and remodeling. (I), (II) and modulators of (II) are useful for

XX propylaxis or treatment of one or more cancers. (II) is also useful for

XX creating transgenic animals useful for studying the in vivo activities of

XX the polypeptide as well as for studying modulators of the polypeptides.

XX (I) induces the proliferation of neural cells and regeneration of nerve

XX and brain tissue and is useful for the treatment of central and

XX peripheral nervous system diseases and neuropathies, such as Alzheimer's,

XX Parkinson's disease, Huntington's disease, and amyotrophic lateral

XX sclerosis. In addition, (I) is involved in chemotactic or chemokinetic

XX activity, regulation of haematopoiesis and is useful for treating myeloid

XX and lymphoid cell disorders, platelet disorders such as thrombocytopenia

XX and for regeneration of bone, cartilage, tendon, ligament and/or nerve

XX tissue growth, and in tissue repair, healing of burns, incisions,

XX ulcers, for treating osteoporosis, osteoarthritis, bone degenerative

XX disorders, or periodontal disease. Furthermore, (I) is also useful for

XX gut protection or regeneration and treatment of lung or liver fibrosis,

XX reperfusion injury in various tissues, various immune deficiencies and

CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (i) affects diurnal rhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC anagenic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention.

XX Sequence 244 AA;

Query Match 72.3%: Score 193; DB 22; Length 244;
 Best Local Similarity 100.0%; Pred. NO. 2e-172;
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 DSVSTFSKRLREOLGPVTQEFMDNLEKETEGRLQEMSKDLEEVAKVQPYLDDFQKKQOE 134
 DB 52 dsvstfskrlreqlgprvqetfwdnleketegrlqemskdleevakvqpylddfqkkqoe 111
 QY 135 EMELYRQVPEPRALQEGARQKHELOEKLSPGEEKRDRARAHVDAIRTHLAPYSDEL 194
 DB 112 emelyrqvpepralqegargqklhelqeklsplgeemdrarahvdalrthlapydel 171
 QY 195 RORLAARLEALKENGARLALEYHAKTEHLSTSEKAPALEDRQGLRPLVESFKYSFL 254
 DB 172 rgrlaarleaalkengarlaeayhakatehstlsekapaledrlrqlplvesfkysfl 231
 QY 255 SALEEYTRKRLNTQ 267
 DB 232 saleeytkrlntq 244

RESULT 10
 AAU33170
 ID AAU33170 standard; Protein; 299 AA.

AC AAU33170;
 XX
 DT 18-DEC-2001 (first entry)
 DE Novel human secreted protein #3661.
 XX
 KW Human: vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 FT Nucleic acids encoding a range of human polypeptides, useful in genetic
 FT vaccination, testing and therapy -
 XX
 PS Claim 20; Page 718; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukemias. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.

XX Sequence 299 AA;

Query Match 71.5%: Score 191; DB 22; Length 299;
 Best Local Similarity 100.0%; Pred. NO. 1.8e-170;
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAAYLTIAVLFITGSGARHFQODEPPSPMDRVKDLATVYDVYDKSGRYSQFECS 60
 DB 33 mkaayltiavlfitgsgarhfwqdeppspmdrvkdlatvydvdydksgryvsqfegs 92
 QY 61 ALCQKLNKLDNWDVSTFSKRLREOLGPVTQEFMDNLEKETEGRLQEMSKDLEEVAK 120
 DB 93 alqkqlnkldnwdsvstfskrlreqlgprvqetfwdnleketegrlqemskdleevak 152
 QY 121 VQPYLDDFQKKQOEEMELYRQVPEPRALQEGARQKHELOEKLSPGEEKRDRARAHV 180
 DB 153 vqpylddfqkkqoeemelyrqvpepralqegargqklhelqeklsplgeemdrarahv 212
 QY 181 DALRTHLAPYS 191
 DB 213 dalrthlapy 223

RESULT 11
 AAM08602
 ID AAM08602 standard; Protein; 267 AA.

AC AAM08602;
 XX
 DT 04-SEP-1997 (first entry)
 DE Human apolipoprotein A-1 variant "Paris" protein sequence.
 XX
 KW Human: apolipoprotein A-1; variant; mutation; serum lipid; cholesterol;
 KW high density lipoprotein; triglyceride; symptom; cardiovascular disease;
 KW atherosclerosis; restenosis; myocardial infarct; angina; death; stroke;
 KW cardiac decompensation; metabolic deficit.

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT Region /note="prepro peptide"
 FT /note="this sequence which contains the mutated amino
 FT /note="acid residue is claimed - claim 2"
 FT Misc-difference 175
 FT /note="changed from Arg residue in wild type protein,
 FT due to a C to T transition mutation"

XX MO9637608-A1.
 XX
 PD 28-NOV-1996.
 XX
 PF 20-MAY-1996; 96WO-FR00747.

XX 22-MAY-1995; 95FR-0006061.
 XX (INSP) INST PASTEUR LILLE.
 PA (RHON) RHONE-POULENC ROBER SA.
 PA (UYPA-) UNIV CURIE PARIS VI P & M.
 XX Benoit P, Bruckert E, Deneffe P, Duverger N, Fruchart J;
 PI Luc G, Turping, Assmann G, Funke H;
 XX WPI: 1997-021218/02.
 DR N-PSDB; AA743691.
 XX New variant of human apoA-1 with Cys at position 151 - has
 PT anti-atherogenic activity for treatment and prevention of
 PT cardiovascular disease
 XX Claim 2; Page -: 58pp; French.
 XX This is the amino acid sequence of a human apolipoprotein A-1 variant
 CC designated the "Paris" variant which has a Cys replacing the Arg residue
 CC at position 151. The substitution is generated by a mutation of
 CC the C nucleotide at position 523 in the wild type gene to a T residue,
 CC changing the encoded residue from an Arg to a Cys. The gene was isolated
 CC from a patient with an unusual pattern of serum lipids i.e. low levels of
 CC apoA-1 and high density lipoprotein (HDL)-cholesterol and high
 CC triglycerides, but showing symptoms of atherosclerosis. The new variant
 CC protein has anti-atherogenic activity so is useful for treatment and
 CC prevention of cardiovascular diseases such as atherosclerosis,
 CC stenosis, myocardial infarct, angina, sudden death, stroke and cardiac
 CC decompensation, or more generally any condition involving genetic or
 CC metabolic deficit of apoA-1.
 CC Note: this sequence is not given in the specification but is generated
 CC from the wild type apoA-1 gene disclosed in the specification and has
 CC the appropriate amino acid changed.
 XX Sequence 267 AA;
 SQ

Query Match 65.2%; Score 174; DB 18; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.3e-154;
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAALVTLAVLPTGSOARHFWDDEPPSPWDRVKDLATVYVDVLKDSGRDYVSQFESS 60
 DB 1 mkaavllavllftlgsqarhfwgdeppsgwdrvkdlatvydvvlkdsgrdyvsqfegs 60
 QY 61 ALGKQLNLKLLDMWDSTSTFSKLRQLGPNQEFWDNLKFTREGIROMSKDLREVKAK 120
 DB 61 algqqlnlklldmwdsststfsklrqlgpnvqefwdnlkftreglrgemskdleevkak 120
 QY 121 VQPYLDFOFKWQOEMELYRQKVEPLRAELQEGAROKLHELOEKLSPLEEMMD 174
 DB 121 vqpylddfqkkgemelyrqrveplraelqegarklhelqeklsplgemmd 174

RESULT 12
 AAR56863
 ID AAR56863 standard; Protein: 264 AA.
 XX AAR56863;
 AC AAR56863;
 XX 26-JAN-1995 (first entry)
 XX Apo-lipoprotein AI-M.
 DE Apo-lipoprotein AI-M.
 XX Apo-lipoprotein AI-M; Apo AI-M; Escherichia coli; plasmid pKF683;
 KW vector; atherosclerosis; cardiovascular disease.
 XX Homo sapiens.
 OS
 XX
 PN W09413819-A.
 XX

PD 23-JUN-1994.
 XX 93WO-SE01061.
 PF 09-DEC-1993;
 XX 92SE-0003753.
 PR 11-DEC-1992;
 XX (KABI) KABI PHARMACIA AB.
 PA
 XX Abrahamsen L, Holmgren E, Kalderen C, Lake M, Mikaelsson A;
 PI Sejlitz T;
 XX WPI: 1994-217892/26.
 DR N-PSDB; AA068357.
 XX Expression vector for extracellular prodn of apo-lipoprotein AI-M
 PT in E. coli - includes inducible promoter and signal peptide
 PT sequences providing improved yield, useful in treating
 PT atherosclerosis and cardiovascular disease.
 XX Disclosure: Fig. 3; 33pp; English.
 XX Plasmid pKF683 encodes human apo-lipoprotein AI-M in E. coli. The
 CC NotI-HindIII segment of pKF683 and the deduced amino acid sequence
 CC of the translated Apo AI-M protein were determined. The plasmid
 CC provides high yields of extracellular Apo AI-M.
 XX Sequence 264 AA;
 SQ

Query Match 64.4%; Score 172; DB 15; Length 264;
 Best Local Similarity 100.0%; Pred. No. 9.9e-153;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 DEPPSPWDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDMWDSTSTFSKL 84
 DB 22 deppsgwdrvkdlatvyvdvlkdsgrdyvsqfegsalgkqlnlkldmwdststfsl 81
 QY 85 RBQLGPNQEFWDNLKFTBSGLRQPMKDLREVKAKVQPYLDFOFKWQOEMELYRQVE 144
 DB 82 reqlgpnvqefwdnlkftbsglrgemskdleevkakvpylddfqkkgemelyrqkve 141
 QY 145 PLRAELQEGAROKLHELOEKLSPLEEMDRARAHVVALRTHLAPYSDLELR 196
 DB 142 plraelqegarklhelqeklsplgemdrarahvalrthlapysdelr 193

RESULT 13
 AAR56864
 ID AAR56864 standard; Protein: 264 AA.
 XX AAR56864;
 AC AAR56864;
 XX 26-JAN-1995 (first entry)
 XX Apo-lipoprotein AI-M.
 DE Apo-lipoprotein AI-M.
 XX Apo-lipoprotein AI-M; Apo AI-M; Escherichia coli; plasmid pKF764;
 KW vector; atherosclerosis; cardiovascular disease.
 XX Homo sapiens.
 OS
 XX
 PN W09413819-A.
 XX 23-JUN-1994.
 XX 93WO-SE01061.
 PF 09-DEC-1993;
 XX 92SE-0003753.
 PR 11-DEC-1992;
 XX (KABI) KABI PHARMACIA AB.
 PA
 XX Abrahamsen L, Holmgren E, Kalderen C, Lake M, Mikaelsson A;
 PI Sejlitz T;

XX WPI; 1994-217892/26.
 DR N-PSDB; AA068358.
 XX
 PT Expression vector for extracellular prodn of apo-lipoprotein AI-M
 PT in E. coli - includes inducible promoter and signal peptide
 PT atherosclerosis and cardiovascular disease.
 XX
 PS Disclosure; Fig. 4; 33pp; English.
 XX
 CC Plasmid pK764 encodes human apo-lipoprotein AI-M in E. coli. The
 CC Nott-HindIII segment of pK764 and the deduced amino acid sequence
 CC of the translated Apo AI-M protein were determined. The plasmid
 CC provides high yields of extracellular Apo AI-M.
 XX
 SQ Sequence 264 AA:

Query Match 64.4%; Score 172; DB 15; Length 264;
 Best Local Similarity 100.0%; Pred. No. 9.9e-153;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 DEPPQPMRVRKDLATVYVYDVKDSGRVYSGFEGSALGKQLNLKLDNWDSTVTFEKL 84
 Db 22 deppqpmrivrkdlatvvydvdkdsgrdyvsqfegsalgkqlnlkldnwdsvtstfekl 81
 QY 85 RQDLGFTVTOEFMDNLEKETEGRLROEMSKDLEEVKAKVOPLDDFOKKOEMEELYROKVE 144
 Db 82 rqlgqvgtvtdnleketegrlrgemskdleevkakvpylddfqkkvgeemelyrkykve 141
 QY 145 PIRAEIQEGARQKHLHQLKSPLEGEMRDRARAHVDAIRTHLAPYSDELRLQ 196
 Db 142 piraeltqegarkhlhqlksplegemrdrarahvdairthlapydelrlq 193

RESULT 14
 AAU29835
 ID AAU29835 standard; Protein; 221 AA.
 XX
 AC AAU29835;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #326.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 PS Claim 20; Page 199; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukemias. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 SQ Sequence 221 AA:

Query Match 53.6%; Score 143; DB 22; Length 221;
 Best Local Similarity 100.0%; Pred. No. 1.2e-125;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 LGPYTOEFMDNLEKETEGRLROEMSKDLEEVKAKVOPLDDFOKKOEMEELYROKVEPLR 147
 Db 79 lgvptgftvtdnleketegrlrgemskdleevkakvpylddfqkkvgeemelyrkykveplr 138
 QY 148 AELOEGARQKHLHQLKSPLEGEMRDRARAHVDAIRTHLAPYSDELRLQRLARLEALKE 207
 Db 139 aelqegarkhlhqlksplegemrdrarahvdairthlapydelrlqrlaarlealke 198
 QY 208 NGARLAEYHAKATEHLSTLSEK 230
 Db 199 ngarlaeyhakatehlstlsek 221

RESULT 15
 AAU28372
 ID AAU28372 standard; Protein; 166 AA.
 XX
 AC AAU28372;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secretory protein, Seq ID No 729.
 XX
 KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200166689-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US04942.
 XX
 PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX WPI; 2001-569934/66.
 DR N-PSDB: AAS45272.
 XX Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 PS Example 2; SEQ ID No 729; 107pp; English.
 XX The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating meloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention.
 XX
 XX Sequence 166 AA:
 SO
 Query Match 36.3%; Score 97; DB 22; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1e-82;
 Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 75 DSVSTSPSKLREQLGPTQGFMDNLEKTEGLRQEMSKDLFEYKAKVOPILDFQKWOE 134
 Db 61 dsvststsklreqlgptqgfmdnleketeglrqemskdleevakvpyldtqkwwge 120
 QY 135 EMELYRQKVEPLRAELOEGAROKLHELOEKSPILGEE 171
 Db 121 emelyrqkvpeplraelqegargklheleqekspilgee 157

KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX Homo sapiens.
 XX WO200179449-A2.
 XX 25-OCT-2001.
 XX 16-APR-2001; 2001WO-US08656.
 XX 18-APR-2000; 2000US-0552929.
 XX 26-JAN-2001; 2001US-0770160.
 XX (HYSE-) HYSEQ INC.
 PI Tang YT, Liu C, Drmanac RT;
 DR WPI; 2001-611725/70.
 XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 PS Claim 20; Page 297; 765pp; English.
 XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 XX Sequence 119 AA:
 SO
 Query Match 34.5%; Score 92; DB 22; Length 119;
 Best Local Similarity 100.0%; Pred. No. 3.7e-78;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 67 NKLIDNMDSVSTSPSKLREQLGPTQGFMDNLEKTEGLRQEMSKDLFEYKAKVOPYLD 126
 Db 2 nklidnmdsvststsklreqlgptqgfmdnleketeglrqemskdleevakvpyld 61
 QY 127 DQOKKQEMELYRQKVEPLRAELOEGAROKL 158
 Db 62 dfqkqwgemelyrqkvpeplraelqegargkl 93

RESULT 17
 AAU30267
 ID AAU30267 standard; Protein: 120 AA.
 XX
 AC AAU30267;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #758.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

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XX OS Homo sapiens.
XX PN WO200179449-A2.
XX PD 25-OCT-2001.
XX PF 16-APR-2001; 2001WO-US08656.
XX PR 18-APR-2000; 2000US-0552929.
XX PR 26-JAN-2001; 2001US-0770160.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-611725/70.
XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic
XX PT vaccination, testing and therapy -
XX PS Claim 20; Page 270; 765pp; English.
XX CC The invention relates to novel human secreted polypeptides. The
XX CC polypeptides and antibodies to the polypeptides are useful for
XX CC determining the presence of or predisposition to a disease associated
XX CC with altered levels of polypeptide. The polypeptides are also useful for
XX CC identifying agents (agonists and antagonists) that bind to them. Cells
XX CC for use in treatment of a pathology related to aberrant expression or
XX CC physiological interactions of the polypeptide. Vectors comprising
XX CC the nucleic acids encoding the polypeptides and cells genetically
XX CC engineered to express them are also useful for producing the proteins.
XX CC The proteins are useful in genetic vaccination, testing and
XX CC therapy, and can be used as nutritional supplements. They may be used to
XX CC increase stem cell proliferation; to regulate haematopoiesis; and in
XX CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
XX CC immune suppression and/or stimulation; as anti-inflammatory agents; and
XX CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
XX CC sequences of novel human secreted proteins of the invention.
XX SQ Sequence 120 AA;

Query Match 25.5%; Score 68; DB 22; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.1e-55;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 DSVTSFSKLRBOLGPTVQEFWMDLKEKETGLRQEMSKDLEEVKAKVQPYLDDPQKKMQE 134
DB 52 dsvtsfskrlreqlgprvtqefwmdlkeketglrgemskdleevkavqpylddfqkkwqe 111
QY 135 EMELYRQK 142
DB 112 emelyrqk 119

RESULT 18
AAU30469
ID AAU30469 standard; Protein; 120 AA.
XX AC AAU30469;
XX DT 18-DEC-2001 (first entry)
XX DE Novel human secreted protein #960.
XX KW Human; vaccination; gene therapy; nutritional supplement;
XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX OS Homo sapiens.
XX PN

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PN WO200179449-A2.
XX PD 25-OCT-2001.
XX PF 16-APR-2001; 2001WO-US08656.
XX PR 18-APR-2000; 2000US-0552929.
XX PR 26-JAN-2001; 2001US-0770160.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-611725/70.
XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic
XX PT vaccination, testing and therapy -
XX PS Claim 20; Page 297; 765pp; English.
XX CC The invention relates to novel human secreted polypeptides. The
XX CC polypeptides and antibodies to the polypeptides are useful for
XX CC determining the presence of or predisposition to a disease associated
XX CC with altered levels of polypeptide. The polypeptides are also useful for
XX CC identifying agents (agonists and antagonists) that bind to them. Cells
XX CC for use in treatment of a pathology related to aberrant expression or
XX CC physiological interactions of the polypeptide. Vectors comprising
XX CC the nucleic acids encoding the polypeptides and cells genetically
XX CC engineered to express them are also useful for producing the proteins.
XX CC The proteins are useful in genetic vaccination, testing and
XX CC therapy, and can be used as nutritional supplements. They may be used to
XX CC increase stem cell proliferation; to regulate haematopoiesis; and in
XX CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
XX CC immune suppression and/or stimulation; as anti-inflammatory agents; and
XX CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
XX CC sequences of novel human secreted proteins of the invention.
XX SQ Sequence 120 AA;

Query Match 25.5%; Score 68; DB 22; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.1e-55;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 DSVTSFSKLRBOLGPTVQEFWMDLKEKETGLRQEMSKDLEEVKAKVQPYLDDPQKKMQE 134
DB 52 dsvtsfskrlreqlgprvtqefwmdlkeketglrgemskdleevkavqpylddfqkkwqe 111
QY 135 EMELYRQK 142
DB 112 emelyrqk 119

RESULT 19
AAU30268
ID AAU30268 standard; Protein; 318 AA.
XX AC AAU30268;
XX DT 18-DEC-2001 (first entry)
XX DE Novel human secreted protein #759.
XX KW Human; vaccination; gene therapy; nutritional supplement;
XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX OS Homo sapiens.
XX PN WO200179449-A2.
XX PD 25-OCT-2001.

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XX 16-APR-2001; 2001WO-US08656.
XX
XX 18-APR-2000; 2000US-0552929.
XX
XX 26-JAN-2001; 2001US-0770160.
XX
XX (HXSE-) HXSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI: 2001-611725/70.
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy -
XX
XX Claim 20; Page 270; 765pp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
XX polypeptides and antibodies to the polypeptides are useful for
XX determining the presence of or predisposition to a disease associated
XX with altered levels of polypeptide. The polypeptides are also useful for
XX identifying agents (agonists and antagonists) that bind to them. Cells
XX expressing the proteins are useful for identifying a therapeutic agent
XX for use in treatment of a pathology related to aberrant expression or
XX physiological interactions of the polypeptide. Vectors comprising
XX the nucleic acids encoding the polypeptides and cells genetically
XX engineered to express them are also useful for producing the proteins.
XX The proteins are useful in genetic vaccination, testing and
XX therapy, and can be used as nutritional supplements. They may be used to
XX increase stem cell proliferation; to regulate haematopoiesis; and in
XX bone, cartilage, tendon and/or nerve tissue growth or regeneration;
XX immune suppression and/or stimulation; as anti-inflammatory agents; and
XX in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
XX sequences of novel human secreted proteins of the invention.
XX
XX Sequence 318 AA:
XX
XX Query Match 18.0%; Score 48; DB 22; Length 318;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-36;
XX Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 220 ATEHLSTLSEKAKPALEDLRQGLPVLSEFKVSFLSALEETKKNLTQ 267
XX |||||||||||||||||||||||||||||||||||||||||||||||
XX Db 246 atehlstlsekakpaledlrqglpvlsefkvsflsaleeytkkintq 293
XX
XX RESULT 20
XX AAU30470
XX ID AAU30470 standard; Protein; 359 AA.
XX
XX AC AAU30470;
XX
XX DT 18-DEC-2001 (first entry)
XX
XX DE Novel human secreted protein #961.
XX
XX KW Human: vaccination; gene therapy; nutritional supplement;
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
XX OS Homo sapiens.
XX
XX PN WO200179449-A2.
XX
XX PD 25-OCT-2001.
XX
XX PF 16-APR-2001; 2001WO-US08656.
XX
XX PR 18-APR-2000; 2000US-0552929.
XX
XX PA 26-JAN-2001; 2001US-0770160.
XX
XX (HYSE-) HXSEQ INC.
XX

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XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI: 2001-611725/70.
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy -
XX
XX Claim 20; Page 297; 765pp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
XX polypeptides and antibodies to the polypeptides are useful for
XX determining the presence of or predisposition to a disease associated
XX with altered levels of polypeptide. The polypeptides are also useful for
XX identifying agents (agonists and antagonists) that bind to them. Cells
XX expressing the proteins are useful for identifying a therapeutic agent
XX for use in treatment of a pathology related to aberrant expression or
XX physiological interactions of the polypeptide. Vectors comprising
XX the nucleic acids encoding the polypeptides and cells genetically
XX engineered to express them are also useful for producing the proteins.
XX The proteins are useful in genetic vaccination, testing and
XX therapy, and can be used as nutritional supplements. They may be used to
XX increase stem cell proliferation; to regulate haematopoiesis; and in
XX bone, cartilage, tendon and/or nerve tissue growth or regeneration;
XX immune suppression and/or stimulation; as anti-inflammatory agents; and
XX in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
XX sequences of novel human secreted proteins of the invention.
XX
XX Sequence 359 AA:
XX
XX Query Match 18.0%; Score 48; DB 22; Length 359;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-36;
XX Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 220 ATEHLSTLSEKAKPALEDLRQGLPVLSEFKVSFLSALEETKKNLTQ 267
XX |||||||||||||||||||||||||||||||||||||||||||||||
XX Db 312 atehlstlsekakpaledlrqglpvlsefkvsflsaleeytkkintq 359
XX
XX RESULT 21
XX AAR20164
XX ID AAR20164 standard; peptide; 42 AA.
XX
XX AC AAR20164;
XX
XX DT 01-APR-1992 (first entry)
XX
XX DE Apo AI polypeptide (A).
XX
XX KW Monoclonal antibody; MAB AI-11; epitope; diagnosis.
XX
XX OS Synthetic.
XX
XX FH Key
XX FT Peptide 1..28 Location/Qualifiers
XX FT Peptide 2..28
XX FT Peptide 7..28
XX FT Peptide 10..28
XX FT Peptide 11..28
XX FT Peptide 11..42
XX FT Peptide 13..28
XX
XX PN WO9118619-A.
XX
XX PD 12-DEC-1991.
XX
XX PF 07-JUN-1991; 91WO-US04038.
XX
XX PR 07-JUN-1990; 90US-0534761.
XX
XX PA (SCRT-) SCRIPPS CLINIC & RE.
XX

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PI Curtiss LK, Banka CL, Bonnet DJ, Smith RS;
 XX WPI; 1992-007201/01.
 XX
 PT New Apo AI polypeptide(s) and anti-Apo antibodies - used to
 PT detect Apo AI in vascular fluid samples and increase
 PT LCAT-mediated cholesterol esterification in humans
 XX
 PS Claim 2: Page 68; 87pp; English.
 XX
 CC The peptides represented in AAR20164-65 are capable of immunologically
 CC mimicking an Apo AI epitope. They are useful in diagnosis and
 CC detection of Apo AI in fluids and for preparing anti-Apo AI
 CC antibodies. It is useful in therapeutic methods for increasing LCAT-
 CC mediated cholesterol esterification in humans.
 CC The Apo AI polypeptide is selected from the peptides indicated in
 CC the features and includes amino acids 13-28 defining a conserved
 CC native epitope on Apo AI capable of immunoreacting with monoclonal
 CC antibody MAb A1-11.
 XX
 SQ Sequence 42 AA;
 XX
 Query Match 15.7%; Score 42; DB 13; Length 42;
 Best Local Similarity 100.0%; Pred. No. 9e-32;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 108 QENSKDLEEVKAKVPYLDFOKMOEMELYRQKVEPLRAE 149
 DB 1 qemskdleevkavpylddfqkkgemelyrqkveplrae 42
 XX
 RESULT 22
 AAG62609
 ID AAG62609 standard; peptide: 26 AA.
 XX
 AC AAG62609;
 XX
 DT 06-SEP-2001 (first entry)
 XX
 DE Apolipoprotein fragment #3.
 XX
 KW Apolipoprotein: ApoA-1; atherosclerosis; coronary disease;
 KW cardiovascular disease; ischaemic heart disease; dyslipidaemia.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 11 /label= OTHER
 FT /note= "optionally oxidised"
 XX
 PN WO200138395-A1.
 XX
 PD 31-MAY-2001.
 XX
 PF 27-NOV-2000; 2000WO-AU01463.
 XX
 PR 26-NOV-1999; 99AU-0004293.
 XX
 PA (HEAR-) HEART RES INST LTD.
 XX
 PI Stocker R, Wang XL, Wilcken D;
 XX
 DR WPI; 2001-355909/37.
 XX
 PT Novel oxidized form of apolipoprotein useful in diagnosis and treatment
 PT of diseases associated with oxidative stress such as cardiovascular
 PT diseases, in particular, atherosclerosis -
 XX
 PS Example 1: Page 28; 55pp; English.
 XX
 CC The present invention relates to oxidised apolipoprotein A-I (ApoA-I)

CC where at least Met residue 86 is oxidised to Met(O). This can be used in
 CC the prevention, diagnosis and treatment of lipid associated disorders,
 CC including coronary vascular disease, ischaemic heart disease,
 CC atherosclerosis and dyslipidaemias. The present sequence is a fragment of
 CC the ApoA-I protein isolated in the exemplification of the invention.
 XX
 SQ Sequence 26 AA;
 XX
 Query Match 9.7%; Score 26; DB 22; Length 26;
 Best Local Similarity 100.0%; Pred. No. 5.6e-17;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 126 DDFQKMQEMELYRQKVEPLRAELQ 151
 DB 1 ddfqkkgemelyrqkveplraelq 26
 XX
 RESULT 23
 AAU29834
 ID AAU29834 standard; Protein: 134 AA.
 XX
 AC AAU29834;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #325.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 PS Claim 20: Page 199; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 SQ Sequence 134 AA;

Query Match 9.7%; Score 26; DB 22; Length 134;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 IFLTGSQARHFWQODEPQSPWDRVK 36
 ||||||||||||||||||
 DB 11 IFLTGSQARHFWQODEPQSPWDRVK 36

RESULT 24

AA002278
 ID AA002278 standard; Protein: 151 AA.

AC AA002278;

DT 06-NOV-2001 (first entry)

DE Human polypeptide SEQ ID NO 16170.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

PN WO200164835-A2.

PD 07-SEP-2001.

PE 26-FEB-2001; 2001MO-US04927.

XX 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI: 2001-514838/56.

DR N-PSDB; AAI82209.

XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

PS Claim 20; SEQ ID NO 16170; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 151 AA;

Query Match 9.4%; Score 25; DB 22; Length 151;
 Best Local Similarity 100.0%; Pred. No. 2.3e-15;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 118 KAKVQPYLDDPQKKWQEMELYRQK 142

DB 73 kakvpylddfqkkwqemelyrqk 97
 ||||||||||||||||||

RESULT 25

AA092072

ID AAP92072 standard; peptide: 22 AA.

AC AAP92072;

DT 10-APR-1990 (first entry)

DE Apolipoprotein AI (Apo AI) polypeptide.

XX Apolipoprotein AI; Apo AI; high-density lipoprotein; HDL;
 KW coronary artery disease; CAD; Apo AI epitope.

XX Key Location/Qualifiers

FT Peptide 12..22 /label= AI101-111

FT Peptide 4..12 /label= AI93-101

FT Peptide 1..22 /label= AI90-111

FT Peptide 11..16 /label= AI100-105

FT Peptide 7..12 /label= AI96-101

FT Peptide 1..22 /label= AI90-111

FT Peptide 1..16 /label= AI90-105

FT Peptide 6..16 /label= AI95-105

XX WO8904486-A.

XX 18-MAY-1989.

XX 02-NOV-1988; 88MO-US03903.

XX 02-NOV-1987; 87US-0116248.

XX (SCRT-) SCRIPPS CLINIC & RE.

PI Curtiss LK, Smith RR;

DR WPI: 1989-165740/22.

XX New monoclonal antibody and polypeptide antigens
 PT - directed against Apo AI-HDL epitope, useful in
 PT diagnostic assays

PS Claim 2; Table 1; Table 2; 62pp; English.

XX AI90-111 and smaller peptides contained within this sequence. AI95-105,
 CC AI190-105 and AI190-111 are specifically claimed. Such Apo AI peptides
 CC are capable of immunologically mimicking a native conserved Apo AI
 CC epitope. They may be helpful in the diagnosis of risk of coronary heart
 CC disease.

XX Sequence 22 AA;

Query Match 8.2%; Score 22; DB 10; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.6e-13;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 IEEVAKAVQPYLDDPQKKWQEE 135
 ||||||||||||||||||

DB 1 leevkakvpylddfqkkwgee 22


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RESULT 26
AAC62608
ID AAC62608 standard; peptide: 22 AA.
XX
XX AAC62608;
AC
XX 06-SEP-2001 (first entry)
DT
XX
XX Apolipoprotein fragment #2.
DE
XX
XX Apolipoprotein; Apoa-1; atherosclerosis; coronary disease;
KM cardiovascular disease; Ischaemic heart disease; dyslipidaemia.
KM
XX
XX Unidentified.
OS
XX
XX WO200138395-A1.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 27-NOV-2000; 2000WO-AU01463.
PF
XX
XX 26-NOV-1999; 99AU-0004293.
PR
XX
XX (HEAR-) HEART RES INST LTD.
PA
XX
XX Stocker R, Wang XL, Wilcken D;
PI
XX
XX WPI: 2001-355909/37.
DR
XX
XX Novel oxidized form of apolipoprotein useful in diagnosis and treatment
PT of diseases associated with oxidative stress such as cardiovascular
PT diseases, in particular, atherosclerosis
PS
XX
XX Example 1: Page 28; 55pp; English.
XX
XX The present invention relates to oxidised apolipoprotein A-I (ApoA-I)
CC where at least Met residue 86 is oxidised to Met(O). This can be used in
CC the prevention, diagnosis and treatment of lipid associated disorders,
CC including coronary vascular disease, Ischaemic heart disease,
CC atherosclerosis and dyslipidemias. The present sequence is a fragment of
CC the ApoA-I protein isolated in the exemplification of the invention.
SQ
XX
XX Sequence 22 AA:

Query Match      8.2%; Score 22; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.6e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 EGAROKLHELOEKISPLGEEMR 173
   |||||||||||||||||||
Db 1 egarqkheiqeklsplgeemr 22

RESULT 27
AAO12095
ID AAO12095 standard; Protein; 154 AA.
XX
XX AAO12095;
AC
XX
XX 06-NOV-2001 (first entry)
DT
XX
XX Human polypeptide SEQ ID NO 25987.
DE
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KM tissue growth factor; immunomodulatory; cancer; leukemia;
KM nervous system disorders; arthritis; inflammation.
XX
XX Homo sapiens.
OS
XX
XX WO200164835-A2.
PN
XX

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PD 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US04927.
PF
XX
XX 28-FEB-2000; 2000US-0515126.
PR
XX
XX 18-MAY-2000; 2000US-0577409.
PA
XX
XX (HYSE-) HYSEQ INC.
PI
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI: 2001-514838/56.
DR
XX
XX N-FSDB; AA192026.
PT
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukemia, inflammation and immune
PT disorders
PS
XX
XX Claim 20; SEQ ID NO 25987; 1399pp + Sequence Listing; English.
CC
XX
XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
SQ
XX
XX Sequence 154 AA:

Query Match      8.2%; Score 22; DB 22; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAAVTLAVLFLTGSQARHF 22
   |||||||||||||||||||
Db 9 mkaavtlavlfltgsgarhfw 30

RESULT 28
AAP90956
ID AAP90956 standard; peptide: 21 AA.
XX
XX AAP90956;
AC
XX
XX 19-FEB-1990 (first entry)
DT
XX
XX Apo AI epitope.
DE
XX
XX High density lipoproteins.
KM
XX
XX Synthetic.
OS
XX
XX WO8909403-A.
PN
XX
XX 05-OCT-1989.
PD
XX
XX 27-MAR-1989; 89WO-US01262.
PF
XX
XX 29-MAR-1988; 88US-0174698.
PR
XX
XX (SCRI ) SCRIPPS CLINIC RES.
PA
XX
XX Curtiss LK, Smith RS;
PI
XX

```

DR WPI; 1989-309644/42.
 XX Apo 1 lipoprotein peptide and monoclonal antibody against it - used to
 PT assay peptide in vascular fluid to identify risk of coronary artery
 PT disease.
 XX
 PS Claim 2; page 41; 49pp; English.
 XX
 CC Apo AI contains the sequence below (Claim 1 claims AAs 1-15). There is
 CC an inverse correlation between plasma levels of Apo AI and coronary
 CC artery disease risk. The monoclonal antibody recognises this epitope
 CC on native Apo AI.
 XX
 SQ Sequence 21 AA;
 XX
 Query Match 7.9%; Score 21; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.2e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 25 DEPPSPMDRVKDLATVYDV 45
 ||||||||||||||||
 Db 1 deppspmdrvkdlatvydv 21
 XX
 RESULT 29
 AAR20165
 ID AAR20165 standard; Protein; 32 AA.
 XX
 AC AAR20165;
 XX
 DT 01-APR-1992 (first entry)
 XX
 DE Apo AI polypeptide (B).
 XX
 KW Monoclonal antibody; MAB AI-14; epitope; diagnosis.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 11
 FT Peptide 1..21 /label= GLU, PHE
 FT Peptide 1..32
 FT Peptide 5..21
 FT Peptide 5..28
 FT Peptide 6..21
 FT Peptide 6..28
 XX
 PN WO9118619-A.
 XX
 PD 12-DEC-1991.
 XX
 PF 07-JUN-1991; 91WO-US04038.
 XX
 PR 07-JUN-1990; 90US-0534761.
 XX
 PA (SCRT-) SCRIPPS CLINIC & RE.
 XX
 PI Curtiss LK, Banka CL, Bonnet DJ, Smith RS;
 XX
 DR WPI; 1992-007201/01.
 XX
 PT New Apo AI polypeptide(s) and anti-Apo antibodies - used to
 PT detect Apo AI in vascular fluid samples and increase
 PT LCAT-mediated cholesterol esterification in humans
 XX
 PS Claim 5; Page 68; 87pp; English.
 XX
 CC The peptides represented in AAR20164-65 are capable of immunologically
 CC mimicking an Apo AI epitope. They are useful in diagnosis and
 CC detection of Apo AI in fluids and for preparing anti-Apo AI
 CC antibodies. It is useful in therapeutic methods for increasing LCAT-

CC mediated cholesterol esterification in humans.
 CC The Apo AI polypeptide is selected from the peptides indicated in
 CC the features and includes amino acids 6-21 defining a conserved
 CC native epitope on Apo AI capable of immunoreacting with monoclonal
 CC antibody MAB AI-4.
 XX
 SQ Sequence 32 AA;
 XX
 Query Match 7.9%; Score 21; DB 13; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.2e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 129 OKKROEEMELYRQKVEPLRAE 149
 ||||||||||||||||
 Db 12 qkrqeemelyrqkveplrae 32
 XX
 RESULT 30
 AAP92073
 ID AAP92073 standard; peptide; 19 AA.
 XX
 AC AAP92073;
 XX
 DT 10-APR-1990 (first entry)
 XX
 DE Apolipoprotein AI (Apo AI) polypeptide.
 XX
 KW Apolipoprotein AI; Apo AI; high-density lipoprotein; HDL;
 KW coronary artery disease; CAD; Apo AI epitope; AI87-105.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..15
 FT Peptide /label= AI87-101
 FT Peptide 7..15
 FT Peptide /label= AI93-101
 FT Peptide 9..19
 FT Peptide /label= AI95-105
 FT Peptide 4..19
 FT Peptide /label= AI90-105
 XX
 PN WO8904486-A.
 XX
 PD 18-MAY-1989.
 XX
 PF 02-NOV-1988; 88WO-US03903.
 XX
 PR 02-NOV-1987; 87US-0116248.
 XX
 PA (SCRT-) SCRIPPS CLINIC & RE.
 XX
 PI Curtiss LK, Smith RR;
 XX
 DR WPI; 1989-165740/22.
 XX
 PT New monoclonal antibody and polypeptide antigens
 PT - directed against Apo AI-HDL epitope, useful in
 PT diagnostic assays
 XX
 PS Claim 2; Table 1; Table 2; 62pp; English.
 XX
 CC AI87-105 and smaller peptides contained within this sequence - see FT.
 CC Such Apo AI peptides are capable of immunologically mimicking a native
 CC conserved Apo AI epitope. They may be helpful in the diagnosis of risk of
 CC coronary heart disease.
 XX
 SQ Sequence 19 AA;
 XX
 Query Match 7.1%; Score 19; DB 10; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 SKDLEEVKAKVQPYLDDEQ 129
 |||||
 DB 1 skdleevkakvpylddfq 19

RESULT 31

AAV18676
 ID AAV18676 standard; Peptide; 18 AA.

AC AAV18676;

DT 09-JUL-1999 (first entry)

DE Peptide SEQ ID NO:270.

OS Synthetic.
 KW Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder;
 KM ApoA-I; cardiovascular disease; atherosclerosis; restenosis; LCAT;
 XX hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.

PN WO916409-A2.

PD 08-APR-1999.

PF 28-SEP-1998; 98MO-US20329.

PR 29-SEP-1997; 97US-0940136.

PA (BUTT/) BUTTNER K.

PA (CORN/) CORNUT I.

PA (DASS/) DASSEUX J.

PA (DURO/) DUROURCO J.

PA (METZ/) METZ G.

PA (SEK/) SEKUL R.

PI Butner K, Cornut I, Dasseux J, Dufourcq J, Metz G;

PI Sekul R;

DR WPI; 1999-254921/21.

XX Nucleic acid encoding apolipoprotein A-I agonist peptides

PT Nucleic acid encoding apolipoprotein A-I agonist peptides

PS Disclosure; Page 207; 232pp; English.

XX The present invention describes a nucleic acid (A) encoding an

CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,

CC which forms an amphipathic alpha-helix in presence of lipids. (A),

CC optionally as a complex with lipids, and host cells that contain (A),

CC are useful for gene therapy, or prevention, of diseases associated with

CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,

CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I

CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat

CC endotoxemia (septic shock). Host cells containing (A) can also be used

CC to study the role of apoA-I in lipid metabolism. (B) can also be used

CC diagnostically, e.g. to measure serum HDL (particularly its

CC subpopulation involved in retrograde cholesterol transport) and for

CC imaging the circulatory system or HDL accumulations at fatty streaks.

CC The present sequence represents a peptide from the present invention.

XX Sequence 18 AA;

QY Query Match

Best Local Similarity 6.7%; Score 18; DB 20; Length 18;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAAYFLAVLELTGSGA 18

DB 1 mkaavltlavltlgtsga 18

RESULT 32

AA008726
 ID AA008726 standard; Protein; 38 AA.

AC AA008726;

DT 06-NOV-2001 (first entry)

DE Human polypeptide SEQ ID NO 22618.

OS Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;

KM tissue growth factor; immunomodulatory; cancer; leukemia;

XX nervous system disorders; arthritis; inflammation.

PN WO200164835-A2.

PD 07-SEP-2001.

PF 26-FEB-2001; 2001WO-US04927.

PR 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

PA (HYSE-) HYSEQ INC.

PA Tang YF, Liu C, Drmanac RT;

PA WPI; 2001-514838/56.

PA N-PSDB; AA188657.

PT Isolated nucleic acids and polypeptides, useful for preventing

PT diagnosing and treating e.g. leukemia, inflammation and immune

PT disorders -

XX Claim 20; SEQ ID NO 22618; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA19941-AA19984) and

CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to

CC cytokine, cell proliferation or cell differentiation or which may induce

CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or

CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, haematopoiesis regulating

CC activity, tissue growth factor activity, immunomodulatory activity and

CC activin/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukemia, nervous system disorders, arthritis and

CC inflammation.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 38 AA;

QY Query Match

Best Local Similarity 6.7%; Score 18; DB 22; Length 38;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 KVSFLSALAEYTKLNQ 267

DB 21 kvsflsalseytklnq 38

RESULT 33

AA089474

ID AA089474 standard; peptide; 17 AA.

AC AA089474;

XX 25-FEB-1997 (first entry)

DE Anti-arteriosclerotic peptide A.
 XX
 XX Anti-arteriosclerotic; human; apolipoprotein A-I; apoA-I;
 KM treatment; arteriosclerosis; prevention; restenosis;
 KM percutaneous transluminal coronary angioplasty; PTCA.
 XX
 OS Homo sapiens.
 XX
 PN JF08157492-A.
 XX
 PD 18-JUN-1996.
 XX
 PF 07-DEC-1994: 94JP-0331293.
 XX
 PR 07-DEC-1994: 94JP-0331293.
 XX
 PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 DR WPI: 1996-339187/34.
 XX
 XX Anti-arteriosclerotic peptide(s) derived from apo:lipoprotein A-I -
 PT used in the treatment of arteriosclerosis and re-stenosis
 XX
 PS Claim 3; Page 2; 7pp; Japanese.
 XX
 CC The present sequence is a specifically claimed
 CC anti-arteriosclerotic peptide derived from amino acid residues
 CC 227-243 of human apolipoprotein A-I, and its analogues. It may be
 CC used in the treatment of arteriosclerosis, and in the prevention
 CC of restenosis after percutaneous transluminal coronary
 CC angioplasty. An orally administered dose of 50 microg to 5 mg/kg
 CC of the peptide prevented arteriosclerosis in rabbits.
 CC
 SQ Sequence 17 AA:
 Query Match 6.4%; Score 17; DB 17; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 251 VSFSLALEYTKKLTNQ 267
 DB 1 VSFSLALEYTKKLTNQ 17
 RESULT 34
 AAR34033
 ID AAR34033 standard; Protein; 16 AA.
 XX
 AC AAR34033;
 XX
 DT 13-AUG-1993 (first entry)
 XX
 DE Sequence of apo A-I from about residue 120 through about residue
 DE 135.
 XX
 KM Lipoprotein; apoprotein; B-100; A-I; LDL; HDL; assay.
 XX
 OS Synthetic.
 XX
 PN W09307165-A.
 XX
 PD 15-APR-1993.
 XX
 PF 09-OCT-1992: 92WO-US08634.
 XX
 PR 09-OCT-1991: 91US-0774633.
 PR 08-OCT-1992: 92US-0555555.
 PR 28-JUN-1992: 92US-0901706.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Curtiss LK, Koduri KR, Smith RS, Wiltzium JL, Young SG;

XX
 DR WPI: 1993-134378/16.
 XX
 XX Polypeptide mimic of native apo B-100 and native apo A-I - useful
 PT in assays for LDL and HDL in plasma samples
 XX
 PS Disclosure; Page 13 and page 35; 137pp; English.
 XX
 CC The inventors claim a portion of the polypeptide contg. apo B-100
 CC that immunoreacts with antibodies secreted by the hybridoma M947
 CC having ATCC Accession No. 8746. Polypeptides specifically claimed
 CC include residues 217-297, 216-310, 216-331, 216-352, 216-377, 1-377,
 CC 205-297, 173-297, 140-297. DNA sequences encoding the polypeptides
 CC are also claimed. Also claimed are a fusion polypeptide that
 CC contains: (a) a first amino acid residue sequence up to 250 residues
 CC in length that includes residues 120-135 of apo A-I, (b) a second
 CC amino acid residue sequence up to 375 residues in length that
 CC includes residues 217-297 of apo B-100 and DNA encoding it.
 CC
 SQ Sequence 16 AA:
 Query Match 6.0%; Score 16; DB 14; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.2e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 120 KYQPYLDLDFQKKWQEE 135
 DB 1 KYQPYLDLDFQKKWQEE 16
 RESULT 35
 AAR72706
 ID AAR72706 standard; Peptide; 16 AA.
 XX
 AC AAR72706;
 XX
 DT 31-OCT-1995 (first entry)
 XX
 DE Human apo A-I fragment comprising residues 120-135.
 XX
 KM Apo A-I; LDL cholesterol; low density lipoprotein; lipid.
 XX
 OS Homo sapiens.
 XX
 PN US5408038-A.
 XX
 PD 18-APR-1995.
 XX
 PF 09-OCT-1991: 91US-0774633.
 XX
 PR 09-OCT-1991: 91US-0774633.
 PR 18-JUN-1992: 92US-0901706.
 PR 08-OCT-1992: 92US-0959946.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Curtiss LK, Koduri KR, Smith RS, Wiltzium JL, Young SG;
 XX
 DR WPI: 1995-161146/21.
 DR N-PSDB; AAQ89634.
 XX
 PT New apo:lipoprotein B-100 peptide(s) and fusion peptide(s) - used
 PT in assay systems for detecting LDL and HDL cholesterol levels in
 PT body fluids.
 XX
 PS Claim 10; Column 17; 41pp; English.
 XX
 CC A dispersible apo A-I/B-100 fusion polypeptide is claimed which
 CC contains a first AA sequence of apo A-I (see AAR72605) and that includes
 CC at least AA sequence positions 120-135 (see AAR72606). The two
 CC sequences are operatively linked. An exemplary linking sequence is
 CC AAR72707 whose encoding DNA can be ligated between an apo A-I and a

CC B-100 encoding DNA sequence.
XX
SQ Sequence 16 AA:

Query Match 6.0%; Score 16; DB 16; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 120 KVQPIIDDFOKMOEE 135
| | | | | | | | | | | | | | | | | |
Db 1 kvppyloddqkkgwgee 16

RESULT 36
AAV27065
ID AAV27065 standard; peptide; 16 AA.
XX
AC AAV27065;
XX
DT 18-OCT-1999 (first entry)
XX
DE Peptide seq ID No: 1 of JP11209399.
XX

KW Medicinal composition: lipoprotein; megakaryocytic; antithrombin III;
KW alveolar forming activity; C1 inhibitor; human; thrombocytopenia;
KW platelet.
XX
OS Synthetic.
XX
PN JP11209399-A.
XX
PD 03-AUG-1999.
XX
PF 28-MAY-1998; 98JP-0146860.
XX
PR 20-NOV-1997; 97JP-0319587.
XX
PA (ASAH) ASAH KASEI KOGYO KK.
XX
DR WPI: 1999-488816/41.
XX

PT New medicinal composition composed of an effective ingredient of
PT heavy specific gravity lipoprotein - useful for effective production
PT of platelets and treatment of thrombocytopenia
XX
PS Disclosure; Page 12; 14pp; Japanese.
XX

CC The invention provides a new medicinal composition composed of an
CC effective ingredient of a heavy specific gravity lipoprotein containing
CC megakaryocytic projected alveolar forming activity, particularly non-
CC absorptive in zinc chelating gel, especially containing antithrombin III,
CC having C1 inhibitor activity. The lipoprotein is prepared by: (a) heating
CC human blood at 60 deg. C for 10 minutes; (b) removal of protein to give a
CC supernatant; (c) dialysis of the resultant supernatant against 10 mM
CC NaOAc buffer at pH 4.5, to give a supernatant; (d) dialysis of the
CC resultant supernatant against 10 mM HEPES buffer containing 150 mM NaCl
CC at pH 7.4, to give a supernatant; (e) gel filtration with 10 mM HEPES
CC buffer containing 150 mM NaCl at pH 7.4 to give a fraction having the
CC activity; (f) contacting the active fraction with a zinc chelating gel
CC under 10 mM HEPES buffer containing 150 mM NaCl at pH 7.4; (g) collection
CC of non-absorptive fraction; (h) ultracentrifugation of the fraction
CC adjusted to S₀.6.1.21; and (i) collection of the floating yellow fraction
CC to give the aimed heavy specific gravity lipoprotein containing
CC megakaryocytic projected alveolar forming activity; used for treatment of
CC thrombocytopenia. The new composition is useful for effective production
CC of platelets and treatment of thrombocytopenia.
XX
SQ Sequence 16 AA:

Query Match 6.0%; Score 16; DB 20; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 DEPPQSPWDRVKDLAT 40
| | | | | | | | | | | | | | | | | |
Db 1 deppqspwdrvkdlat 16

RESULT 37
AAG62607
ID AAG62607 standard; peptide; 16 AA.
XX
AC AAG62607;
XX
DT 06-SEP-2001 (first entry)
XX
DE Apolipoprotein fragment #1.
XX

KW Apolipoprotein; ApoA-1; atherosclerosis; coronary disease;
KW cardiovascular disease; ischaemic heart disease; dyslipidaemia.
XX
OS Unidentified.
XX

EH Key Location/Qualifiers
FT Modified-site 14
FT /Label= OTHER
FT /note= "optionally oxidised"
XX

PN WO200138395-A1.
XX

PD 31-MAY-2001.
XX

PF 27-NOV-2000; 2000WO-AU01463.
XX

PR 26-NOV-1999; 99AU-0004293.
XX

PA (HEAR-) HEART RES INST LTD.
XX

PI Stocker R, Wang XL, Wilcken D;
XX

DR WPI: 2001-355909/37.
XX

PT Novel oxidized form of apolipoprotein useful in diagnosis and treatment
PT of diseases associated with oxidative stress such as cardiovascular
PT diseases, in particular, atherosclerosis
XX
PS Example 1; Page 28; 55pp; English.
XX

CC The present invention relates to oxidised apolipoprotein A-I (ApoA-I)
CC where at least Met residue 86 is oxidised to Met(O). This can be used in
CC the prevention, diagnosis and treatment of lipid associated disorders,
CC including coronary vascular disease, ischaemic heart disease, atherosclerosis
CC and dyslipidaemias. The present sequence is a fragment of
CC the ApoA-I protein isolated in the exemplification of the invention.
XX
SQ Sequence 16 AA:

Query Match 6.0%; Score 16; DB 22; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DNLEKETGLRQEMSK 112
| | | | | | | | | | | | | | | | | |
Db 1 dnleketglrqlgmsk 16

RESULT 38
AAP60986
ID AAP60986 standard; Peptide; 16 AA.
XX
AC AAP60986;
XX
DT 08-AUG-1991 (first entry)

```

XX DE Sequence of immunogenic fragment of apolipoprotein (APL) ApoA1.
XX KW Apolipoprotein; immunoassay; antibody.
XX OS Homo sapiens.
XX PN W08604144-A.
XX PD 17-JUL-1986.
XX PF 26-DEC-1985; 85WO-US02569.
XX PR 31-DEC-1984; 84US-0688040.
XX PR 26-DEC-1985; 85US-0905584.
XX PA (ITGE-) INT GENETIC ENG INC.
XX PI Fareed G, Sen A;
XX DR WPI; 1986-196930/30.
XX CC Peptide fragments of human apo:lipoprotein - used for producing
XX PT type-specific antibodies for immunoassay
XX PS Claim 19; page 38; 53pp; English.
XX CC The peptides of the invention are conjugated with carrier proteins
XX CC and used to produce type-specific, non-cross-reactive antibodies by
XX CC immunisation. The antibodies may then be used in immunoassays to
XX CC identify and quantitate specific APLs. Peptide fragments without
XX CC the C-terminal Cys residue are also claimed.
XX SQ Sequence 16 AA:

Query Match 5.6%; Score 15; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 RTHLAPYSDELRLRL 198
   |||||
DB 1 rthlapysdelrql 15

RESULT 39
AAP60985
ID AAP60985 standard; Protein; 14 AA.
XX
XX AAP60985;
XX
XX 08-AUG-1991 (first entry)
XX DT
XX DE Sequence of immunogenic fragment of apolipoprotein (APL) ApoA1.
XX KW Apolipoprotein; immunoassay; antibody.
XX OS Homo sapiens.
XX PN W08604144-A.
XX PD 17-JUL-1986.
XX PF 26-DEC-1985; 85WO-US02569.
XX PR 31-DEC-1984; 84US-0688040.
XX PR 26-DEC-1985; 85US-0905584.
XX PA (ITGE-) INT GENETIC ENG INC.
XX PI Fareed G, Sen A;
XX DR WPI; 1986-196930/30.

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XX PT Peptide fragments of human apo:lipoprotein - used for producing
XX PT type-specific antibodies for immunoassay
XX PS Claim 18; page 37; 53pp; English.
XX CC The peptides of the invention are conjugated with carrier proteins
XX CC and used to produce type-specific, non-cross-reactive antibodies by
XX CC immunisation. The antibodies may then be used in immunoassays to
XX CC identify and quantitate specific APLs. Peptide fragments without
XX CC the C-terminal Cys residue are also claimed.
XX SQ Sequence 14 AA:

Query Match 4.9%; Score 13; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 DEPPQSPMDRVKD 37
   |||||
DB 1 deppqspmdrvkd 13

RESULT 40
AAP92076
ID AAP92076 standard; peptide; 12 AA.
XX
XX AAP92076;
XX
XX 10-APR-1990 (first entry)
XX DT
XX DE Apolipoprotein AI (Apo AI) polypeptide.
XX KW Apolipoprotein AI; Apo AI; high-density lipoprotein; HDL;
XX KW coronary artery disease; CAD; Apo AI epitope; A1105-116.
XX PN W08904486-A.
XX PD 18-MAY-1989.
XX PF 02-NOV-1988; 88WO-US03903.
XX PR 02-NOV-1987; 87US-0116248.
XX PA (SCRI-) SCRIPPS CLINIC & RE.
XX PI Curtiss IK, Smith RR;
XX DR WPI; 1989-165740/22.
XX
XX New monoclonal antibody and polypeptide antigens
XX PT - directed against Apo AI-HDL epitope, useful in
XX PT diagnostic assays
XX PS Page 31; 62pp; English.
XX CC An Apo AI peptide capable of immunologically mimicking a native
XX CC conserved Apo AI epitope. It may be helpful in the diagnosis of risk of
XX CC coronary heart disease.
XX SQ Sequence 12 AA:

Query Match 4.5%; Score 12; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 OKKQDEMEELR 140
   |||||
DB 1 gkkwqemelyr 12

```

RESULT 41
 ID AAY41961 standard; Peptide: 12 AA.
 AC AAY41961;
 DT 09-DEC-1999 (first entry)
 DE Rheumatoid arthritis diagnostic protein isoform peptide #112.
 KW Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;
 KW rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;
 KW rheumatoid arthritis diagnostic protein isoform; screening;
 KW expression reference protein isoform; prognosis.
 OS Homo sapiens.
 PN WO9947925-A2.
 PD 23-SEP-1999.
 PF 15-MAR-1999; 99WO-GB00763.
 PR 13-MAR-1998; 98GB-0005477.
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PI Parekh RB, Patel TP, Townsend RR;
 DR WPI; 1999-571871/48.
 PT Diagnosis of human rheumatoid arthritis by two-dimensional
 PT electrophoresis -
 PS Disclosure; Page 20; 157pp; English.
 CC A method has been developed for the diagnosis of human rheumatoid
 CC arthritis (RA) using two-dimensional electrophoresis to generate a
 CC two-dimensional array of features. The method can be used for screening,
 CC diagnosis and prognosis of RA in a subject or for monitoring the effect
 CC of an anti-RA drug or therapy administered to a subject. The method
 CC comprises: (a) analysing a sample of serum or plasma and optionally
 CC synovial fluid by two-dimensional electrophoresis, to generate a two-
 CC dimensional array of features; (b) identifying at least one chosen
 CC feature whose relative abundance correlates with the presence or absence
 CC of RA; and (c) comparing the abundance of each chosen feature in the
 CC sample with the abundance of that chosen feature in serum or plasma from
 CC one or more persons without RA, where the relative abundance of the
 CC chosen feature or features in the sample indicates the presence or
 CC absence of RA in the subject. The method can also be used in clinical
 CC studies for testing drugs for therapy of RA, for purification of RA-
 CC diagnostic protein isoforms (RPIs), and for production of antibodies to
 CC RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify
 CC compounds that promote or inhibit their activity, which are then used as
 CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy
 CC protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to
 CC AAY42103 represent expression reference protein isoform peptides and
 CC AA225066 to AA225068 represent degenerate probes for RPIs, which are all
 CC used in the exemplification of the present invention.
 SQ Sequence 12 AA:

Query Match 4.5%; Score 12; DB 20; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00035;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 VSFLSALFEYTK 262
 |||||
 Db 1 vsflsalseytk 12

RESULT 42

AAY42027
 ID AAY42027 standard; Peptide: 12 AA.
 AC AAY42027;
 DT 09-DEC-1999 (first entry)
 DE Rheumatoid arthritis diagnostic protein isoform peptide #178.
 KW Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;
 KW rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;
 KW rheumatoid arthritis diagnostic protein isoform; screening;
 KW expression reference protein isoform; prognosis.
 OS Homo sapiens.
 PN WO9947925-A2.
 PD 23-SEP-1999.
 PF 15-MAR-1999; 99WO-GB00763.
 PR 13-MAR-1998; 98GB-0005477.
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PI Parekh RB, Patel TP, Townsend RR;
 DR WPI; 1999-571871/48.
 PT Diagnosis of human rheumatoid arthritis by two-dimensional
 PT electrophoresis -
 PS Disclosure; Page 21; 157pp; English.
 CC A method has been developed for the diagnosis of human rheumatoid
 CC arthritis (RA) using two-dimensional electrophoresis to generate a
 CC two-dimensional array of features. The method can be used for screening,
 CC diagnosis and prognosis of RA in a subject or for monitoring the effect
 CC of an anti-RA drug or therapy administered to a subject. The method
 CC comprises: (a) analysing a sample of serum or plasma and optionally
 CC synovial fluid by two-dimensional electrophoresis, to generate a two-
 CC dimensional array of features; (b) identifying at least one chosen
 CC feature whose relative abundance correlates with the presence or absence
 CC of RA; and (c) comparing the abundance of each chosen feature in the
 CC sample with the abundance of that chosen feature in serum or plasma from
 CC one or more persons without RA, where the relative abundance of the
 CC chosen feature or features in the sample indicates the presence or
 CC absence of RA in the subject. The method can also be used in clinical
 CC studies for testing drugs for therapy of RA, for purification of RA-
 CC diagnostic protein isoforms (RPIs), and for production of antibodies to
 CC RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify
 CC compounds that promote or inhibit their activity, which are then used as
 CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy
 CC protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to
 CC AAY42103 represent expression reference protein isoform peptides and
 CC AA225066 to AA225068 represent degenerate probes for RPIs, which are all
 CC used in the exemplification of the present invention.
 SQ Sequence 12 AA:

Query Match 4.5%; Score 12; DB 20; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00035;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 VSFLSALFEYTK 262
 |||||
 Db 1 vsflsalseytk 12

RESULT 43
AAB87196

Query Match	4.5%; Score 12; DB 22; Length 12;
Best Local Similarity	100.0%; Pred. No. 0.00035;
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY 251 VSFLSALEETK 262	
Db 1 vsfsaleeytk 12	
RESULT 44	
AAFP60987	
ID AAF60987 standard; Peptide; 13 AA.	
XX	

AC	AAP60987;	
XX		
DT	08-AUG-1991 (first entry)	
XX		
DE	Sequence of immunogenic fragment of apolipoprotein (Apo) ApoE1.	
XX		
KW	Apolipoprotein; immunoassay; antibody.	
XX		
OS	Homo sapiens.	
XX		
EN	W08604144-A.	
XX		
PD	17-JUL-1986.	
XX		
PF	26-DEC-1985; 85WO-US02569.	
XX		
PR	31-DEC-1984; 84US-0688040.	
XX		
PR	26-DEC-1985; 85US-0905584.	
XX		
PA	(ITGE-) INT GENETIC ENG INC.	
XX		
PI	Farred G, Sen A;	
XX		
DR	WPI; 1986-196930/30.	
XX		
PT	Peptide fragments of human apolipoprotein - used for producing	
XX	type-specific antibodies for immunoassay	
XX		
PS	Claim 20; page 38; 53pp; English.	
XX		
CC	The peptides of the invention are conjugated with carrier proteins	
CC	and used to produce type-specific, non-cross-reactive antibodies by	
CC	immunisation. The antibodies may then be used in immunoassays to	
CC	identify and quantitate specific Apus. Peptide fragments without	
CC	the C-terminal Cys residue are also claimed.	
XX		
SO	Sequence 13 AA;	
XX		
QY	117 VKAKVQPYLDLF 128	
DB	1 VKAKVQPYLDLF 12	
XX		
RESULT 45		
ID	AAB87236	
XX	AAB87236 standard; Peptide; 22 AA.	
XX		
AC	AAB87236;	
XX		
DT	10-MAY-2001 (first entry)	
XX		
DE	Breast-cancer associated protein isoform BPI-28 peptide #4.	
XX		
KW	Human; breast cancer; breast cancer associated protein isoform; BPI;	
XX	breast cancer associated feature; BPI diagnosis; cytostatic.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200113117-A2.	
XX		
PD	22-FEB-2001.	
XX		
PF	14-AUG-2000; 2000WO-GB03143.	
XX		
PR	13-AUG-1999; 99GB-0019258.	
XX		
PR	30-MAR-2000; 2000GB-0007754.	
XX		
PA	(OXFO-) OXFORD GLYCOSCIENCES UK LTD.	

XX Herath HMC;

XX WPI; 2001-211252/21.

PT Screening, diagnosis or prognosis of breast cancer, by analyzing a sample of serum or plasma by two dimensional electrophoresis to detect the presence or level of a breast cancer-associated feature -

PS Disclosure: Page 25; 146pp; English.

CC The present invention describes a method for the screening, diagnosis or prognosis of breast cancer (BC), determining the stage or severity of BC, and monitoring the effect of therapy administered to a subject having BC, comprising analysing a sample of body fluid by two dimensional electrophoresis to generate a two-dimensional array of features, comprising a chosen feature whose relative abundance correlates with BC or predicts the onset of BC; and (b) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in the body fluid from one or more persons free from BC, or with a previously determined reference range for that feature in subjects free from BC, or with the abundance of an expression reference feature (ERF) in the test sample. The method is useful for screening, diagnosis or prognosis of breast cancer, determining the stage or severity of BC, monitoring the effect of therapy administered to a subject having BC, and for identifying a subject at risk of developing BC. AAB87186 to AAB87340 represents breast cancer associated protein isoform (BPI) peptide sequences, and AAF91643 to AAF91848 represent BPI probes used in the exemplification of the present invention.

SQ Sequence 22 AA;

Query Match 4.5%; Score 12; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 251 VSFSLALEEYTK 262
|||||
DB 1 veflsaleeytk 12

RESULT 46

AAAY1957
ID AAY1957 standard; Peptide; 11 AA.

AC AAY1957;

DT 09-DEC-1999 (first entry)

DE Rheumatoid arthritis diagnostic protein isoform peptide #108.

XX Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;
KW Rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;
KW Rheumatoid arthritis diagnostic protein isoform; screening;
KW expression reference protein isoform; prognosis.

OS Homo sapiens.

PN WO9947925-A2.

PD 23-SEP-1999.

PF 15-MAR-1999; 99WO-GB00763.

PR 13-MAR-1998; 98GB-0005477.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Parekh RB, Patel TP, Townsend RR;

XX WPI; 1999-571871/48.

PT Diagnosis of human rheumatoid arthritis by two-dimensional electrophoresis -

PS Disclosure: Page 20; 157pp; English.

CC A method has been developed for the diagnosis of human rheumatoid arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA; and (c) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic protein isoforms (RPIs), and for production of antibodies to RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify CC compounds that promote or inhibit their activity, which are then used as CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy CC protocols. AAY1844 to AAY42100 represent RPI peptides, AAY42101 to AAY42506 represent expression reference protein isoform peptides and CC AAY25066 to AAY25068 represent degenerate probes for RPIs, which are all CC used in the exemplification of the present invention.

SQ Sequence 11 AA;

Query Match 4.1%; Score 11; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 DLATYVDVVK 47
|||||
DB 1 dlatyvadvk 11

RESULT 47

AAAY2023
ID AAY2023 standard; Peptide; 11 AA.

AC AAY2023;

DT 09-DEC-1999 (first entry)

DE Rheumatoid arthritis diagnostic protein isoform peptide #174.

XX Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;
KW Rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;
KW Rheumatoid arthritis diagnostic protein isoform; screening;
KW expression reference protein isoform; prognosis.

OS Homo sapiens.

PN WO9947925-A2.

PD 23-SEP-1999.

PF 15-MAR-1999; 99WO-GB00763.

PR 13-MAR-1998; 98GB-0005477.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Parekh RB, Patel TP, Townsend RR;

XX WPI, 1999-571871/48.

XX Diagnosis of human rheumatoid arthritis by two-dimensional electrophoresis -

PS Disclosure: Page 21; 157pp; English.

XX A method has been developed for the diagnosis of human rheumatoid arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA; and (c) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic protein isoforms (RPIs), and for production of antibodies to RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy protocols. AA141844 to AA142100 represent RPI peptides, AA142101 to AA142103 represent expression reference protein isoform peptides and AA225066 to AA225068 represent degenerate probes for RPIs, which are all used in the exemplification of the present invention.

SO Sequence 11 AA;

Query Match 4.1%; Score 11; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 DLATVYVDYLK 47
| | | | | | | | | | | | | | |
Db 1 dlatvyvdyllk 11

RESULT 48

ABBS56060 standard; Peptide; 11 AA.

AC ABBS56060;

DT 15-FEB-2002 (first entry)

DE Vascular dementia-associated protein isoform (VPI) 260.

KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening; diagnosis; prognosis; gene therapy.

OS Homo sapiens.

PN WO200169261-A2.

PD 20-SEP-2001.

PF 14-MAR-2001; 2001WO-GB01106.

PR 15-MAR-2000; 2000GB-0006285.

PR 24-NOV-2000; 2000GB-0028734.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Hefath HMAC, Parekh RB, Rohlf C;
XX

DR WPI; 2001-557937/62.

XX Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy.

PT comprises analysing body fluid by 2-dimensional electrophoresis for features correlated with VD -

PS Claim 6; Page 35; 151pp; English.

XX The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIs) (ABBS5801-ABBS6295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy.

SO Sequence 11 AA;

Query Match 4.1%; Score 11; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 185 THAPYSDELR 195
| | | | | | | | | | | | | | |
Db 1 thlapyseldr 11

RESULT 49

AAU24926 standard; Peptide; 11 AA.

AC AAU24926;

DT 18-DEC-2001 (first entry)

DE Schizophrenia-Associated Protein Isoform (SPI) peptide #155.

KW Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.

OS Homo sapiens.

PN WO200162785-A2.

PD 30-AUG-2001.

PF 23-FEB-2001; 2001WO-GB00792.

PR 24-FEB-2000; 2000GB-0004415.

PR 28-NOV-2000; 2000US-0750395.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

DR WPI; 2001-570624/64.

XX New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets -

PS Disclosure; Page 32; 148pp; English.
XX

CC The sequence represents a schizophrenia-associated protein isoform (SPI).
 CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
 CC in cerebrospinal fluid, serum or plasma and are useful markers of
 CC schizophrenia. The sequences can be used for treatment and diagnosis of
 CC schizophrenia, screening, prognosis, monitoring the results of therapy,
 CC identifying patients most likely to respond to a particular therapy and
 CC identification of new targets for drug treatment. SPI DNA is useful as a
 CC nucleic acid probe to detect the presence of nucleic acids or SPIs.
 CC
 SQ Sequence 11 AA:

Query Match 4.1%; Score 11; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 185 THLAPYSDLR 195
 |||||
 DB 1 thlapydelr 11

RESULT 50
 AAU15270

ID AAU15270 standard; Peptide: 11 AA.

XX AAU15270;

DT 24-OCT-2001 (first entry)

DE Schizophrenia-associated isoform peptide #155.

KW Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;

KM neurological disorder; neuropathy.

XX Homo sapiens.

OS WO200163293-A2.

PN 30-AUG-2001.

PD 23-FEB-2001; 2001WO-GB00783.

PR 24-FEB-2000; 2000GB-0004415.

PR 28-NOV-2000; 2000US-0750395.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMC, Parekh RB, Rohlf C;

DR WPI; 2001-502868/55.

PT Diagnosing and monitoring Schizophrenia by detecting the presence of
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein
 PT Isoforms in samples of cerebrospinal fluid -

PS Claim 6; Page 32; 160pp; English.

CC The invention relates to methods and compositions for screening,
 CC diagnosis and prognosis of Schizophrenia. The method involves detecting
 CC the presence of Schizophrenia (SCH) Associated Features (Sf) and SCH
 CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,
 CC immunosay or hybridisation assay, for diagnosing and monitoring SCH,
 CC studying the effectiveness of treatments and for identifying potential
 CC therapeutic agents. The method is used for (1) screening or diagnosis of
 CC SCH and the relative abundance of at least 1 chosen feature correlates
 CC with the presence or absence of SCH; and (2) monitoring the effect of
 CC therapy administered to a subject with SCH and the relative abundance of
 CC at least 1 chosen feature which correlates with the severity of SCH.
 CC The expression and activity of the Sf, SPIs and related molecules
 CC (e.g. secondary messengers) are studied to diagnose SCH, monitor the
 CC progress of the disorder and produce potential therapeutic agents for the
 CC targets to identify and produce potential therapeutic agents for the
 CC treatment of SCH. The paucity of detectable neuronal defects

CC distinguishes neuropsychiatric disorders such as SCH from neurological
 CC disorders, where manifestations of anatomical and biochemical changes
 CC have been identified in many cases. Consequently the identification and
 CC characterisation of cellular and/or molecular causative defects and
 CC neuropathies are necessary for improved treatment of neuropsychiatric
 CC disorders. AAU15114-AAU15762 represent the amino acid sequences of
 CC schizophrenia-associated isoforms used in the method of the invention.
 CC
 SQ Sequence 11 AA:

Query Match 4.1%; Score 11; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 185 THLAPYSDLR 195
 |||||
 DB 1 thlapydelr 11

Search completed: September 22, 2002, 12:22:53
 Job time: 978 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:01:05 ; Search time 66.91 Seconds

(without alignments)
383,438 Million cell updates/sec

Title: US-09-803-918a-2

Perfect score: 1362
Sequence: 1 MKAAVLTLLAVLFLTGSGQARH.....SFKVSFLSALREYTKKLMTQ 267

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_71.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1362	100.0	267	1	LPHUAI
2	1306	95.9	267	2	JS0079
3	1299	95.4	267	1	A26529
4	1161.5	85.3	266	1	LPDGA1
5	1100.5	80.8	266	1	apoliipoprotein A-I
6	1100	80.8	265	2	A46018
7	1093	80.2	265	2	JT0672
8	1087.5	79.8	264	2	S11394
9	1082	79.4	265	1	LPRB1B
10	1082	79.4	265	1	A56858
11	974.5	71.5	241	1	A24998
12	924	67.8	231	2	JU00704
13	904.5	66.4	264	2	S22420
14	898.5	66.0	262	2	JC1237
15	849.5	62.4	259	2	A24700
16	688.5	50.6	264	1	JC5456
17	683.5	48.7	264	2	A61448
18	644.5	47.3	246	2	S21830
19	617.5	45.3	164	2	S29565
20	291	21.4	429	2	apoliipoprotein A-I
21	278.5	20.4	396	1	LPHU44
22	267	19.6	391	1	LPR7A4
23	253	18.6	399	2	C40892
24	251	18.4	391	2	B40892
25	251	18.4	395	2	A40892
26	249.5	18.3	401	2	A47141
27	238.5	17.5	394	2	A25281
28	225.5	16.6	258	2	JH0472
29	209	15.3	311	2	JU0036

30	198	14.5	312	1	LPRTE	apoliipoprotein E p
31	194.5	14.3	1547	2	T28657	blackjack protein,
32	190.5	14.0	317	2	A28792	apoliipoprotein E p
33	189.5	13.9	317	2	S03185	apoliipoprotein E p
34	188	13.8	317	2	S33450	apoliipoprotein E p
35	184	13.5	298	2	S12635	apoliipoprotein E p
36	182	13.4	329	2	JC5566	apoliipoprotein E p
37	178.5	13.1	291	2	C60940	apoliipoprotein E p
38	174.5	12.8	317	1	LPHUE	apoliipoprotein E p
39	166.5	12.2	316	2	JC6549	apoliipoprotein E p
40	160	11.7	316	2	S26478	apoliipoprotein E p
41	160	11.7	316	2	I4596	apoliipoprotein E p
42	147	10.8	311	2	A45951	apoliipoprotein E p
43	146	10.7	513	2	S08381	apoliipoprotein E p
44	143.5	10.5	771	1	A33430	keratin, 58K type
45	137	10.1	470	2	T23512	h-caldesmon - chic hypothetical prote

ALIGNMENTS

RESULT 1
LPHUAI
apoliipoprotein A-I precursor [validated] - human
N:Alternate names: apoa-I-2; apoa-I-4; preproapoa-I; prostacyclin stabilizing factor
C:Species: Homo sapiens (man)
C:Date: 14-Nov-1983 #sequence.revision 14-Nov-1983 #extl.change 08-Dec-2000
C:Accession: A90947; B90947; S02373; A93465; A21147; A93519; B93519; A93472; A94010;
6197
R:Seilhamer, J.J.; Protter, A.A.; Frossard, P.; Levy-Wilson, B.
DNA 3, 309-317, 1984
A:Title: Isolation and DNA sequence of full-length cDNA and of the entire gene for hu
A:Reference number: A90947; M01D:8502665
A:Accession: A90947
A:Molecule type: DNA
A:Residues: 1-267 <SEI>
A:Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635
A:Accession: B90947
A:Molecule type: mRNA
A:Residues: 1-267 <SE2>
A:Cross-references: GB:X01038; NID:g28769; PIDN:CAA25519.1; PID:g296635
R:Makrides, S.C.; Ruiz-Opazo, N.; Hayden, M.; Nussbaum, A.L.; Breslow, J.L.; Zannis,
Eur. J. Biochem. 173, 465-471, 1988
A:Title: Sequence and expression of Tangier apoa-I gene.
A:Reference number: S02373; M01D:88196137
A:Accession: S02373
A:Molecule type: DNA
A:Residues: 1-267 <MAK>
A:Cross-references: EMBL:X07496; NID:g28774; PIDN:CAA30377.1; PID:g296729
R:Shoulders, R.C.; Kornblith, A.R.; Munro, B.S.; Baralle, F.E.
Nucleic Acids Res. 11, 2827-2837, 1983
A:Title: Gene structure of human apoliipoprotein A1.
A:Reference number: A93465; M01D:83220822
A:Accession: A93465
A:Molecule type: DNA
A:Residues: 1-267 <SHO>
A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518;
R:Karathanasis, S.K.; Zannis, V.I.; Breslow, J.L.
Proc. Natl. Acad. Sci. U.S.A. 80, 6147-6151, 1983
A:Title: Isolation and characterization of the human apoliipoprotein A-I gene.
A:Reference number: A21147; M01D:84016011
A:Accession: A21147
A:Molecule type: DNA
A:Residues: 1-267 <KAR>
A:Cross-references: GB:J00098; GB:J03222; NID:g178765; PIDN:AA559514.1; PID:g178768
R:Sharpe, C.R.; Sidoli, A.; Shelley, C.S.; Lucero, M.A.; Shoulders, C.C.; Baralle, F.
Nucleic Acids Res. 12, 3917-3932, 1984
A:Title: Human apoliipoproteins A1, AII, CII and CIII. cDNA sequences and mRNA abundan
A:Reference number: A93519; M01D:84221405
A:Accession: A93519
A:Molecule type: mRNA
A:Residues: 1-267 <SHA>
A:Cross-references: GB:X00566; NID:g28765; PIDN:CAA25232.1; PID:g732753

A:Accession: B93519
 A:Molecule type: DNA
 A:Residues: 1-24 <SH2>
 R:Cheng, P.; Chan, L.
 Nucleic Acids Res. 11, 3703-3715, 1983
 A:Title: Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.
 A:Reference number: A93472; MUID:83220772
 A:Accession: A93472
 A:Molecule type: mRNA
 A:Residues: 1-267 <CH2>
 A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GE
 R:Law, S.W.; Brewer Jr., H.B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 66-70, 1984
 A:Title: Nucleotide sequence and the encoded amino acids of human apolipoprotein A-I mRNA
 A:Reference number: A94010; MUID:84119464
 A:Accession: A94010
 A:Molecule type: mRNA
 A:Residues: 1-267 <LAN>
 A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GE
 R:Rannals, V.I.; Karathanasis, S.K.; Keutmann, H.T.; Goldberger, G.; Breslow, J.L.
 Proc. Natl. Acad. Sci. U.S.A. 80, 2574-2578, 1983
 A:Title: Intracellular and extracellular processing of human apolipoprotein A-I: secreted
 A:Reference number: A21118; MUID:83195100
 A:Accession: A21118
 A:Molecule type: mRNA
 A:Residues: 1-24 <ZAN>
 R:Brewer Jr., H.B.; Fairwell, T.; Kay, L.; Meng, M.; Roman, R.; Law, S.; Light, J.A.
 Biochem. Biophys. Res. Commun. 113, 626-632, 1983
 A:Title: Human plasma proapoA-I: isolation and amino-terminal sequence.
 A:Reference number: A90112; MUID:83256553
 A:Accession: A90112
 A:Molecule type: protein
 A:Residues: 19-27 <BRE>
 R:Brewer Jr., H.B.; Fairwell, T.; Larue, A.; Roman, R.; Houser, A.; Bronzert, T.J.
 Biochem. Biophys. Res. Commun. 80, 623-630, 1978
 A:Title: The amino acid sequence of human ApoA-I, an apolipoprotein isolated from high d
 A:Reference number: A90209; MUID:78123731
 A:Accession: A90209
 A:Molecule type: protein
 A:Residues: 25-57, 'Q', 59-169, 'QQ', 172-267 <BR2>
 R:Yui, Y.; Aoyama, T.; Morishita, H.; Takahashi, H.; Takatsu, Y.; Kawai, C.
 J. Clin. Invest. 82, 803-807, 1988
 A:Title: Serum prostacyclin stabilizing factor is identical to apolipoprotein A-I (Apo A
 A:Reference number: A30516; MUID:88331387
 A:Accession: A30516
 A:Molecule type: protein
 A:Residues: 25-56 <YUI>
 R:Nichols, W.C.; Dwyer, F.E.; Liepnieks, J.; Benson, M.D.
 Biochem. Biophys. Res. Commun. 156, 762-768, 1988
 A:Title: Variant apolipoprotein AI as a major constituent of a human hereditary amyloid.
 A:Reference number: A31582; MUID:89050104
 A:Accession: A31582
 A:Molecule type: protein
 A:Residues: 25-49, 'R', 51-85, 'D', 87-107 <NIC>
 A:Note: variant sequence from patient with familial amyloidotic polyneuropathy type III
 R:Manjunath, P.; Marcel, Y.L.; Uma, J.; Seidah, N.G.; Chretien, M.; Chappelaine, A.
 J. Biol. Chem. 264, 16853-16857, 1989
 A:Title: Apolipoprotein A-I binds to a family of bovine seminal plasma proteins.
 A:Reference number: A34409; MUID:89380318
 A:Accession: A34409
 A:Molecule type: protein
 A:Residues: 25-48 <MAN>
 R:Stoffel, W.; Binczek, E.
 Biol. Chem. Hoppe-Seyler 369, 1055-1063, 1988
 A:Title: Structural requirements of human preproapolipoprotein AI for translocation and
 A:Reference number: S02737; MUID:89149957
 A:Accession: S02737
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-6, 'AV', 9, 'LV', 12-29 <STO>
 A:Note: part of this sequence, including the amino end of the mature protein, was confir
 R:Stoffel, W.; Binczek, E.
 Biol. Chem. Hoppe-Seyler 372, 481-488, 1991

A:Title: Transient expression of wild type and mutant human apolipoprotein AI in COS
 A:Reference number: S16197; MUID:92029676
 A:Contents: annotation: extension of studies in reference S02737
 R:Stoffel, W.; Kruger, E.; Deutzmann, R.
 Hoppe-Seyler's Z. Physiol. Chem. 364, 227-237, 1983
 A:Title: Cell-free translation of human liver apolipoprotein AI and AI1 mRNA processi
 A:Reference number: A19913; MUID:83236195
 A:Accession: B19913
 A:Molecule type: protein
 A:Residues: 1-6, 'X', 8-13, 'XXX', 17-18, 'XX', 21, 'X', 23-25, 'X', 27-29 <ST2>
 R:Einhorn, C.; Bozas, S.E.; Tekkanen, H.; Kirsbaum, L.; Metsco, J.; Murphy, B.; Walke
 Biochim. Biophys. Acta 1086, 255-260, 1991
 A:Title: The apolipoprotein A-I binding protein of placenta and the SP-40,40 protein
 A:Reference number: A56815; MUID:92075698
 A:Accession: A56815
 A:Molecule type: protein
 A:Residues: 25-31, 'P', 33 <EHN>
 A:Experimental source: serum
 A:Note: sequence extracted from NCBI backbone (NCBIP:69759)
 A:Note: 32-Trip was also found
 R:Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vlagne, J.; Kane, J.P.
 Biochemistry 33, 1988-1993, 1994
 A:Title: Identification of proteins associated with apolipoprotein A-I-containing lip
 A:Reference number: A54223; MUID:94162201
 A:Accession: A54223
 A:Molecule type: protein
 A:Residues: 25-39 <RUN>
 R:Mouilevsky, N.; Roobol, C.; Loriau, R.; Guillaume, J.P.; Jacobs, P.; Cravador, A.;
 DNA 8, 429-436, 1989
 A:Title: Production of human recombinant proapolipoprotein A-I in Escherichia coli: p
 A:Reference number: I39476; MUID:89377481
 A:Accession: I39476
 A:Molecule type: mRNA
 A:Residues: 19-267 <RES>
 A:Cross-references: GB:M29068; NID:q178774; PIDN:AAA51747.1; PID:q178775
 R:Higuchi, K.; Law, S.W.; Hoeg, J.M.; Schumacher, U.K.; Meglin, N.; Brewer, H.B.
 J. Biol. Chem. 263, 18530-18536, 1988
 A:Title: Tissue-specific expression of apolipoprotein A-I (ApoA-I) is regulated by th
 A:Reference number: I39475; MUID:89054040
 A:Accession: I39475
 A:Molecule type: DNA
 A:Residues: 1-14 <RE2>
 A:Cross-references: GB:J04066; NID:q178763; PIDN:AAA51746.1; PID:q553183
 R:Breslow, J.L.
 Annu. Rev. Biochem. 54, 699-727, 1985
 A:Title: Human apolipoprotein molecular biology and genetic variation.
 A:Reference number: A90042; MUID:85278004
 A:Contents: annotation: review of sequences, variants and gene location
 R:Hoeg, J.M.; Meng, M.S.; Roman, R.; Fairwell, T.; Brewer Jr., H.B.
 J. Biol. Chem. 261, 3911-3914, 1986
 A:Title: Human apolipoprotein A-I. Post-translational modification by fatty acid acyl
 A:Reference number: A92577; MUID:86140194
 A:Contents: annotation: acylation with palmitate
 A:Note: an undetermined serine or threonine is acylated by fatty acid; the acylating
 R:Law, S.W.; Brewer, H.B.
 J. Biol. Chem. 260, 12810-12814, 1985
 A:Title: Tangier disease: The complete mRNA sequence encoding for preproapo-A-I.
 A:Reference number: I55236; MUID:86008382
 A:Accession: I55236
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-143, 'D', 145-267 <RE3>
 A:Cross-references: GB:M1191; NID:q178776; PIDN:AAA5545.1; PID:q178777
 C:Comment: Apolipoprotein A-I precursor is synthesized in the liver and small intesti
 proteins (HDL) in plasma.
 C:Genetics:
 A:Gene: GDB:APOA1
 A:Cross-references: GDB:119684; OMIM:107680
 A:Map position: 11q23.3-11q23.3
 A:Introns: 15/1; 67/2
 C:Function:
 A:Description: participates in the reverse transport of cholesterol from tissues to t
 sterol acyltransferase (LCAT); noncovalently binds and stabilizes prostacyclin (PGI-2

C:Superfamily: apolipoprotein A-I
 C:Keywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid binding; lipid
 F:1-18/Domain: signal sequence #status experimental <SIG>
 F:19-24/Domain: propeptide #status experimental <PRO>
 F:25-267/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 100.0%; Score 1362; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.5e-69;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAAYLTAVLFLTGSGARHFWQDEPPQSPMDRVKDLATVYVDLKDGRDYVSQFEGS 60
 DB 1 MKAAYLTAVLFLTGSGARHFWQDEPPQSPMDRVKDLATVYVDLKDGRDYVSQFEGS 60
 QY 61 ALGKQNLKLLDNWDSVSTFSKLRQGLGVTOEFMDNLEKEFEGLRQEMSKDLEEVAK 120
 DB 61 ALGKQNLKLLDNWDSVSTFSKLRQGLGVTOEFMDNLEKEFEGLRQEMSKDLEEVAK 120
 QY 121 VQPYLDFOKKQWQEMELRYQKVEPLRAELQEGAROKLHELQKLSPLGEMRDRARAHV 180
 DB 121 VQPYLDFOKKQWQEMELRYQKVEPLRAELQEGAROKLHELQKLSPLGEMRDRARAHV 180
 QY 181 DALRTHLAPYSDLRQRLAARLEALKENGARLAETHAKATEHLSTLSKAKPALEDLRQ 240
 DB 181 DALRTHLAPYSDLRQRLAARLEALKENGARLAETHAKATEHLSTLSKAKPALEDLRQ 240
 QY 241 GLLPVLESFKVSFLSALEETTKLNTQ 267
 DB 241 GLLPVLESFKVSFLSALEETTKLNTQ 267

RESULT 2

JS0079
 apolipoprotein A-I precursor - baboon
 C:Species: Papio sp. (baboon)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Jun-1997
 C:Accession: JS0079
 R:Hiton, J.E.; Borenstein, S.; Cox, L.A.; Rainwater, D.L.; Vandenberg, J.L.
 Gene 74, 483-490, 1988
 A:Title: The baboon gene for apolipoprotein A-I: characterization of a cDNA clone and its
 A:Reference number: JS0079; MUID:89232739
 A:Accession: JS0079
 A:Molecule type: mRNA
 A:Residues: 1-267 <HI>
 A:Experimental source: Liver
 C:Comment: This protein is the principal protein component of high density lipoprotein
 C:Comment: This protein serves as a cofactor for lecithin cholesterol acyltransferase
 C:Comment: This protein contains a region of repeated amino acids which form amphipathic
 C:Genetics:
 A:Gene: apoA1
 C:Superfamily: apolipoprotein A-I
 C:Keywords: HDL; lipid binding; lipoprotein
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-267/Product: apolipoprotein A-I #status predicted <LAI>
 F:123-144,145-166,167-188,189-210,211-232,233-254/Region: tandem repeats

Query Match 95.9%; Score 1306; DB 2; Length 267;
 Best Local Similarity 95.1%; Pred. No. 2e-66;

Matches 254; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKAAYLTAVLFLTGSGARHFWQDEPPQSPMDRVKDLATVYVDLKDGRDYVSQFEGS 60
 DB 1 MKAAYLTAVLFLTGSGARHFWQDEPPQSPMDRVKDLATVYVDLKDGRDYVSQFEGS 60
 QY 61 ALGKQNLKLLDNWDSVSTFSKLRQGLGVTOEFMDNLEKEFEGLRQEMSKDLEEVAK 120
 DB 61 ALGKQNLKLLDNWDSVSTFSKLRQGLGVTOEFMDNLEKEFEGLRQEMSKDLEEVAK 120
 QY 121 VQPYLDFOKKQWQEMELRYQKVEPLRAELQEGAROKLHELQKLSPLGEMRDRARAHV 180
 DB 121 VQPYLDFOKKQWQEMELRYQKVEPLRAELQEGAROKLHELQKLSPLGEMRDRARAHV 180

QY 181 DALRTHLAPYSDLRQRLAARLEALKENGARLAETHAKATEHLSTLSKAKPALEDLRQ 240
 DB 181 DALRTHLAPYSDLRQRLAARLEALKENGARLAETHAKATEHLSTLSKAKPALEDLRQ 240
 QY 241 GLLPVLESFKVSFLSALEETTKLNTQ 267
 DB 241 GLLPVLESFKVSFLSALEETTKLNTQ 267

RESULT 3

A26529
 apolipoprotein A-I precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 30-Sep-1989 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999
 C:Accession: A26529; A26627; S23135; A57766
 R:Polites, H.G.; Melchior, G.W.; Castle, C.K.; Marotli, K.R.
 Gene 49, 103-110, 1986
 A:Title: The primary structure of cynomolgus monkey apolipoprotein A-I deduced from c
 A:Reference number: A26529; MUID:87191989
 A:Accession: A26529
 A:Molecule type: mRNA
 A:Residues: 1-267 <POL>
 A:Cross-references: GB:M5411; NID:g342074; PIDN:AAA36834.1; PID:g342075
 R:Herbert, P.N.; Bausserman, L.L.; Lynch, K.M.; Saitelli, A.L.; Kantor, M.A.; Nicolo
 Biochimistry 26, 1457-1463, 1987
 A:Title: Homologues of the human C and A apolipoproteins in the Macaca fascicularis (C
 A:Reference number: A26627; MUID:87185451
 A:Accession: A26627
 A:Molecule type: protein
 A:Residues: 25-48 <HER>
 R:Murray, R.W.; Marotli, K.R.
 Biochim. Biophys. Acta 1131, 207-210, 1992
 A:Title: Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene and cor
 A:Reference number: S23135; MUID:92305062
 A:Accession: S23135
 A:Molecule type: DNA
 A:Residues: 1-12, 'L', 14-267 <MUR>
 A:Cross-references: GB:M83242; NID:g342070; PIDN:AAA36832.1; PID:g342071
 R:Sorci, Thomas, M.; Kearns, M.W.
 J. Biol. Chem. 266, 18045-18050, 1991
 A:Title: Transcriptional regulation of the apolipoprotein A-I gene.
 A:Reference number: A57766; MUID:92011532
 A:Accession: A57766
 A:Molecule type: DNA
 A:Residues: 1-10 <RES>
 A:Cross-references: GB:M69223; NID:g342066; PIDN:AAA36831.1; PID:g553820
 C:Comment: The precursor is synthesized in the liver and small intestine. The propept
 C:Comment: ApoA-I makes up about 70% of the protein of the high density lipoproteins
 C:Comment: promoting cholesterol efflux from tissues and by acting as a cofactor for the lecith
 C:Genetics:
 A:Introns: 15/1; 67/2
 C:Superfamily: apolipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem r
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PP>
 F:25-267/Product: apolipoprotein A-I #status predicted <MAT>

Query Match 95.4%; Score 1299; DB 1; Length 267;
 Best Local Similarity 94.8%; Pred. No. 5e-66;

Matches 253; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKAAYLTAVLFLTGSGARHFWQDEPPQSPMDRVKDLATVYVDLKDGRDYVSQFEGS 60
 DB 1 MKAAYLTAVLFLTGSGARHFWQDEPPQSPMDRVKDLATVYVDLKDGRDYVSQFEGS 60
 QY 61 ALGKQNLKLLDNWDSVSTFSKLRQGLGVTOEFMDNLEKEFEGLRQEMSKDLEEVAK 120
 DB 61 ALGKQNLKLLDNWDSVSTFSKLRQGLGVTOEFMDNLEKEFEGLRQEMSKDLEEVAK 120
 QY 121 VQPYLDFOKKQWQEMELRYQKVEPLRAELQEGAROKLHELQKLSPLGEMRDRARAHV 180
 DB 121 VQPYLDFOKKQWQEMELRYQKVEPLRAELQEGAROKLHELQKLSPLGEMRDRARAHV 180

Db 121 VQPYLDPOKKWQEMELRYKQVEPLRLAEHSGTRQKHLHEKLSPLGEEVDRARAHV 180
 QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAIEYHAKAHEHSTLSEKAKPALEDLRQ 240
 Db 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAIEYHAKAHEHSTLSEKAKPALEDLRQ 240
 QY 241 GLLPVLESFKVSFLSALEETKRLNTQ 267
 Db 241 GLLPVLESFKVSFLSALEETKRLNTQ 267

RESULT 4

LPGAI

apolipoprotein A-I precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C>Date: 17-Dec-1982 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
 C:Accession: A60940; A03092; A61418
 C:Accession: A60940; A03092; A61418
 J:Luco, C.C.; Li, W.H.; Chan, L.
 J: Lipid Res. 30, 1735-1746, 1989
 A:Title: Structure and expression of dog apolipoprotein A-I, E, and C-I mRNAs: implications
 A:Reference number: A60940; MUID:90132271
 A:Accession: A60940
 A:Molecule type: mRNA
 A:Residues: 1-266 <LUO>
 R:Chung, H.; Randolph, A.; Reardon, I.; Heinrikson, R.L.
 J: Biol. Chem. 257, 2961-2967, 1982
 A:Title: The covalent structure of apolipoprotein A-I from canine high density lipoproteins
 A:Reference number: A03092; MUID:82142425
 A:Accession: A03092
 A:Molecule type: protein
 A:Residues: 25-167, 'G', 169-201, 'Q', 203-234, 'Q', 236-266 <CHU>
 R:Nakai, T.; Whayne, T.F.; Tang, J.
 FEBS Lett. 64, 409-411, 1976
 A:Title: The amino- and carboxyl-terminal sequences of canine apolipoprotein A-I.
 A:Reference number: A61418; MUID:76210910
 A:Accession: A61418
 A:Molecule type: protein
 A:Residues: 25-56, 'Z', 261-262, 'A' <NAK>
 C:Superfamily: apolipoprotein A-I
 C:Keywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid transport; L1
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PRO>
 F:25-266/Product: apolipoprotein A-I #status experimental <MAT>

Query Match

Best Local Similarity 85.3%; Score 1161.5; DB 1; Length 266;
 Matches 227; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

QY 1 MKAVALTLAVLFLTGSQARHFHWOODEPSPMDRVKDLATVYVDLAKSGRDYVSOFEGS 60
 Db 1 MKAVALTLAVLFLTGSQARHFHWOODE-POSPMDRVKDLATVYVDLAKSGRDYVSOFEGS 59
 QY 61 ALGKOLNKLNDMWDVSTFSKLRLEQIGVTOEFMDNLEKEFEGRLQEMSKDLEEVKAK 120
 Db 60 ALGKOLNKLNDMWDVSTFSKLRLEQIGVTOEFMDNLEKEFEGRLQEMSKDLEEVKAK 119
 QY 121 VQPYLDPOKKWQEMELRYKQVEPLRLAEHSGTRQKHLHEKLSPLGEEVDRARAHV 180
 Db 120 VQPYLDPOKKWQEMELRYKQVEPLRLAEHSGTRQKHLHEKLSPLGEEVDRARAHV 179
 QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAIEYHAKAHEHSTLSEKAKPALEDLRQ 240
 Db 180 DALRTHLAPYSDELRLQRLAARLEALKENGARLAIEYHAKAHEHSTLSEKAKPALEDLRQ 239
 QY 241 GLLPVLESFKVSFLSALEETKRLNTQ 267
 Db 240 GLLPVLESFKVSFLSALEETKRLNTQ 266

RESULT 5

LPRB12

apolipoprotein A-I precursor (clone 2zap A1) - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999
 C:Accession: S06064
 R:Parakevopoulos, T.B.; Krilis, A.; Zannis, V.
 Submitted to the EMBL Data Library, July 1989
 A:Reference number: S06064
 A:Accession: S06064
 A:Molecule type: mRNA
 A:Residues: 1-266 <PAR>
 A:Cross-references: EMBL:X15908; NID:g1457; PIDN:CAA34024.1; PID:g1458
 C:Comment: This protein is synthesized in the small intestine.
 C:Comment: This protein is a major component of the high density lipoproteins in plas
 C:Superfamily: apolipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem r
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PRO>
 F:25-266/Product: apolipoprotein A-I #status experimental <MAT>

Query Match

Best Local Similarity 80.8%; Score 1100.5; DB 1; Length 266;
 Matches 214; Conservative 25; Mismatches 27; Indels 1; Gaps 1;

QY 1 MKAVALTLAVLFLTGSQARHFHWOODEPSPMDRVKDLATVYVDLAKSGRDYVSOFEGS 60
 Db 1 MKAVALTLAVLFLTGSQARHFHWOODE-PRSSWKIKDFATVYVDLAKSGRDYVSOFEGS 59
 QY 61 ALGKOLNKLNDMWDVSTFSKLRLEQIGVTOEFMDNLEKEFEGRLQEMSKDLEEVKAK 120
 Db 60 ALGKOLNKLNDMWDVSTFSKLRLEQIGVTOEFMDNLEKEFEGRLQEMSKDLEEVKAK 119
 QY 121 VQPYLDPOKKWQEMELRYKQVEPLRLAEHSGTRQKHLHEKLSPLGEEVDRARAHV 180
 Db 120 VQPYLDPOKKWQEMELRYKQVEPLRLAEHSGTRQKHLHEKLSPLGEEVDRARAHV 179
 QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAIEYHAKAHEHSTLSEKAKPALEDLRQ 240
 Db 180 DLTKTLAPYSDELRLQRLAARLEALKENGARLAIEYHAKAHEHSTLSEKAKPALEDLRQ 239
 QY 241 GLLPVLESFKVSFLSALEETKRLNTQ 267
 Db 240 GLLPVLESFKVSFLSALEETKRLNTQ 266

RESULT 6

apolipoprotein A1 - pig

C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
 C:Accession: A46018
 R:Birchbauer, A.; Knippling, G.; Juritsch, B.; Aschauer, H.; Zechner, R.
 Genomics 15, 643-652, 1993
 A:Title: Characterization of the apolipoprotein A1 and CIII genes in the domestic pig
 A:Reference number: A46018; MUID:93224154
 A:Accession: A46018
 A:Status: preliminary
 A:Molecule type: DNA; protein
 A:Residues: 1-265 <BIR>
 A:Cross-references: GB:L00626; NID:g164358; PIDN:AAA3092.1; PID:g164359
 A:Note: sequence extracted from NCBI backbone (NCBI:129509, NCBI:129511)
 C:Superfamily: apolipoprotein A-I

Query Match

Best Local Similarity 80.8%; Score 1100; DB 2; Length 265;
 Matches 216; Conservative 19; Mismatches 30; Indels 2; Gaps 2;

QY 1 MKAVALTLAVLFLTGSQARHFHWOODEPSPMDRVKDLATVYVDLAKSGRDYVSOFEGS 60
 Db 1 MKAVALTLAVLFLTGSQARHFHWOODE-POSPMDRVKDLATVYVDLAKSGRDYVSOFEGS 59
 QY 61 ALGKOLNKLNDMWDVSTFSKLRLEQIGVTOEFMDNLEKEFEGRLQEMSKDLEEVKAK 120
 Db 61 ALGKOLNKLNDMWDVSTFSKLRLEQIGVTOEFMDNLEKEFEGRLQEMSKDLEEVKAK 120

[illegible]

A; Introns: 15/1; 66/2

A:Title: Synthesis of apolipoprotein A-I in pig brain microvascular endothelial cells.
A:Reference number: JQ0704; MUID:90132667
A:Accession: JQ0704
A:Molecule type: mRNA
A:Residues: 1-231 <WEI>
A:Note: the authors translated the codon CAG for residue 124 as His and GAC for residue 231 as Asp.
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; lipid binding; lipid transport; lipoprotein; pig

		67.8%;	Score 924;	DB 2;	Length 231;	
	Query Match	Similarity 79.0%;	Pred. No. 4e-45;			
	Best Local	Similarity 18;	Mismatches 29;	Indels 2;	Gaps 2;	
	Matches 184;	Conservative				
QY	35	VKDLATVYVDVLKDSGRDYVSQFEGSALGKOLNKLIDNMDSDVSPFSKLREQLGPVTOE	94			
Db	1	VKDFATVYDAIIGDSGRDYVAQFEASALGKHNLKLIIDNMDSDSTFTYKREDLGPVTOE	60			
QY	95	FMDNKKETEGRLROEMSKDLEEVKAKKQPYRLDDQKKMOEMELTYRQKVEPLPAELIQEGA	154			
Db	61	FMDNLEKEETALQKKMSKDLKEEVKKRQVPYRDDQPNKKMOEMEETYYRKKM-PLAEEFREGA	119			
QY	155	RQRLHLELOEKLSPLEGEEMDRARAHAHVADLRTHLAPYSDLELQRLRLAARLELKNNGARLGA	214			
Db	120	RQKVOELOERLSPLEBELRDLRAHAHVADLRQHAVAPYSDDLQRRNAARFEALKE-GGDSILA	178			
QY	215	EYAAKATTEHLSTLSEKAKPALDRLQGLLPVLESEFKVSFLSALAEVYTKKLNTO	267			
Db	179	EYAAKAOEOLKALGEAKPALDRLQGLLPVLENIKKVIAAILAIDEMSKKLNQ	231			

RESULT 13

apolipoprotein A-I precursor - mouse
S22420

C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence,revision 13-Jan-1995 #text,change 13-Aug-1999
C:Accession: S22420; S22421; A44364
R:Stoffel, W.; Mueller, R.; Blinczek, E.; Hofmann, K.
Biol. Chem. Hoppe-Seyler 373, 187-193, 1992

A:Title: Mouse apolipoprotein AI. cDNA-derived primary structure, gene organisation and
A:Reference number: S22420; MUID:92281682

A:Accession: S22420

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-264 <STO>

A:Cross-references: EMBL:X64262; NID:g50014; PIDN:CA445560.1; PID:g50015
A:Accession: S22421

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <STR2>

A:Cross-references: EMBL:X64263; NID:g50020; PIDN:CA445561.1; PID:g50021
R:Janusz, J.L.; Azrolan, N.; O'Connell, A.; Aalto-Setälä, K.; Breslow, J.L.
Genomics 14, 1081-1088, 1992

A:Title: Characterization of the mouse apolipoprotein ApoA-1/ApoC-3 gene locus: genomic
A:Reference number: A44364; MUID:93122774

A:Accession: A44364

A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-264 <JAN>

A:Note: sequence extracted from NCBI backbone (NCBIN:122400, NCBI:P:122407)
C:Genetics:

A:Introns: 15/1; 66/2
A:Superfamily: apolipoprotein A-I

[illegible]

RESULT 14
JC1237
apolipoprotein A-I precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-1993
C:Accession: JC1237
R:Boyle, T. P.; Marotti, K. R.
Gene 117, 243-247, 1992
A:Title: Structure of the murine gene encoding apolipoprotein A-I.
A:Reference number: JC1237; MUID:92347700
A:Accession: JC1237
A:Molecule type: DNA
A:Residues: 1-262 <BO>
A:Cross-references: GR:M77801
C:Genetics:
A:Gene: ApoA-I
A:Introns: 15/1; 66/2
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; I
T:1-24/Domains: signal sequence #status predicted <SIG>
T:25-267/Product: apolipoprotein A-I #status predicted <MAT>

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Query Match:	Similarity	67.1%;	Pred.	No.1-2e-43;			
Matches	173;	Conservative	37;	Mismatches	45;	Indels	3; Gaps
QY	1	KKAAYLTAVLVLGSGAARHFWOODEPPPOSPWDRKADLATVYVDLKDSDRDYVSQFEES	60				
Dd	1	KKAAVLLVAFLVFPLTGSQAHHVVCODE-PQSQDKWKCDPANYVVAVKDSGRDYVSDESS	59				
QY	61	ALGKOLULKLNDWDSDVTSTFSKRLREQLGAPVIOEPMIDLKEFTGLSLOEKSKOLEVKKK	120				
Dd	60	SLEGGCLNMLILEMWDITLGSTVSQDLERIGPLTRDFMDNLKETDWMLEKEDNNKDLVEKKR	119				
QY	121	VQPYLDLPQKWEOEMELYRQRVEPLRAELDEGAROKLHELOEKLSPLEGMEDRRARAHV	180				
Dd	120	VQPIIDEFQKKMEVDLYLRQVAPLGALEBESAROKLOETLOGRLSPVAEEFPDRMRTHV	179				
QY	181	DALSTHLAPYSDDLRLRALRLALEKNGARIAEVNAHKATEHTSTSEAKPALDELHQ	240				
Dd	180	DSLRTQLAHPISDEDMRSLSLORLAELKS--PLINETHTRAKTHIKTLGERARPALDELKH	237				
QY	241	GILPVLSESEKVSFSLALE	258				
Dd	238	SLMPMETIETLKTKAOSVIE	255				

Query Match	66.43;	Score 904.5;	DB 2;	Length 264;
Best Local Similarity	65.28;	Prod. No. 5.8e-44;		
Matches 174;	Conservative 41;	Mismatches 49;	Indels 3;	Gaps 2;
OY	1	MKAAYTLAVLVLTSQARHFWQDEPQSMDEKRLATVYVDVLKDSGRDVSQFEGS	60	
		:::		
Db	1	MKAAYTLAVLVLTSQAMHWQDE-PQSMDEKRFANFYVDAYDAKDSGRDVSQFESS	59	

A;Title: Linkage, evolution, and expression of the rat apolipoprotein A-I, C-III, and A-IV
 A;Reference number: A92558; MID:87008540
 A;Accession: A24700
 A;Molecule type: DNA
 A;Residues: 1-259 <HAD>
 A;Cross-references: EMBL:J02597; NID:g202935; PIDN:AAA0745.1; PID:g202939
 R;Poncin, J.E.; Martial, J.A.; Gielen, J.E.
 Eur. J. Biochem. 140, 493-498, 1984
 A;Title: Cloning and structure analysis of the rat apolipoprotein A-I cDNA.
 A;Reference number: S00298; MID:84207987
 A;Accession: S00298
 A;Molecule type: mRNA
 A;Residues: 1-259 <PON>
 A;Cross-references: GB:M00001; EMBL:X00558; NID:g202944; PIDN:AAA0749.1; PID:g202945
 R;Gordon, J.I.; Smith, D.P.; Andy, R.; Alpers, D.H.; Schonfeld, G.; Strauss, A.W.
 J. Biol. Chem. 257, 971-978, 1982
 A;Title: The primary translation product of rat intestinal apolipoprotein A-I mRNA is an
 A;Accession number: A05314; MID:82098162
 A;Molecule type: protein
 A;Residues: 1-18, 'X', 20-21, 'X', 23-28, 'X', 30-38, 'X', 40-41, 'X', 43-45 <GOR>
 C;Comment: This protein is synthesized in the liver and small intestine. The propeptide
 C;Genetics: This protein is a major component of the high density lipoproteins in plasma.
 A;Introns: 15/1; 66/2
 C;Superfamily: apolipoprotein A-I
 C;Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipoprotein
 F;1-18/Domain: signal sequence #status experimental <Sig>
 F;19-24/Domain: propeptide #status experimental <Pro>
 F;25-259/Product: apolipoprotein A-I #status experimental <Mat>

Query Match 62.4%; Score 849.5; DB 2; Length 259;
 Best Local Similarity 63.0%; Pred. No. 6.7e-41;
 Matches 167; Conservative 35; Mismatches 56; Indels 7; Gaps 3;

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QY      1 MKAAVLTIAVLTGSGARHFQODEPPOSMPDRVKDLATVYVDVLKDSGRDVSQEGS 60
      1 MKAAVLAVALVFLTGCAWFEWQODE-POSQMDRVKDFATVYDAVKDSGRDVSQESS 59
DB
QY      61 ALGKQNLKLLDNMDSVTSFSLRQOLGPTQEFWDNLEKETEGILRQMSKDLSEVKAK 120
      60 TLGKQNLNLNDWMDTLGSLGRLQGLPTQEFMANLEKETDMLRNEMNKDLENVKOK 119
DB
QY      121 VQPYLDDFQKKQOEMELTRQKVEPTLRAELQEGAROKLHLEQKLSPLGEMRDRAHAY 180
      120 MOPHLDEFQEKWNEEYARQKLEPLGTGLHKNKAK---EMOPHLKVVAAEEFRDRRVNA 175
DB
QY      181 DALRTHLAPEYSDRLRRLAARLEALKENGARLAELYHAKATEHTLSLSEKAPALDDLRQ 240
      176 DALRAKFGLYSDQRENLARLQRLTEIRKNH--PTLIEYHTKASDHKTLGKAKAPALDDLGQ 233
DB
QY      241 GLLPVLESFQKVSFLSALLEEYTKLN 265
      234 GLMPVLEAWKAKIMSMIDEAKKTLN 258
DB
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Search completed: September 22, 2002, 12:06:28
 Job time: 323 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:05:20 ; Search time 35.02 Seconds
(without alignments)
295.206 Million cell updates/sec

Title: US-09-803-918a-2

Perfect score: 1362

Sequence: 1 MKAAVLTAVLFLTGSQARH.....SPKVSFLSALEETKRLNTQ 267

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1362	100.0	267	1 APAL_HUMAN	P02647 homo sapien
2	1306	95.9	267	1 APAL_MACFA	P15568 macaca fasc
3	1161.5	85.3	266	1 APAL_CANFA	P02648 canis fami
4	1105	81.1	265	1 APAL_PIG	P18648 sus scrofa
5	1100.5	80.8	266	1 APAL_RABIT	P09809 oryctolagus
6	1077	79.1	265	1 APAL_BOVIN	P15487 bos taurus
7	975.5	71.6	265	1 APAL_TUPGB	O18759 tupia glis
8	904.5	66.4	264	1 APAL_MOUSE	O00623 mus musculu
9	842.5	61.9	259	1 APAL_RAT	P04639 rattus norv
10	705.5	51.8	264	1 APAL_ANAPL	P04236 anas platyr
11	688.5	50.6	264	1 APAL_CHICK	P08280 gallus gall
12	663.5	48.7	264	1 APAL_COTJA	P32918 coturnix co
13	291	21.4	429	1 APAL_MACFA	P33621 macaca fasc
14	275	20.2	366	1 APAL_BRARE	O42363 brachydanto
15	274.5	20.2	366	1 APAL_HUMAN	P06727 homo sapien
16	269	19.8	382	1 APAL_PIG	O46409 sus scrofa
17	268	19.7	391	1 APAL_RAT	P02651 rattus norv
18	259	19.0	362	1 APAL_ONCMY	O57525 oncorhynch
19	251	18.4	395	1 APAL_MOUSE	P06728 mus musculu
20	249.5	18.3	401	1 APAL_PAPAN	O28758 papio anubi
21	247	18.1	262	1 AP12_ONCMY	O57524 oncorhynch
22	247	18.1	262	1 APAL_SALTR	O91488 salmo trutt
23	243.5	17.9	281	1 APAL_BRARE	O42364 brachydanto
24	230.5	16.9	260	1 APAL_SPAKU	O42175 spartus aura
25	220.5	16.2	238	1 APAL_MOUSE	P27007 salmo salar
26	209	15.3	311	1 APAL_MOUSE	P08226 mus musculu
27	198	14.5	312	1 APAL_RAT	P05770 papio anubi
28	190.5	14.0	317	1 APAL_PAPAN	P10517 macaca fasc
29	189.5	13.9	317	1 APAL_MACFA	P18650 sus scrofa
30	188	13.8	317	1 APAL_PIG	P23529 canis fami
31	184	13.5	298	1 APAL_CANFA	P18649 canis fami
32	178.5	13.1	305	1 APAL_HUMAN	P02649 homo sapien
33	174.5	12.8	317	1 APAL_HUMAN	P02649 homo sapien

ALIGNMENTS

RESULT	ID	APAL_HUMAN	STANDARD:	PRT:	267 AA.
AC	P02647;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Apolipoprotein A-I precursor (Apo-AI).				
GN	APOL.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=64221405; PubMed=6328445;				
RA	Sharpe C.R., Sidoli A., Shelley C.S., Lucero M.A., Shoulders C.C.,				
RA	Baralle F.E.;				
RT	"Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA				
RT	abundance.";				
RL	Nucleic Acids Res. 12:3917-3932(1984).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8502665; PubMed=6207999;				
RA	Selhamer J.J., Protter A.A., Frossard P., Levy-Wilson B.;				
RT	"Isolation and DNA sequence of full-length cDNA and of the entire				
RT	gene for human apolipoprotein AI-- discovery of a new genetic				
RT	polymorphism in the apo AI gene.";				
RL	DNA 3:309-317(1984).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83220822; PubMed=6406984;				
RA	Shoulders C.C., Kornblith A.R., Munro B.S., Baralle F.E.;				
RT	"Gene structure of human apolipoprotein AI.";				
RL	Nucleic Acids Res. 11:2827-2837(1983).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83220772; PubMed=6304641;				
RA	Cheung P., Chan L.;				
RT	"Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.";				
RL	Nucleic Acids Res. 11:3703-3715(1983).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84119464; PubMed=6198645;				
RA	Law S.W., Brewer H.B. Jr.;				
RT	"Nucleotide sequence and the encoded amino acids of human				
RT	apolipoprotein A-I mRNA.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 81:66-70(1984).				
RN	[6]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=86008382; PubMed=2995392;				
RA	Law S.W., Brewer H.B. Jr.;				
RT	"Tangier disease. The complete mRNA sequence encoding for				
RT	preproapo-A-I.";				
RL	J. Biol. Chem. 260:12810-12814(1985).				
RN	[7]				

003247 bos taurus
P18287 oryctolagus
P16878 xenopus lae
P12957 gallus gall
O10758 rattus norv
P39922 hydra atten
O08638 mus musculu
O13439 homo sapien
P08799 dictyosteli
O08378 homo sapien
P08776 xenopus lae
Q9uzc8 pyrococcus

- RP SEQUENCE FROM N.A.
RX MEDLINE=84016011; PubMed=6413973;
RA Karathanasis S.K., Zannis V.I., Breslow J.L.;
RT "Isolation and characterization of the human apolipoprotein A-I
RT gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:6147-6151(1983).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=89377481; PubMed=2673706;
RA Mogullevsky N., Roobol C., Loriau R., Guillaume J.P., Jacobs P.,
RA Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,
RA Holmquist L., Carlson L.A., Bollen A.;
RT "Production of human recombinant apolipoprotein A-I in Escherichia
RT coli: purification and biochemical characterization.";
RL DNA 8:429-436(1989).
RN [9]
RP SEQUENCE FROM N.A. (VARIANT TANGIER).
RX MEDLINE=88196137; PubMed=3129297;
RA Makrides S.C., Ruiz-Opazo N., Hayden M., Nussbaum A.L., Breslow J.L.,
RA Zannis V.I.;
RT "Sequence and expression of Tangier apoA-I gene.";
RL Eur. J. Biochem. 173:465-471(1988).
RN [10]
RP SEQUENCE OF 118-267 FROM N.A.
RX MEDLINE=83091059; PubMed=6294659;
RA Breslow J.L., Ross D., McPherson J., Williams H.W., Kurnit D.,
RA Nussbaum A.L., Karathanasis S.K., Zannis V.I.;
RT "Isolation and characterization of cDNA clones for human
RT apolipoprotein A-I.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6861-6865(1982).
RN [11]
RP SEQUENCE OF 19-27.
RX MEDLINE=83256553; PubMed=6409108;
RA Brewer H.B. Jr., Fairwell T., Kay L., Meng M., Roman R., Law S.,
RA Light J.A.;
RT "Human plasma proapoA-I: isolation and amino-terminal sequence.";
RL Biochem. Biophys. Res. Commun. 113:626-632(1983).
RN [12]
RP SEQUENCE OF 25-267.
RX MEDLINE=78123731; PubMed=204308;
RA Brewer H.B. Jr., Fairwell T., Larue A., Roman R., Houser A.,
RA Bronzert T.J.;
RT "The amino acid sequence of human APOA-I, an apolipoprotein isolated
RT from high density lipoproteins.";
RL Biochem. Biophys. Res. Commun. 80:623-630(1978).
RN [13]
RP SEQUENCE OF 25-267.
RX MEDLINE=75133493; PubMed=164450;
RA Baker H.N., Gotto A.M. Jr., Jackson R.L.;
RT "The primary structure of human plasma high density apolipoprotein
RT glutamine I (APOA-I). II. The amino acid sequence and alignment of
RT cyanoogen bromide fragments IV, III, and I.";
RL J. Biol. Chem. 250:2725-2738(1975).
RN [14]
RP SEQUENCE OF 25-56.
RX MEDLINE=88331387; PubMed=3047170;
RA Yui Y., Aoyama T., Morishita H., Takahashi M., Takatsu Y., Kawai C.;
RT "Serum prostacyclin stabilizing factor is identical to apolipoprotein
RT A-I (Apo A-I). A novel function of Apo A-I.";
RL J. Clin. Invest. 82:803-807(1988).
RN [15]
RP SEQUENCE OF 25-48.
RX MEDLINE=89380318; PubMed=2506184;
RA Manjunath P., Marcel Y.L., Uma J., Seidah N.G., Chretien M.,
RA Chapelaire A.;
RT "Apolipoprotein A-I binds to a family of bovine seminal plasma
RT proteins.";
RL J. Biol. Chem. 264:16853-16857(1989).
RN [16]
RP SEQUENCE OF 25-43.
RX MEDLINE=88070603; PubMed=3120314;
RA Pirioli R.P., Ordovas J.M., Rosenberg I., Schaeffer E.J.,
RA Pereira M.E.A.;
RT "Similarity of cruzin, an inhibitor of Trypanosoma cruzi
RT neuraminidase, to high-density lipoprotein.";
RL Science 238:1417-1419(1987).
RN [17]
RP SEQUENCE OF 25-42.
RX TISSUE-Heart;
RT MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1459-1465(1994).
RN [18]
RP PALMITOYLATION.
RX MEDLINE=86140194; PubMed=3005308;
RA Hoeg J.M., Meng M.S., Roman R., Fairwell T., Brewer H.B. Jr.;
RT "Human apolipoprotein A-I. Post-translational modification by fatty
RT acid acylation.";
RL J. Biol. Chem. 261:3911-3914(1986).
RN [19]
RP PROCESSING.
RX MEDLINE=83195100; PubMed=6405383;
RA Zannis V.I., Karathanasis S.K., Keutmann H.T., Goldberger G.,
RA Breslow J.L.;
RT "Intracellular and extracellular processing of human apolipoprotein
RT A-I: secreted apolipoprotein A-I isoprotein 2 is a propeptide.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2574-2578(1983).
RN [20]
RP STRUCTURE BY NMR OF 190-209.
RX MEDLINE=96270776; PubMed=8664326;
RA Wang G., Trelleaven W.D., Cushman R.J.;
RT "Conformation of human serum apolipoprotein A-I(166-185) in the
RT presence of sodium dodecyl sulfate or dodecylphosphocholine by ¹H-NMR
RT and CD. Evidence for specific peptide-SDS interactions.";
RL Biochim. Biophys. Acta 1301:174-184(1996).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (4.0 ANGSTROMS) OF 67-267.
RX MEDLINE=98024124; PubMed=9356442;
RA Borchani D.W., Rogers D.P., Engler J.A., Brouillette C.G.;
RT "Crystal structure of truncated human apolipoprotein A-I suggests a
RT lipid-bound conformation.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12291-12296(1997).
RN [22]
RP VARIANT MILANO.
RX MEDLINE=83109095; PubMed=6401735;
RA Weisgraber K.H., Rall S.C. Jr., Bersot T.P., Mahley R.W.,
RA Franceschini G., Sirtori C.R.;
RT "Apolipoprotein A-IMilano. Detection of normal A-I in affected
RT subjects and evidence for a cysteine for arginine substitution in the
RT variant A-I.";
RL J. Biol. Chem. 258:2508-2513(1983).
RN [23]
RP VARIANT TANGIER.
RX MEDLINE=83300108; PubMed=6412234;
RA Schmitz G., Assmann G., Rall S.C. Jr., Mahley R.W.;
RT "Tangier disease: defective recombination of a specific Tangier
RT apolipoprotein A-I isoforrm (pro-apo A-I) with high density
RT lipoproteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:6081-6085(1983).
RN [24]
RP VARIANT NORWAY.
RX MEDLINE=84289383; PubMed=6432779;
RA Rall S.C. Jr., Weisgraber K.H., Mahley R.W., Ogawa Y., Fielding C.J.,
RA Utermann G., Haas J., Steinmetz A., Menzel H.J., Assmann G.;
RT "Abnormal lecithin:cholesterol acyltransferase activation by a human
RT apolipoprotein A-I variant in which a single lysine residue is
RT deleted.";
RL J. Biol. Chem. 259:10063-10070(1984).
RN [25]
RP SEQUENCE OF 25-107 (VARIANT IOWA).
RX MEDLINE=89050104; PubMed=3142462;
RA Nichols W.C., Dwulet F.E., Liepnieks J., Benson M.D.;
RT "Variant apolipoprotein AI as a major constituent of a human
RT hereditary amyloid.";

Query Match 100.0%; Score 1362; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3,8e-71;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRAVITLAVPLTSGQAHFHWQDEPPSPMDRKADLATVYVVDLKSGRDYVSQFEGS 60
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 DB 1 MKRAVITLAVPLTSGQAHFHWQDEPPSPMDRKADLATVYVVDLKSGRDYVSQFEGS 60
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QY 61 ALGKQNLKLDNDMSVSTFSKLRQGLRPVQEFMDNLEKTEGLRQMSKDLSEYAK 120
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QY 181 DALRTHLAVSDRLRQRLAARLEALKENGARLAETVHAKATHEHLSLSEKAPALEDLRQ 240
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 DB 181 DALRTHLAVSDRLRQRLAARLEALKENGARLAETVHAKATHEHLSLSEKAPALEDLRQ 240
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QY 241 GLPYLESEFKVSFLSALEETTKLNTQ 267
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 DB 241 GLPYLESEFKVSFLSALEETTKLNTQ 267
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RESULT 2
 APAL_MACFA STANDARD; PRT: 267 AA.
 AC P1568: P17929:
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Macaca fascicularis (Crah eating macaque) (Cynomolgus monkey), and
 OS Papio hamadryas (Hamadryas baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NCBI_TaxID=9541, 9557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=87191989; PubMed=3106152;
 RA Pollitts H.G., Melchior G.W., Castle C.K., Marotti K.R.;
 RT "The primary structure of cynomolgus monkey apolipoprotein A-I
 deduced from the cDNA sequence: comparison to the human sequence.";
 RL Gene 49:103-110(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=92305062; PubMed=1610902;
 RA Murray R.W., Marotti K.R.;
 RT "Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene
 and corresponding flanking regions";
 RL Biochim. Biophys. Acta 1131:207-210(1992).
 RN [3]
 RP SEQUENCE OF 25-48.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=87185451; PubMed=3105581;
 RA Herbert P.N., Bauseman L.L., Lynch K.M., Saritelli A.L.,
 RA Kantor M.A., Nicolosi R.J., Shulman R.S.;
 RT "Homologues of the human C and A apolipoproteins in the Macaca
 fascicularis (cynomolgus) monkey";
 RL Biochemistry 26:1457-1463(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas; TISSUE=Liver;
 RX MEDLINE=89232739; PubMed=2907746;
 RA Hixson J.E., Borenstein S., Cox L.A., Rainwater D.L., Vandeberg J.L.;
 RT "The baboon gene for apolipoprotein A-I: characterization of a cDNA
 clone and identification of DNA polymorphisms for genetic studies of

RT cholesterol metabolism.";
 RL Gene 74:483-490(1988).
 RN [5]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC SPECIES=M.fascicularis;
 RA Sorci-Thomas M.;
 RL Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
 CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: M15411; AAA36834.1; -;
 DR EMBL: M83242; AAA36832.1; -;
 DR EMBL: M35634; AAA35380.1; -;
 DR EMBL: M69223; AAA36831.1; -;
 DR PIR: A26529; A26529.
 DR PIR: A26627; A26627.
 DR PIR: JS0079; JS0079.
 DR PIR: S23135; S23135.
 DR HSSP: P02647; 10DR.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 267
 FT DOMAIN 68 267
 FT REPEAT 68 89
 FT REPEAT 90 111
 FT REPEAT 112 122
 FT REPEAT 123 144
 FT REPEAT 145 166
 FT REPEAT 167 188
 FT REPEAT 189 210
 FT REPEAT 211 232
 FT REPEAT 233 243
 FT REPEAT 244 267
 FT REPEAT 267 267
 FT CONFLICT 13 13 L -> P (IN REF. 1).
 FT SEQUENCE 267 AA; 30735 MW; 869955C024088E21 CRC64;

Query Match 95.9%; Score 1306; DB 1; Length 267;
 Best Local Similarity 95.1%; Pred. No. 5,7e-68;
 Matches 254; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKRAVITLAVPLTSGQAHFHWQDEPPSPMDRKADLATVYVVDLKSGRDYVSQFEGS 60
 |||||||
 DB 1 MKRAVITLAVPLTSGQAHFHWQDEPPSPMDRKADLATVYVVDLKSGRDYVSQFEGS 60
 |||||||

QY 61 ALGKQNLKLDNDMSVSTFSKLRQGLRPVQEFMDNLEKTEGLRQMSKDLSEYAK 120
 |||||||
 DB 61 ALGKQNLKLDNDMSVSTFSKLRQGLRPVQEFMDNLEKTEGLRQMSKDLSEYAK 120
 |||||||

QY 121 VOPYLDDFOKKWOEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLGEEMRDRARAHV 180
 |||||||
 DB 121 VOPYLDDFOKKWOEMELYRQKVEPLRAELQEGARQKLHELOEKLSPLGEEMRDRARAHV 180
 |||||||

QY 181 DALRTHLAVSDRLRQRLAARLEALKENGARLAETVHAKATHEHLSLSEKAPALEDLRQ 240
 |||||||
 DB 181 DALRTHLAVSDRLRQRLAARLEALKENGARLAETVHAKATHEHLSLSEKAPALEDLRQ 240
 |||||||

QY 241 GLIPVLESEKVSFLSALEEYTKKLNTQ 267
 |||||||||||||||||||||
 Db 241 GLIPVLESEKVSFLSALEEYTKKLNTQ 267
 RESULT 3
 APAL_CANFA STANDARD; PRT; 266 AA.
 ID APAL_CANFA
 AC P02648;
 DT 21-JUN-1986 (Rel. 01, Created)
 DF 15-DEC-1998 (Rel. 37, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=90132271; PubMed=2515239;
 RA Luo C.-C., Li W.-H., Chan L.;
 RT "Structure and expression of dog apolipoprotein A-I, E, and C-I
 RT mRNAs: implications for the evolution and functional constraints of
 RT apolipoprotein structure.";
 RL J. Lipid Res. 30:1735-1746(1989).
 RN [2]
 RP SEQUENCE OF 25-266.
 RX MEDLINE=82142425; PubMed=6801039;
 RA Chung H., Randolph A., Reardon I., Heinrikson R.L.;
 RT "The covalent structure of apolipoprotein A-I from canine high
 RT density lipoproteins.";
 RL J. Biol. Chem. 257:2961-2967(1982).
 RN [3]
 RP SEQUENCE OF 25-57 AND 262-265.
 RX MEDLINE=76210910; PubMed=179887;
 RA Nakai T., Whayne T.F., Tang J.;
 RT "The amino- and carboxyl-terminal sequences of canine apolipoprotein
 RT A-I.";
 RL FEBS Lett. 64:409-411(1976).
 RN [4]
 RP SEQUENCE OF 25-37.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS. SYNTHESIZED IN THE LIVER AND SMALL INTESTINE.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 DR HSP: P02647; LDPGAL.
 DR HSC-2DPAGE: P02648; DOG.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 FT Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 266 APOLOPROTEIN A-I.
 FT DOMAIN 67 266 10 X APPROXIMATE TANDEM REPEATS.
 FT REPEAT 67 88 1.
 FT REPEAT 89 110 2.
 FT REPEAT 111 121 3 (HALF-LENGTH).
 FT REPEAT 122 143 4.
 FT REPEAT 144 165 5.

FT REPEAT 166 187 6.
 FT REPEAT 188 209 7.
 FT REPEAT 210 231 8.
 FT REPEAT 232 242 9 (HALF-LENGTH).
 FT REPEAT 243 266 10.
 FT CONFLICT 168 168 A -> G (IN REF. 2).
 FT CONFLICT 202 202 E -> Q (IN REF. 2).
 FT CONFLICT 235 235 E -> Q (IN REF. 2).
 FT CONFLICT 264 266 NAO -> A (IN REF. 3).
 SQ SEQUENCE 266 AA; 30196 MW; A3202620C28A869D CRC64;
 Query Match 85.3%; Score 1161.5; DB 1; Length 266;
 Best Local Similarity 85.0%; Pred. No. 9.2e-60;
 Matches 227; Conservative 19; Mismatches 20; Indels 1; Gaps 1;
 QY 1 MRAVITLAVLELTGSOAHFWQDEPPQSPWDRKDLATVYVDVKSGSDYVQFSGS 60
 |||||
 Db 1 MRAALTLTAVLELTGSOAHFWQDE-PPSPWDRKDLATVYVDVKSGSDYVQFSGS 59
 QY 61 ALGKQNLKLLDNWDSVTSFSLREQLGPTVQEFWMDLEKETEGLRQMSKDLSEYRAK 120
 |||||
 Db 60 ALGKQNLKLLDNWDSLSSTVTKLRQIGPTVQEFWMDLEKETEVLRQMSKDLSEYRAK 119
 QY 121 VQPYLDDFOKKQWQEMELYRQVVEPLRAELQGCARQKHELOKISPLGEEKRDRAAHV 180
 |||||
 Db 120 VQPYLDDFOKKQWQEEVELYRQVAPLGSSELREGARQKLOELOKLSPLAEELRDARVHV 179
 QY 181 DAKTHLAPYSDLRRLRLARLEALKENGCGARLAETNHAETNLSLSEKAPALEDLRO 240
 |||||
 Db 180 DAKRAQLAPYSDLRRLRLARLEALKENGCGARLAETNHAETNLSLSEKAPALEDLRO 239
 QY 241 GLIPVLESEKVSFLSALEEYTKKLNTQ 267
 |||||
 Db 240 GLIPVLESEKVSFLSALEEYTKKLNTQ 266
 RESULT 4
 APAL_PIG STANDARD; PRT; 265 AA.
 ID APAL_PIG
 AC P18648;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93224154; PubMed=8468059;
 RA Birchbauer A., Knippling G., Juritsch B., Aschauer H., Zechner R.;
 RT "Characterization of the apolipoprotein AI and CIII genes in the
 RT domestic pig.";
 RL Genomics 15:643-652(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver, and Brain;
 RX MEDLINE=94125128; PubMed=8294940;
 RA Meckel B., Zinke H., Flach R., Weiss B., Weller-Guettler H.,
 RA Gassen H.;
 RT "Expression of apolipoprotein A-I in porcine brain endothelium in
 RT vitro.";
 RL J. Neurochem. 62:788-798(1994).
 RN [3]
 RP SEQUENCE OF 34-265 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=90132667; PubMed=2105375;
 RA Weller-Guettler H., Sommerfeldt M., Pappadimitrakopoulou A., Mischek U.,
 RA Bonitz D., Frey A., Gume M., Scheerer J., Gassen H.G.;
 RT "Synthesis of apolipoprotein A-I in pig brain microvascular

RT enoethelial cells.";
 RL J. Neurochem. 54:444-450(1990).
 [4]
 RP SEQUENCE OF 105-265 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93154581; PubMed=8428656;
 RA Tieu V.N., Hasler-Rapacz J., Rapacz J., Black D.D.;
 RT "Sequences and expression of the porcine apolipoprotein A-I and C-III
 mRNAs";
 RL Gene 123:173-179(1993).
 RN [5]
 RP SEQUENCE OF 25-265.
 RA Hasler-Rapacz J.O., Chaudhary R., Chowdhary B.P., Tieu V.N.,
 RL Jackson K., Gustavsson I., Rapacz J.;
 RN Submitted (OCT-1995) to the SWISS-PROT data bank.
 [6]
 RP SEQUENCE OF 25-34.
 RX MEDLINE=76184721; PubMed=178359;
 RA Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;
 RT "Characterization of the plasma lipoproteins and apolipoproteins of the
 RY Erthrocytes pates monkey";
 RL Biochemistry 15:1928-1933(1976).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL EFFLUX FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECTITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS. SYNTHESIZED PREDOMINANTLY IN THE INTESTINE AND THE
 CC LIVER.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC -----
 DR EMBL; L00626; AAA30992.1; -;
 DR EMBL; X69477; CAA49234.1; -;
 DR EMBL; X17057; -; NOT ANNOTATED_CDS.
 DR EMBL; X59414; CAA42050.1; -;
 DR PIR; J00704; J00704.
 DR PIR; A05311; A05311.
 DR PIR; A46018; A46018.
 DR PIR; S21830; S21830.
 DR PIR; S31394; S31394.
 DR HSSP; P02647; 10DR.
 DR InterPro; IPR000074; Apolipoprotein.
 DR Pfam; PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 265
 FT DOMAIN 67 265
 FT REPEAT 67 86
 FT REPEAT 89 110
 FT REPEAT 111 121
 FT REPEAT 122 142
 FT REPEAT 144 165
 FT REPEAT 166 187
 FT REPEAT 188 209
 FT REPEAT 210 230
 FT REPEAT 231 241
 FT REPEAT 242 265
 FT REPEAT 265 265
 FT CONFLICT 108 108
 FT CONFLICT 143 143
 FT CONFLICT 173 173
 FT CONFLICT 180 180
 FT CONFLICT 185 186
 FT CONFLICT 209 209
 G -> D (IN REF. 2 AND 3).

FT CONFLICT 224 224 A -> G (IN REF. 4).
 SQ SEQUENCE 265 AA; 30325 MW; 2C6E578318CF69C CRC64;
 Query Match 81.1%; Score 1105; DB 1; Length 265;
 Best Local Similarity 80.9%; Pred. No. 1,5e-56;
 Matches 216; Conservative 20; Mismatches 29; Indels 2; Gaps 2;
 QY 1 MKAAVLTAVLFLTGSQARHFWDPEPSPMDRVKATLVYVDLKDSDGRVYSQFEGS 60
 DB 1 MKAAVLTAVLFLTGSQARHFWDPEPSPMDRVKATLVYVDLKDSDGRVYSQFEGS 59
 QY 61 ALGKOLNKLNDWDSVTSFSTKRLQGLPVQGFNDNLEKTEGLRQMSKDLSEYAK 120
 DB 60 ALGKHLNKLNDWDSVTSFSTKRLQGLPVQGFNDNLEKTEGLRQMSKDLSEYAK 119
 QY 121 VQPYLDLFQKQWQEMELYRQKVEPLRALQEGAROKLHELOKSPSGEERDARAHV 180
 DB 120 VQPYLDLFQKQWQEMELYRQKVEPLRALQEGAROKLHELOKSPSGEERDARAHV 179
 QY 181 DALRHLAPSDRLRRLARLEALKENGARLAETHAKATEHLSTSEKAPALEDLRQ 240
 DB 180 EALRQHVAPSDRLRRLARLEALKENGARLAETHAKATEHLSTSEKAPALEDLRQ 238
 QY 241 GLPLVLESPFVPSLAEYTKKLNQ 267
 DB 239 GLPLVLENLKVLTAIDASKLNQ 265
 RESULT 5
 ID APAL_RABIT STANDARD; PRT; 266 AA.
 AC P09809;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2ZAP AI; TISSUE=small intestine;
 RA Paraskevopoulou T.B., Kritsis A., Zannis V.I.;
 RL Submitted (JUL-1989) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=88082866; PubMed=3121329;
 RA Pan T.C., Hao Q.L., Yamin T.T., Dai P.H., Chen B.S., Chen S.L.,
 RT Kroon P.A., Chao Y.S.;
 RT "Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit
 RT apolipoprotein A-I is synthesized in the intestine but not in the
 RT liver";
 RL Eur. J. Biochem. 170:99-104(1987).
 RN [3]
 RP SEQUENCE OF 25-266.
 RX MEDLINE=87030294; PubMed=3095115;
 RA Yang C., Yang T., Pownall H.J., Gotto A.M. Jr.;
 RT "The primary structure of apolipoprotein A-I from rabbit high-density
 RT lipoprotein";
 RL Eur. J. Biochem. 160:427-431(1986).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
 CC THE LECTITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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CC EMBL: X15908; CAA34024.1; -
DR EMBL: X06658; CAA29857.1; -
DR EMBL: X06659; CAA29858.1; -
DR PIR: S06064; LPRB12.
DR PIR: S00230; LPRB1B.
DR PIR: A24998; A24998.
DR HSSP: P02647; IAV1.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein; 1.
KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
FT STGNAL 1 18
FT PROPEP 1 24
FT CHAIN 25 266
FT DOMAIN 67 266
FT REPEAT 67 88
FT REPEAT 89 110
FT REPEAT 111 121
FT REPEAT 122 143
FT REPEAT 144 165
FT REPEAT 166 187
FT REPEAT 188 209
FT REPEAT 210 231
FT REPEAT 232 242
FT REPEAT 243 266
FT REPEAT 18 18
FT CONFLICT 18 18
FT CONFLICT 44 44
FT CONFLICT 45 45
FT CONFLICT 107 107
FT CONFLICT 123 123
FT CONFLICT 147 147
FT CONFLICT 150 150
FT CONFLICT 191 191
FT CONFLICT 195 195
FT CONFLICT 211 211
FT CONFLICT 255 256
FT CONFLICT 256 256
FT SEQUENCE 266 AA; 30591 MW; 0FF6DB386497C7D2 CRC64;

Query Match 80.8%; Score 1100.5; DB 1; Length 266;
Best local similarity 80.1%; Pred. No. 2.7e-56;
Matches 214; Conservative 25; Mismatches 27; Indels 1; Gaps 1;

QY 1 MKAVALTAVLFLTGSQARHFWOODPEPQSPWDRVKLATVYVDLKDSDGRDYVSQEGS 60
DB 1 MKAVALTAVLFLTGSQARHFWOODPEPQSPWDRVKLATVYVDLKDSDGRDYVSQEGS 59
QY 61 ALGKQLNKLDDNDSTVTSFKLEBOLGVTYQEFWNLKLETKLROEMSKDLEEVKAK 120
DB 60 AFGKQLNKLDDNDSTVTSFKLEBOLGVTYQEFWNLKLETKLROEMSKDLEEVKAK 119
QY 121 VQPYLDDQKKWQEMELVROKVEPLRAELOEGAROKLHEOEKLSPIGGEEMRORARAHV 180
DB 120 VQPYLDDQKKWQEMELVROKVEPLRAELOEGAROKLHEOEKLSPIGGEEMRORARAHV 179
QY 181 DALRTHLAPYSDLEQRORLAARLEALKEGARGLALEYNAKATHEHSTSEKAKPALEDLRQ 240
DB 180 DLARKTKAPYSNELOQRALARESTKEGGSIALEYQAKAREHLSVSEKARPALEDLRQ 239
QY 241 GLLPVLESFKVSFSLALEBYTKKLTQ 267
DB 241 GLLPVLESFKVSFSLALEBYTKKLTQ 267

DB 240 GLLPVLESFKASVONVLDKATKINTQ 266

RESULT 6
ID APAL_BOVIN STANDARD: PRT; 265 AA.
AC P15497;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90348478; PubMed=2117227;
RA O'Huigin C., Chan L., Li W.H.;
RT "Cloning and sequencing of bovine apolipoprotein A-I cDNA and
RT molecular evolution of apolipoproteins A-I and B-100.";
RL Mol. Biol. Evol. 7:327-339(1990).
RN [2]
RP SEQUENCE OF 19-265.
RX Sparrow D.A., Lee B.R., Laplaud M.P., Auboliron S., Bauchart D.,
RA Chapman J.M., Gotto A.M. Jr., Yang C.Y., Sparrow J.T.;
RT "Plasma lipid transport in the perinatal calf, Bos spp: primary
RT structure of bovine apolipoprotein A-I.";
RL Biochim. Biophys. Acta 1123:145-150(1992).
RN [3]
RP SEQUENCE OF 25-70.
RX MEDLINE=90147795; PubMed=2105728;
RA Auboliron S., Sparrow D.A., Beauchart L., Bauchart D., Sparrow J.T.,
RA Laplaud M.P., Chapman J.M.;
RT "Characterization and amino-terminal sequence of apolipoprotein AI
RT from plasma high density lipoproteins in the perinatal calf, Bos
RT spp.";
RL Biochem. Biophys. Res. Commun. 166:833-839(1990).
CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC
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FT REPEAT 166 187 6.
 FT REPEAT 188 209 7.
 FT REPEAT 210 230 8.
 FT REPEAT 231 241 9 (HALF-LENGTH).
 FT REPEAT 242 265 10.
 FT CONFLICT 185 186 OL -> HV (IN REF. 2).
 SQ SEQUENCE 265 AA; 30276 MW; 06A2681EA2ABA50F CRC64;

Query Match 79.1%; Score 1077; DB 1; Length 265;
 Best Local Similarity 78.7%; Pred. No. 5.7e-55;
 Matches 210; Conservative 23; Mismatches 32; Indels 2; Gaps 2;

QY 1 MKAVALTLAVLFTLGSQARHFWQODEPSPWDRKDLATVYVDLKDSGRDYVSQFECS 60
 1 MKAVVLTAVLFTLGSQARHFWQODEPSPWDRKDLATVYVDLKDSGRDYVSQFECS 59
 DB 61 ALGKQNLKLDNDVSTFSTSKRLRQGLGYTOGFMDNLEKTEBGLRQEMSKDLEEVKAK 120
 60 ALGKQNLKLDNDVSTFSTSKRLRQGLGYTOGFMDNLEKTEBGLRQEMSKDLEEVKAK 119
 QY 121 VQPYLDFFQKKWQEMELRYKQVEPLRAELQEGAROKLHELOEKLSPLEGMNDRAHAY 180
 120 VQPYLDFFQKKWQEMELRYKQVEPLRAELQEGAROKLHELOEKLSPLEGMNDRAHAY 179
 DB 181 DALRTHLAPYSDELRLQRLARLEALKENGAGARLAEYHAKATEHLSTSEKAKPALEDLRQ 240
 180 ETLRQOLAPYSDDLRLQRLARLEALKENGAGARLAEYHAKATEHLSTSEKAKPALEDLRQ 238
 QY 241 GLPLVLESFVKSFLSALAEYTKKLNQ 267
 239 GLPLVLESFVKSFLSALAEYTKKLNQ 265
 DB

RESULT 7
 APAL_TUPGB STANDARD; PRT; 265 AA.
 ID APAL_TUPGB
 AC 018759;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Tupia glis belangeri (Common tree shrew).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.
 OX NCBI_Taxid=9396;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Lu X., Chen B., Zhao Y., Wang K., Xue H., Zeng W.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC - FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECTININ CHOLESTEROL ACUTRANSFERASE (LCAT).
 CC - SUBCELLULAR LOCATION: Extracellular.
 CC - TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS (BY SIMILARITY).
 CC - SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC or send an email to license@isb-sib.ch).
 DR EMBL: AF005638; AAB82326.1; -
 DR HSSP: P02647; IAV1.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.

KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24 BY SIMILARITY.
 FT CHAIN 25 265 BY SIMILARITY.
 FT DOMAIN 67 265 APOLOPROTEIN A-1.
 FT REPEAT 89 110 10 X APPROXIMATE TANDEM REPEATS.
 FT REPEAT 111 121 2.
 FT REPEAT 112 121 3 (HALF-LENGTH).
 FT REPEAT 122 143 4.
 FT REPEAT 144 165 5.
 FT REPEAT 166 187 6.
 FT REPEAT 188 209 7.
 FT REPEAT 210 231 8.
 FT REPEAT 232 242 9 (HALF-LENGTH).
 FT REPEAT 243 265 10.
 SQ SEQUENCE 265 AA; 30332 MW; 60076BC39FAEA165 CRC64;

Query Match 71.6%; Score 975.5; DB 1; Length 265;
 Best Local Similarity 69.7%; Pred. No. 3.3e-49;
 Matches 184; Conservative 38; Mismatches 41; Indels 1; Gaps 1;

QY 1 MKAVALTLAVLFTLGSQARHFWQODEPSPWDRKDLATVYVDLKDSGRDYVSQFECS 60
 1 MKAVVLTAVLFTLGSQARHFWQODEPSPWDRKDLATVYVDLKDSGRDYVSQFECS 59
 DB 61 ALGKQNLKLDNDVSTFSTSKRLRQGLGYTOGFMDNLEKTEBGLRQEMSKDLEEVKAK 120
 60 ALGKQNLKLDNDVSTFSTSKRLRQGLGYTOGFMDNLEKTEBGLRQEMSKDLEEVKAK 119
 QY 121 VQPYLDFFQKKWQEMELRYKQVEPLRAELQEGAROKLHELOEKLSPLEGMNDRAHAY 180
 120 VQPYLDFFQKKWQEMELRYKQVEPLRAELQEGAROKLHELOEKLSPLEGMNDRAHAY 179
 DB 181 DALRTHLAPYSDELRLQRLARLEALKENGAGARLAEYHAKATEHLSTSEKAKPALEDLRQ 240
 180 ETLRQOLAPYSDDLRLQRLARLEALKENGAGARLAEYHAKATEHLSTSEKAKPALEDLRQ 239
 QY 241 GLPLVLESFVKSFLSALAEYTKKLNQ 264
 240 GLPLVLESFVKSFLSALAEYTKKLNQ 263
 DB

RESULT 8
 APAL_MOUSE STANDARD; PRT; 264 AA.
 ID APAL_MOUSE
 AC 000623;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stoffel W., Mueller R., Binczek E., Hofmann K.;
 RT "Mouse apolipoprotein AI. cDNA-derived primary structure, gene
 RT organisation and complete nucleotide sequence.";
 RT Biol. Chem. Hoppe-Seyler 373:187-193(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93122774; PubMed=1478650;
 RA Januzzi J.L., Azrolan N., O'Connell A., Aalto-Setälä K., Breslow J.L.;
 RT "Characterization of the mouse apolipoprotein ApoA-1/ApoC-3 gene
 RT locus: genomic, mRNA, and protein sequences with comparisons to other
 RT species.";
 RT Genomics 14:1081-1088(1992).
 CC - FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING

CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
 CC THE LECTHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC -----
 DR EMBL: X64262; CAA45560.1; -;
 DR EMBL: X64263; CAA45561.1; -;
 DR EMBL: L04149; -; NOT_ANNOTATED_CDS.
 DR EMBL: L04151; -; NOT_ANNOTATED_CDS.
 DR PIR: S22420; S22420.
 DR PIR: A44364; A44364.
 DR HSSP: P02647; IAV1.
 DR SWISS-2DPAGE: Q00623; MOUSE.
 DR MGD: MGI:88049; APOA1.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18 BY SIMILARITY.
 FT PROPEP 19 24 APOLIPOPROTEIN A-I.
 FT CHAIN 25 264 10 X APPROXIMATE TANDEM REPEATS.
 FT DOMAIN 67 264 1.
 FT REPEAT 67 88 2.
 FT REPEAT 89 110 3 (HALF-LENGTH).
 FT REPEAT 111 121 4.
 FT REPEAT 122 143 5.
 FT REPEAT 144 165 6.
 FT REPEAT 166 187 7 (INCOMPLETE).
 FT REPEAT 188 207 8.
 FT REPEAT 208 229 9 (HALF-LENGTH).
 FT REPEAT 230 240 10.
 FT REPEAT 241 264
 FT REPEAT 264 AA; 30587 MM; C453FF2019634AAC CRC64;
 SO SEQUENCE

Query Match 66.4%; Score 904.5; DB 1; Length 264;
 Best Local Similarity 65.2%; Pred. No. 3.6e-45;
 Matches 174; Conservative 41; Mismatches 49; Indels 3; Gaps 2;

DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84207987; Pubmed=6426956;
 RA Poncin J.E., Martial J.A., Gielen J.E.;
 RT Cloning and structure analysis of the rat apolipoprotein A-I cDNA."
 RL Eur. J. Biochem. 140:493-498(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87008540; Pubmed=3020028;
 RA Haddad I.A., Ordovas J.M., Fitzpatrick T., Karathanasis S.K.;
 RT "Linkage, evolution, and expression of the rat apolipoprotein A-I, C-
 RL III, and A-IV genes."
 RL J. Biol. Chem. 261:13268-13277(1986).
 RN [3]
 RP SEQUENCE OF 1-45.
 RC STRAIN=SPRAGUE-DAWLEY;
 RX MEDLINE=82098162; Pubmed=6798036;
 RA Gordon J.I., Smith D.P., Andy R., Alpers D.H., Schonfeld G.,
 RA Straus A.W.;
 RT "The primary translation product of rat intestinal apolipoprotein A-I
 RT mRNA is an unusual preproprotein."
 RL J. Biol. Chem. 257:971-978(1982).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL EFFLUX FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECTHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC -----
 DR EMBL: M00001; AAA40749.1; -;
 DR EMBL: X00558; CAA25224.1; -;
 DR EMBL: J02597; AAA40745.1; -;
 DR PIR: A24700; A24700.
 DR HSSP: P02647; IAV1.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24 APOLIPOPROTEIN A-I.
 FT CHAIN 25 259 10 X APPROXIMATE TANDEM REPEATS.
 FT DOMAIN 67 259 1.
 FT REPEAT 67 88 2.
 FT REPEAT 89 110 3 (HALF-LENGTH).
 FT REPEAT 111 121 4.
 FT REPEAT 122 143 5 (INCOMPLETE).
 FT REPEAT 144 161 6.
 FT REPEAT 162 183 7 (INCOMPLETE).
 FT REPEAT 184 203 8.
 FT REPEAT 204 225 9 (HALF-LENGTH).
 FT REPEAT 226 236 10.
 FT REPEAT 237 259
 FT REPEAT 201 201 R -> K (IN REF. 2).
 FT CONFLICT 214 214 G -> S (IN REF. 2).
 FT CONFLICT 218 218 R -> K (IN REF. 2).
 FT CONFLICT

SQ SEQUENCE 259 AA; 3008 MW; 2E8D5E845FEAE88 CRC64;
 Query Match 61.9%; Score 842.5; DB 1; Length 259;
 Best Local Similarity 62.6%; Pred. No. 1.2e-41;
 Matches 166; Conservative 35; Mismatches 57; Indels 7; Gaps 3;

QY 1 MKAATLAVLFLTGSOARHFQODEPPQSPMDRYKDLATVVDYLDKSGRDYVSQFEGS 60
 DB 1 MKAATLAVLFLTGSOARHFQODEPPQSPMDRYKDLATVVDYLDKSGRDYVSQFEGS 59
 QY 61 ALGQOLNKLNDNDVSTFSKLRBQGLPVTOEFWDNLEKETEGSLROEMSKDLEEVKAK 120
 DB 60 TLGQOLNKLNDNDVSTFSKLRBQGLPVTOEFWDNLEKETEGSLROEMSKDLEEVKAK 119
 QY 121 VQPYLDPOFKKOEEMELVROKVEPLRAELOGAROKLHELOEKLSPGEMDRARAHV 180
 DB 120 MQPHLDPOFKKOEEMELVROKVEPLRAELOGAROKLHELOEKLSPGEMDRARAHV 175
 QY 181 DALRTHLAPYSDELROKRLAARLEALKENGARLAELYHAKATEHLSTSEKAKPALEDLRQ 240
 DB 176 DALRTHLAPYSDELROKRLAARLEALKENGARLAELYHAKATEHLSTSEKAKPALEDLRQ 233
 QY 241 GLLPVLESFVSVFLSALAEYTKLN 265
 DB 234 GLMPVLEAMKAKIMSMIDEAKKLN 258

RESULT 10
 APAL_ANAPL STANDARD; PRT; 264 AA.
 AC 042296;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Anas platyrhynchos (Domestic duck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 NCBI_TaxID=839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEKIN BREED; TISSUE=Liver;
 RA Chen B., Lu X., Wang K., Xue H., Zeng W., Zhu D., Chi L.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
 THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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 CC or send an email to license@sdb-sdb.ch).
 CC
 DR EMBL: U086131; AAB64381.1; -.
 DR HSSP: P02647; IODR.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein.
 KM Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNA 1 18
 FT PROPEP 19 24 BY SIMILARITY.
 FT CHAIN 25 264 APOLIPOPROTEIN A-I.
 FT DOMAIN 67 264 10 X APPROXIMATE TANDEM REPEATS.
 FT REPEAT 67 88 1.
 RN

FT REPEAT 89 110 2.
 FT REPEAT 111 121 3 (HALF-LENGTH).
 FT REPEAT 122 143 4.
 FT REPEAT 144 165 5.
 FT REPEAT 166 187 6.
 FT REPEAT 188 209 7.
 FT REPEAT 210 231 8.
 FT REPEAT 232 242 9 (HALF-LENGTH).
 FT REPEAT 243 264 10.
 SQ SEQUENCE 264 AA; 30659 MW; 7546F4BAF2846900 CRC64;

Query Match 51.8%; Score 705.5; DB 1; Length 264;
 Best Local Similarity 51.5%; Pred. No. 7.2e-34;
 Matches 135; Conservative 55; Mismatches 71; Indels 1; Gaps 1;

QY 1 MKAATLAVLFLTGSOARHFQODEPPQSPMDRYKDLATVVDYLDKSGRDYVSQFEGS 60
 DB 1 MRVVVVTALLFLTGQARYFWQGHDE-PQAPLDRLDLYLVLETYKASGKDAIOTFAS 59
 QY 61 ALGQOLNKLNDNDVSTFSKLRBQGLPVTOEFWDNLEKETEGSLROEMSKDLEEVKAK 120
 DB 60 AVGQOLDKLADNLDLTGAAGAKLRDMAPYKKEVREMKLKTESLRAELTKDLEEVKAK 119
 QY 121 VQPYLDPOFKKOEEMELVROKVEPLRAELOGAROKLHELOEKLSPGEMDRARAHV 180
 DB 120 IRFELDPOFSAKTTELEQYRQRLAELKELTKOKELVMOOKLTPVAEERDRLRGV 179
 QY 181 DALRTHLAPYSDELROKRLAARLEALKENGARLAELYHAKATEHLSTSEKAKPALEDLRQ 240
 DB 180 EELRKLAPYSDELROKRLAARLEALKENGARLAELYHAKATEHLSTSEKAKPALEDLRQ 239
 QY 241 GLLPVLESFVSVFLSALAEYTK 262
 DB 240 RLTPYAENLKTFRISLDELQK 261

RESULT 11
 APAL_CHICK STANDARD; PRT; 264 AA.
 AC P08250;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=86049703; PubMed=3118875;
 RA Byrnes L., Luo C.-C., Li W.-H., Yang C.-Y., Chan L.;
 RL "The complete sequence of chick apolipoprotein A-I: cDNA sequence, tissue expression and evolution.";
 CC Biochem. Biophys. Res. Commun. 148:485-492(1987).
 CC [2]
 CC SEQUENCE FROM N.A.
 RC MEDLINE=86152500; PubMed=3126099;
 RA Ferrari S., Tarugi P., Drusiani E., Calandra S., Fregni M.;
 RL "The complete sequence of chick apolipoprotein A-I mRNA and its expression in the developing chick.";
 CC Gene 60:39-46(1987).
 CC [3]
 CC SEQUENCE FROM N.A.
 RC MEDLINE=87222301; PubMed=3108248;
 RA Rajavashisth T.B., Dawson P.A., Williams D.L., Shackelford J.E.,
 RL Leberer H., Lussis A.J.;
 CC "Structure, evolution, and regulation of chicken apolipoprotein A-I.";
 CC J. Biol. Chem. 262:7058-7065(1987).
 CC [4]
 RN

ID	AP04_MACFA	STANDARD:	PRT:	429 AA.
AC	P33621:			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	Apolipoprotein A-IV precursor (Apo-AIV).			
GN	AP04.			
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;			
OC	Cercopitheciinae; Macaca.			
OX	NCBI_Taxid=9541;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Leukocyte;			
RX	MEDLINE=93192350; PubMed=8448212;			
RA	Osada J., Pocovi M., Nicolosi R.J., Schaefer E.J., Ordovas J.M.;			
RT	"Nucleotide sequences of the Macaca fascicularis apolipoprotein C-II			
RL	and A-IV genes.";			
RL	Biochim. Biophys. Acta 1172:335-339(1993).			
CC	-1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND			
CC	CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN			
CC	LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR			
CC	COMPONENT OF HDL AND CHYLOMICRONS.			
CC	-1- SUBCELLULAR LOCATION: Extracellular.			
CC	-1- TISSUE SPECIFICITY: SECRETED IN PLASMA.			
CC	-1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH			
CC	22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-			
CC	MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-			
CC	HELICAL. AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY			
CC	THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL			
CC	ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.			
CC	-1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.			
CC	-----			
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Query Match	21.4%	Score 291	DB 1	Length 429
Best Local Similarity	26.8%	Pred. No. 4.3e-10		
Matches	71	Conservative	61	Mismatches 123; Indels 10; Gaps 2
QY	1	MAKAVLTAVLELTGSOAREHWQODEPSPWDRYKVLATVYDVULDKDSGRDYVSOFEGS	60	
Db	3	LKAVLVLTAVLTAVTGTARAE--VSADQVATVWMD-----YFQGLSSNMKEAVENHLOKS	52	
QY	61	ALGKOLNLKLNNWDSVYTSFESKLRLEQGLPTQGEFWMNLKEETGTGLRQEMSKDLEEVK	120	
Db	53	ELTQQLNALFQDLGEGVNYVYAGDLOKTKVTPATETLHERLAKDSKLEETRLKELEEVK	112	
QY	121	VQPYLDQFKQWQEMEMELYRQKVEPTLRAELQEGAROKLHTEQELSPGEGEMDRARAY	180	
Db	113	LLEHANEVSQKIGENVRELQQRLEPYTQGLTYQNTQTEQRLRGLTPYQARMRVLR	172	
QY	181	DARFTLAVYSDELKQRLAARLEALKENGKGRVLAIEYNAKATENHLSLSEKAPALDELQ	240	
Db	173	DSLQTLSTRHQAOLKAKIDONVEELKEETLTPYADEFVYKIDQVVEELRSLAPYADQGE	232	
QY	241	GLLPVLESFVYSFSLSALEEYTRKLN	265	
Db	233	KLNHQLGLLAFQMKNAEELKARIS	257	
RESULT	14			
APAL_BRARE				
ID	APAL_BRARE	STANDARD;	PRT;	262 AA.
AC	042363;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Apolipoprotein A-I precursor (Apo-A1).			
GN	APOA.			
OS	Brachydanio rerio (Zebrafish) (Zebra danio).			
OC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;			
OC	Actinopterygii: Neopterygii: Teleostei; Euteleostei; Ostariophysi;			
OC	Cyprinodontes: Cyprinidae; Danio.			
OC	NCBI_TaxID=7955;			
NC	[1]			


```
CC -I- POLYMOPHISM: EIGHT ALLELES HAVE BEEN CHARACTERIZED (APOA-IV*0  
CC TO APOA-IV*7). APOA-IV*1 IS THE MAJOR ALLELE (90%), IV*2 IS ALSO  
CC COMMON (8%). THE OTHERS ARE RARE ALLELES.  
CC -I- DISEASE: DEFECTS IN APOA4 MAY CONTRIBUTE, ALONG WITH DEFECTS IN  
CC OTHER GENES OR ENVIRONMENTAL FACTORS, TO THE DEVELOPMENT OF  
CC FAMILIAL COMBINED HYPERLIPIDEMIA (FCHL).  
CC -I- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.  
-----  
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CC or send an email to license@isb-sdb.ch).  
-----  
DR EMBL; M14642; AAAS1745.1; -;  
DR EMBL; X13629; CAA31955.1; -;  
DR EMBL; M14566; AAAS1748.1; -;  
DR EMBL; J02758; AAA96731.1; -;  
DR EMBL; M13654; AAAS1744.1; -;  
DR PIR; A26448; LPHU04.-;  
DR PIR; A29330; A29330.-;  
DR PIR; A26280; A26280.-;  
DR PIR; S02715; S02715.-;  
DR HSSP; P02649; INFO.-;  
DR SWISS-2DPAGE; P06727; HUMAN.-;  
DR MM; 107690; -;  
DR InterPro; IPR000074; Apolipoprotein.  
DR Pfam; PF01442; Apolipoprotein; 1.  
KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; signal;  
KM Disease mutation; Polymorphism.  
FT SIGNAL 1 20  
FT CHAIN 21 396 APOLIPOPROTEIN A-IV.  
FT DOMAIN 33 330 13 X 22 AA APPROXIMATE TANDEM REPEATS.  
FT REPEAT 33 54 1.  
FT REPEAT 60 81 2.  
FT REPEAT 82 103 3.  
FT REPEAT 115 136 4.  
FT REPEAT 137 158 5.  
FT REPEAT 159 180 6.  
FT REPEAT 181 202 7.  
FT REPEAT 203 224 8.  
FT REPEAT 225 246 9.  
FT REPEAT 247 268 10.  
FT REPEAT 269 286 11.  
FT REPEAT 287 308 12.  
FT REPEAT 309 330 13.  
FT DOMAIN 372 389 GLU/GLN-RICH.  
FT VARIANT 13 V->M (IN APOA-IV*1D).  
FT VARIANT 44 /FTId=VAR_000626.  
FT VARIANT 147 147 E->K (IN BUDAPEST-2).  
FT VARIANT 161 N->S (IN APOA-IV*1B).  
FT VARIANT 161 /FTId=VAR_000628.  
FT A->S (IN SEATTLE-3; IN FCHL).  
FT /FTId=VAR_000629.
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Sun Sep 22 12:10:07 2002

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Page 14

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Db      113  LHPANEVSKIGIUNLHELQGRLEPEYADQRTQVONTQAEQLRQQLPEYAOBMRVYRENA 172
Oy      181  DALPETHYAPADELTEROGLARLEKENGSGARLAEYNAKATEHLSSTSEAKPALDELNO 240
Db      173  DSLQASLRPHADELKAITDQNEVELK-----GRLLPRADEKVKVITDQTVELNR 221
Oy      241  GLLPVLESFKVSTSLAEFT 261
Db      222  SLAPYADQTEKLNHQLEGLT 242

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Search completed: September 22, 2002, 12:22:16
Job time: 1016 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2002, 12:03:00 ; Search time 111.17 Seconds
(without alignments)
415.487 Million cell updates/sec

Title: US-09-803-918a-2
Perfect score: 1362
Sequence: 1 MKAAYTLAVLFTGSOARH.....SPKVSFLSALREYTKKLNQ 267

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPRMBL_19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1012.5	74.3	264	11	Q922L4
2	896	65.8	263	11	Q08855
3	895	65.7	263	11	Q09042
4	836	61.4	258	11	Q09054
5	834	61.2	258	11	Q08877
6	727.5	53.4	241	6	Q9TS49
7	327	24.0	67	4	Q9Y355
8	312.5	22.9	82	6	Q29248
9	298.5	21.9	263	13	Q98TG6
10	257.5	18.9	366	13	Q93601
11	253	18.6	435	11	Q01488
12	247	18.1	56	6	Q02762
13	247	18.1	395	11	Q91XF8
14	244	17.9	395	11	Q9DBN0
15	213.5	15.7	275	13	Q9PT02
16	200	14.7	363	4	Q9UBJ3

17	194.5	14.3	1547	5	Q26471	Q26471 schistocerc
18	191	14.0	313	6	Q9GLC0	Q9GLC0 tupala gilis
19	185	13.6	244	4	Q13784	Q13784 homo sapien
20	184.5	13.5	317	6	Q9GLM6	Q9GLM6 hylobates l
21	181.5	13.3	317	6	Q9GLM8	Q9GLM8 gorilla gor
22	181	13.3	259	13	Q98TG5	Q98TG5 anguilla ja
23	179.5	13.2	317	6	Q9GLT3	Q9GLT3 pan troglod
24	178	13.1	259	13	Q98TG4	Q98TG4 anguilla ja
25	177.5	13.0	259	13	Q98TG3	Q98TG3 anguilla ja
26	177.5	13.0	317	6	Q9GLM7	Q9GLM7 pongo pygma
27	171	12.6	367	11	Q9OUH3	Q9OUH3 rattus norv
28	171	12.6	358	11	Q99PE4	Q99PE4 mus muscun
29	170.5	12.5	259	13	Q98TG2	Q98TG2 anguilla ja
30	170	12.5	368	11	Q91X90	Q91X90 mus muscun
31	169	12.4	174	13	Q98S13	Q98S13 cyprinus ca
32	164.5	12.1	259	13	Q98TG1	Q98TG1 anguilla ja
33	153.5	11.3	174	13	Q9DFQ3	Q9DFQ3 glilichthys
34	146	10.7	1478	4	Q9BOS8	Q9BOS8 homo sapien
35	142	10.4	1411	4	Q15075	Q15075 homo sapien
36	141	10.4	26	4	Q9UCT8	Q9UCT8 homo sapien
37	141	10.4	1456	5	Q9V587	Q9V587 drosophila
38	139.5	10.2	194	11	Q9D2P9	Q9D2P9 mus muscun
39	137	10.1	470	5	Q9XTH4	Q9XTH4 caenorhadi
40	137	10.1	1935	5	Q44934	Q44934 loligo peal
41	136	10.0	992	4	Q9NTH6	Q9NTH6 homo sapien
42	136	10.0	1410	4	Q14221	Q14221 homo sapien
43	136	10.0	1455	4	Q9UPV0	Q9UPV0 homo sapien
44	135.5	9.9	1047	11	Q9EP81	Q9EP81 mus muscun
45	135.5	9.9	1708	5	Q9U0S6	Q9U0S6 mytilus gal

ALIGNMENTS

RESULT	ID	Q922L4	PRELIMINARY;	PRT;	264 AA.
AC	Q922L4	01-MAY-1999 (TREMBL)	10, Created		
DT	01-MAY-1999 (TREMBL)	10, Last sequence update			
DT	01-JUN-2001 (TREMBL)	17, Last annotation update			
DE	APOLIPROTEIN A-I.				
GN	APOLI.				
OS	Mesocricetus auratus (Golden hamster).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;				
OC	Mesocricetus.				
OX	NCBI_TaxID=10036;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=GOLDEN SYRIAN; TISSUE=INTESTINE;				
RX	MEDLINE=99061559; PubMed=9843713;				
RA	Wu J.Y.J., Reeves S.K., Wang Y.R., Wu Y., Lei P.P., Lei K.Y.;				
RT	"Zinc deficiency decreases plasma level and hepatic mRNA abundance of				
RT	apolipoprotein A-I in rats and hamsters."				
RL	Am. J. Physiol. 275:Cl516-Cl525(1998).				
DR	EMBL; AF046919; AAC98484.1. -				
DR	HSSP: P02647; IAVI.				
DR	InterPro: IPR00074; Apolipoprotein.				
DR	Pfam: PF01442; Apolipoprotein; 1.				
KW	Lipoprotein.				
SC	SEQUENCE 264 AA; 30739 MW; 280B22F4C0F0B129 CRC64;				

Query Match 74.3%; Score 1012.5; DB 11; Length 264;
Best local Similarity 73.0%; Pred. No. 87e-56;
Matches 195; Conservative 30; Mismatches 39; Indels 3; Gaps 2;

QY	1	MKAAYTLAVLFTGSOARHFMODEPSPMDRKDLATYVVNVLDGSDGYSGE	60
DB	1	MKTVLAVAVFLTGSQARHFMORD-PQTRMDRKDPATYVVAVDGSGREYSQ	59
QY	61	ALGKQLNLKLLDNMDSVTSTFSKLRQLGPTVQGFWMNLEKETGLRQENSKDL	120

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DB 60 ALGKQINLNLLENWDTLGSFVGRLOEOLGPVTOEFWNLKETEMLRKMKNDEEYKAK 119
QY 121 VQPYLDPOFKKWOEMELRYKQVEPLRAELOEGAROKLHELOEKSPLEGEERDRAHAY 180
DB 120 VQPYLDPOFKKWOEMELRYKQVEPLRAELOEGAROKLHELOEKSPLEGEERDRAHAY 179
QY 181 DALRTHLAPYSDELRLORLAARLEALKEKGARLAIEYHAKATEHLSLSEKAPALEDLRQ 240
DB 180 DALRTHLAPYSDELRLORLAARLEALKEKGARLAIEYHAKATEHLSLSEKAPALEDLRQ 237
QY 241 GILPVLESFKVSFLSALIEYTKKLNQ 267
DB 238 GILPVLESFKVSFLSALIEYTKKLNQ 264

RESULT 2
ID 008855 PRELIMINARY; PRT: 263 AA.
AC 008855;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE APOLIPOPROTEIN A-I.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=SPLEEN;
RX MEDLINE=98077648; PubMed=9415807;
RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
RT "Repetitive elements in the third intron of murine apolipoprotein A-I
RT gene.";
RL Biochem. Mol. Biol. Int. 43:989-996(1997).
DR EMBL: U79574; AAB58426.1; -.
DR HSSP: P02647; IAVI.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein; 1.
KW Lipoprotein.
SQ SEQUENCE 263 AA; 30544 MW; 7825DF7483A5B24A CRC64;

```

Query Match 65.8%; Score 896; DB 11; Length 263;
 Best Local Similarity 65.2%; Pred. No. 1.5e-48;
 Matches 174; Conservative 41; Mismatches 48; Indels 4; Gaps 3;

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QY 1 MKAAYLVLAFLVFLNGSQARHFWDQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSGFSS 60
DB 1 MKAAYLVLAFLVFLNGSQARHFWDQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSGFSS 59
QY 61 ALGQNLKILNDNDVSTFSFKLRBOLGPVTOEFWNLKETEGLROEBSKDLIEYKAK 120
DB 60 SLGQNLNLNLLENWDTLGSFVGRLOEOLGPVTOEFWNLKETEGLROEBSKDLIEYKAK 119
QY 121 VQPYLDPOFKKWOEMELRYKQVEPLRAELOEGAROKLHELOEKSPLEGEERDRAHAY 180
DB 120 VQPYLDPOFKKWOEMELRYKQVEPLRAELOEGAROKLHELOEKSPLEGEERDRAHAY 178
QY 181 DALRTHLAPYSDELRLORLAARLEALKEKGARLAIEYHAKATEHLSLSEKAPALEDLRQ 240
DB 179 DSLRTHLAPHSQOMRESLAQRLAELKSN--PTLNEYHTRAKTHLTKLGEKARPALEDLRH 236
QY 241 GILPVLESFKVSFLSALIEYTKKLNQ 267
DB 237 SLMPLETLTKTQVOVDIKASSETLTAQ 263

RESULT 3
ID 009042 PRELIMINARY; PRT: 263 AA.
AC 009042;

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DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-JUL-2001 (Tremblrel. 17, Last annotation update)
DE APOLIPOPROTEIN A-I.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR AND BALB/C, AND C3H; TISSUE=SPLEEN;
RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U79575; AAB58427.1; -.
DR EMBL: U79572; AAB58424.1; -.
DR EMBL: U79573; AAB58425.1; -.
DR HSSP: P02647; IAVI.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein; 1.
KW Lipoprotein.
SQ SEQUENCE 263 AA; 30516 MW; E245DF7483A5A0DD CRC64;

```

Query Match 65.7%; Score 895; DB 11; Length 263;
 Best Local Similarity 65.2%; Pred. No. 1.8e-48;
 Matches 174; Conservative 41; Mismatches 48; Indels 4; Gaps 3;

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QY 1 MKAAYLVLAFLVFLNGSQARHFWDQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSGFSS 60
DB 1 MKAAYLVLAFLVFLNGSQARHFWDQDEPPQSPWDRVKDLATVYVDVLDKSGRDYVSGFSS 59
QY 61 ALGQNLKILNDNDVSTFSFKLRBOLGPVTOEFWNLKETEGLROEBSKDLIEYKAK 120
DB 60 SLGQNLNLNLLENWDTLGSFVGRLOEOLGPVTOEFWNLKETEGLROEBSKDLIEYKAK 119
QY 121 VQPYLDPOFKKWOEMELRYKQVEPLRAELOEGAROKLHELOEKSPLEGEERDRAHAY 180
DB 120 VQPYLDPOFKKWOEMELRYKQVEPLRAELOEGAROKLHELOEKSPLEGEERDRAHAY 178
QY 181 DALRTHLAPYSDELRLORLAARLEALKEKGARLAIEYHAKATEHLSLSEKAPALEDLRQ 240
DB 179 DSLRTHLAPHSQOMRESLAQRLAELKSN--PTLNEYHTRAKTHLTKLGEKARPALEDLRH 236
QY 241 GILPVLESFKVSFLSALIEYTKKLNQ 267
DB 237 SLMPLETLTKTQVOVDIKASSETLTAQ 263

RESULT 4
ID 009054 PRELIMINARY; PRT: 258 AA.
AC 009054;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE APOLIPOPROTEIN A-I.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WKY AND SHRSP; TISSUE=SPLEEN;
RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U79578; AAB58430.1; -.
DR EMBL: U79577; AAB58429.1; -.
DR HSSP: P02647; IAVI.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein; 1.
KW Lipoprotein.
SQ SEQUENCE 258 AA; 29918 MW; 093E6EF2B629C0C8 CRC64;

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[illegible]

RESULT	7
09Y355	
ID	09Y355
AC	09Y355
DT	01-NOV-1999 (TREMBlrel. 12, Created)
DT	01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT	01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE	APOLIPOPROTEIN A1 (FRAGMENT).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumelostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxId=9606;
ON	[1]
RN	
RP	SEQUENCE FROM N.A.
RX	MEDLINE=99216322; PubMed=10198255;
RA	Hamdi ASl K., Liepiens J.O., Nakamura M., Parker F., Benson M.D.,
RT	"A novel apolipoprotein A-I variant, Arg173Pro, associated with
RL	cardiac and cutaneous amyloidosis."
RL	Biochem. Biophys. Res. Commun. 257:584-588(1999).
EMBL	AF148963; AAD34604.1; -

DR HSSP: P02647; 1A.V1.
 KM Lipoprotein.
 FT NON_TER 1
 RT 67
 SQ SEQUENCE 67 AA; 7433 MW; 525ELFEB7BDD5AFB CRC64;

Query Match 24.0%; Score 327; DB 4; Length 67;
 Best Local Similarity 98.5%; Pred. No. 7.4e-14;
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 165 LSPILGEMDRARAHVDALRTHLAPYSDELRLAARLEALKENGAGALAEYHAKATEHL 224
 DB 1 LSPILGEMDRARAHVDALRTHLAPYSDELRLAARLEALKENGAGALAEYHAKATEHL 60

QY 225 STLSEKA 231
 DB 61 STLSEKA 67

RESULT 8
 Q29248 PRELIMINARY; PRT; 82 AA.

AC Q29248; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE APOLIPOPROTEIN A-I (FRAGMENT).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SMALL INTESTINE;
 RX MEDLINE=66327607; PubMed=8672129;
 RA Winteroe A.K., Fredholm M., Davies W.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 RT library."
 RL Mamm. Genome 7:509-517(1996).
 DR EMBL: F14858; CAA3298.1; -
 KW Lipoprotein. 82
 FT NON_TER
 SQ SEQUENCE 82 AA; 9168 MW; 24625C65CBFFEDD8 CRC64;

Query Match 22.9%; Score 312.5; DB 6; Length 82;
 Best Local Similarity 75.9%; Pred. No. 7.5e-13;
 Matches 63; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

QY 1 MKAAYLTLAVLFLTGSQARHFHWOODEPQSPMDRVKDLATVYVDLKDGRDYSQFEGS 60
 DB 1 MKAAYLTLAVLFLTGSQARHFHWOODEPQSPMDRVKDLATVYVDLKDGRDYSQFEGS 59

QY 61 ALGKOLNLKLDNWDSTSTFSFK 83
 DB 60 ALGKOLNLKLDNWDSTSTFSFK 82

RESULT 9
 Q98TG6 PRELIMINARY; PRT; 263 AA.
 AC Q98TG6;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE 28kDa-2 APOLIPOPROTEIN.
 OS Anguilla japonica (Japanese eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OC Anguillidae; Anguilla.
 OX NCBI_TaxID=7937;
 RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;
 RX MEDLINE=21175592; PubMed=11278178;
 RA Kondo H., Kawazoe I., Nakaya M., Kikuchi K., Aida K., Watabe S.;
 RT "The novel sequences of major plasma apolipoproteins in the eel
 RT Anguilla japonica." Acta
 RL Biochim Biophys. Acta 1531:132-142(2001).
 DR EMBL: AB046203; BAB40960.1; -
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Lipoprotein.

SQ SEQUENCE 263 AA; 30087 MW; DB8CB0AF30EBE6B1 CRC64;

Query Match 21.9%; Score 298.5; DB 13; Length 263;
 Best Local Similarity 28.1%; Pred. No. 2.3e-11;
 Matches 74; Conservative 60; Mismatches 124; Indels 5; Gaps 4;

QY 1 MKAAYLTLAVLFLTGSQARHFHWOODEPQSPMDRVKDLATVYVDLKDGRDYSQFEGS 59
 DB 1 MKAAYLTLAVLFLTGSQARHFHWOODEPQSPMDRVKDLATVYVDLKDGRDYSQFEGS 59

QY 60 SALGKOLNLKLDNWDSTSTFSFKLRBQLGPVTOEFWDNLEKETEGLRDMSKDLSEYKA 119
 DB 60 TEY-KOYKRLRSGSLDNIQGYIOSASALSPYTDVASSQFMEFLTKMDRDKIQADVQLKK 118

QY 120 KVQPYLDPOKKWOEMELIRKQYEPRLALQEGARKLHELOKISPLGEMDRARAH 179
 DB 119 DQPKRDELKEVQKHDEYRAKLEPLVETKHKQEMELTKLQPVVEDLRARIQVN 178

QY 180 VDALTHTLAPYSDELRLAARLEALKENGAGALAEYHAKATEHLSTLSKAPAEEDLR 239
 DB 179 VEETKSLVPTVEALIRAKITFERLEELRTLAEPYQVEKDKHLSALPDVKKYQG--EDLQ 236

QY 240 QGLLPVLESEFVSFLSALEEYTK 262
 DB 237 SKLKPVAEELTKKLVALMESLSQ 259

RESULT 10
 Q93601 PRELIMINARY; PRT; 366 AA.
 ID Q93601;
 AC Q93601;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE APOLIPOPROTEIN AIV.
 GN APOAIV.
 OS Gallus gallus (Chicken).
 OC Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98221191; PubMed=9553114;
 RA Steinmetz A., Hermann M., Nimf J., Aebbersold R., Ducret A.,
 RA Weinberg R.B., Schneider W.J.;
 RT "Expression and conservation of apolipoprotein AIV in an avian
 RT species."
 RL J. Biol. Chem. 273:10543-10549(1998).
 DR EMBL: Y16534; CAA76273.1; -
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 SQ SEQUENCE 366 AA; 40852 MW; B47DB49F3EBD91CE CRC64;

Query Match 18.9%; Score 257.5; DB 13; Length 366;
 Best Local Similarity 26.3%; Pred. No. 1.2e-08;
 Matches 72; Conservative 59; Mismatches 110; Indels 33; Gaps 5;

QY 2 MKAAYLTLAVLFLTGSQARHFHWOODEPQSPMDRVKDLATVYVDLKDGRDYSQFEGSA 61

Sun Sep 22 12:10:08 2002

us-09-803-918a-2.rspt

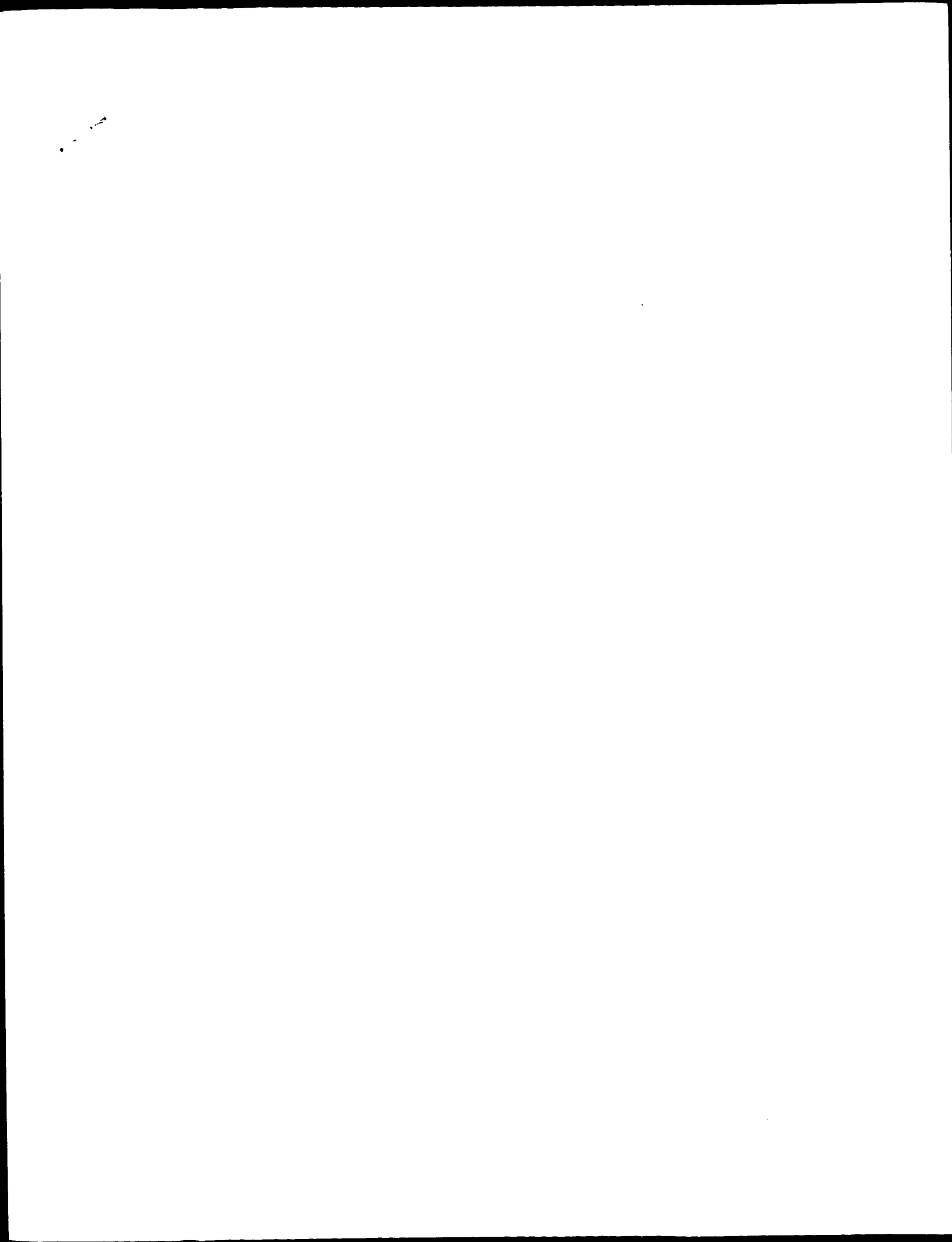
Page 7

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0Y 108 FEE-----GROEHSKLEEVKAKVOPYLDDFOKKMOEEN 136
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Db 120 ST0YIGELKTMEDONADDVHNRVNTYTRKRLKNTKTEIRNTVATYGEIOSRSONM 179
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0Y 137 ELYROKVEPLRAELTOEGAROKLHELOEKLSPJGEMDRARAHVADLRTFLAYSOELQ 196
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Db 180 DIVERVERPFSQAHDPRAQRLSGFTLLKNQADDSQOVSTOAEGRQLEATAEDLRT 239
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0Y 197 RLAALEALKENGARLAELYHAKATEHJLSTLESEK 232
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 240 TLEGRIDEL-----SSLAPYAAKIREHLQRAMDKVK 271

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Search completed: September 22, 2002, 12:21:36
Job time: 1116 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:00:25 : Search time 139.03 Seconds
(without alignments)
213.312 Million cell updates/sec

Title: US-09-803-918a-2
Percent score: 1362
Sequence: 1 MKAAVLTLAVLFLTGSQARH.....SFKVSFLSALEYTKKLTNTQ 267

Scoring table: BIOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
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11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1362	100.0	267	7 AAP61079	Assumed human apol
2	1362	100.0	267	9 AAP82128	Entire human apol
3	1362	100.0	267	14 AAP834032	Sequence of apo AI
4	1362	100.0	267	16 AAR72705	Human apo A-I incl
5	1362	100.0	267	20 AAY18675	Human apolipoprote
6	1362	100.0	267	22 AAB47620	Full length Apo AI
7	1354	99.4	267	18 AAR08602	Human apolipoprote
8	1351.5	99.2	268	9 AAP80668	Recombinant human
9	1328	97.5	239	22 AAU33170	Novel human secret
10	1241	91.1	243	9 AAP81082	Sequence of mature
11	1237.5	90.9	264	15 AAR56863	Apo-lipoprotein AI

12	1237.5	90.9	264	15	AAR56864	Apo-lipoprotein AI
13	1216.5	89.3	244	22	AAU28184	Novel human secret
14	1009	74.1	221	22	AAU29835	Novel human secret
15	912.5	67.0	318	22	AAU30268	Novel human secret
16	831	61.0	359	22	AAU30470	Novel human secret
17	765.5	56.2	166	22	AAU28372	Novel human secret
18	737	54.1	151	22	AAU02278	Novel human secret
19	617.5	45.3	144	22	AAU012095	Novel human secret
20	597.5	43.9	120	22	AAU30267	Novel human secret
21	597.5	43.9	119	22	AAU30469	Novel human secret
22	547	40.2	129	22	AAU30468	Novel human secret
23	278.5	20.4	396	22	AAU90663	Novel human secret
24	269	19.8	382	22	AAU90663	Novel human secret
25	260.5	19.1	346	14	AAU39493	Human secreted pro
26	259.5	19.1	342	14	AAU39493	Human secreted pro
27	257.5	18.9	337	14	AAU39498	Human secreted pro
28	256.5	18.8	333	14	AAU39492	Human secreted pro
29	255.5	18.8	333	14	AAU39497	Human secreted pro
30	254.5	18.7	337	14	AAU39494	Human secreted pro
31	251.5	18.5	333	14	AAU39491	Human secreted pro
32	251	18.4	331	22	AAU90665	Human secreted pro
33	250.5	18.4	342	14	AAU39489	Human secreted pro
34	249	18.3	377	14	AAU39502	Human secreted pro
35	248.5	18.2	342	14	AAU39487	Human secreted pro
36	248.5	18.2	342	14	AAU39496	Human secreted pro
37	247.5	18.2	333	14	AAU39488	Human secreted pro
38	245.5	18.0	333	14	AAU39481	Human secreted pro
39	245.5	18.0	333	14	AAU39495	Human secreted pro
40	245.5	18.0	333	14	AAU39495	Human secreted pro
41	245.5	18.0	377	14	AAU39443	Human secreted pro
42	244.5	18.0	377	14	AAU39444	Human secreted pro
43	243.5	17.9	377	14	AAU39501	Human secreted pro
44	241.5	17.7	363	14	AAU39479	Human secreted pro
45	241.5	17.7	373	14	AAU39486	Human secreted pro

ALIGNMENTS

RESULT	1
AAU61079	standard; Protein; 267 AA.
ID	AAU61079; standard; Protein; 267 AA.
AC	AAU61079;
XX	
DT	07-OCT-1991 (first entry)
XX	
DE	Assumed human apolipoprotein A-1 derivative gene product.
KW	Hyperlipaemia; arteriosclerosis.
XX	
OS	Homo sapiens.
XX	
PN	JP61096998-A.
XX	
PD	15-MAY-1986.
XX	
PF	16-OCT-1984; 84JP-0216986.
XX	
PR	16-OCT-1984; 84JP-0216988.
XX	
PA	(MITU) MITSUBISHI CHEM IND KK.
XX	
DR	WPI; 1986-165025/26.
XX	
DR	N-PSDB; AAN60886.
XX	
PT	Human apo-lipoprotein A-1 (deriv.) prepn. - by providing DNA
XX	fragment in cloning site downstream of expression vector promoter
PT	and introducing into host microorganism.
XX	
PS	Disclosure; Fig 2; 9pp; Japanese.
XX	
CC	The human apolipoprotein may be produced by a suitable transformed

CC host, it is effective in treating hyperlipaemia and arteriosclerosis.
 XX
 SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 7; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKAAVLTIAVFLITGSGARHFWODEPPSPMDRVKDLATVYVYLKDSGRDYVSQFEGS 60
 DB 1 mkaavltiavlitgsgarhfwodeppspmdrvkdlatvvyvylkdsgrdyvsqfegs 60
 OY 61 ALGKQNLKLLDNMDSVSTFSKLRQGLGPTQOEPMNLKEKTEGLRQEMSKDLEEVAK 120
 DB 61 algkqnlklldnmdsvstfsklreqlgpvtqgefnleketeglrgemskdleevak 120
 OY 121 VQPYLDDFQKKWQEMELYRKQVEPLRAELQEGAROKLHELOEKLSPIGEMRDRARAHV 180
 DB 121 vqpylddfqkkwqemelyrkqveplraelqegarqklheleklspigemrdrarahv 180
 OY 181 DALRTHLAPYSDLRQRLAARLEALKENGARLAEYHAKATEHLSTLSEKAPALEDLRQ 240
 DB 181 dalrthlapydselrqrlaarlalengkengarlaeyhakatehlstlsekapaledlrq 240
 OY 241 GLLPVLESFVSFLSALREYTKLNTQ 267
 DB 241 glpvllesfkvsflsaleytkkntq 267

RESULT 2

AAP82128
 ID AAP82128 standard; protein: 267 AA.

AC AAP82128;

DT 24-OCT-1990 (first entry)

DE Entire human preproapoprotein A1.

KW human preproapoprotein A1; high density lipoprotein deficiency; ss.

OS synthetic.

FT Key Location/Qualifiers
 1..18

FT Peptide /label-precursor
 19..24

FT Peptide /label-propeptide
 25..267

FT Protein /label-mature apoprotein

PN EP293357-A.

PD 30-NOV-1988.

PF 24-MAY-1988; 88EP-0870095.

PR 28-MAY-1987; 87GB-0012540.

PA (UNIO) UCB SA.

PI Bollen A, Gobert J, Wulfert E;

DR WPI: 1988-339891/48.

DR N-PSDB; AAN82064.

PT New DNA encoding human preproapoprotein A1 -

PS modified to eliminate hairpin structures

XX Disclosure; ; P; French.

CC The cDNA, 878bp fragment encoding preproapoprotein A1 was detected

CC in clone PUB1609 derived from human liver cells.
 CC See also AAN81258.
 XX
 SQ Sequence 267 AA;

Query Match 100.0%; Score 1362; DB 9; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.7e-99;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKAAVLTIAVFLITGSGARHFWODEPPSPMDRVKDLATVYVYLKDSGRDYVSQFEGS 60
 DB 1 mkaavltiavlitgsgarhfwodeppspmdrvkdlatvvyvylkdsgrdyvsqfegs 60
 OY 61 ALGKQNLKLLDNMDSVSTFSKLRQGLGPTQOEPMNLKEKTEGLRQEMSKDLEEVAK 120
 DB 61 algkqnlklldnmdsvstfsklreqlgpvtqgefnleketeglrgemskdleevak 120
 OY 121 VQPYLDDFQKKWQEMELYRKQVEPLRAELQEGAROKLHELOEKLSPIGEMRDRARAHV 180
 DB 121 vqpylddfqkkwqemelyrkqveplraelqegarqklheleklspigemrdrarahv 180
 OY 181 DALRTHLAPYSDLRQRLAARLEALKENGARLAEYHAKATEHLSTLSEKAPALEDLRQ 240
 DB 181 dalrthlapydselrqrlaarlalengkengarlaeyhakatehlstlsekapaledlrq 240
 OY 241 GLLPVLESFVSFLSALREYTKLNTQ 267
 DB 241 glpvllesfkvsflsaleytkkntq 267

RESULT 3

AAR34032
 ID AAR34032 standard; Protein: 267 AA.

AC AAR34032;

DT 13-AUG-1993 (first entry)

DE Sequence of apo A1.

KW Lipoprotein; apoprotein; B-100; A-I; LDL; HDL; assay.

OS Homo sapiens.

PN W09307165-A.

PD 15-APR-1993.

PF 09-OCT-1992; 92WO-080634.

PR 09-OCT-1991; 91US-0774633.

PR 08-OCT-1992; 92US-055555.

PR 28-JUN-1992; 92US-0901706.

PA (SCRI) SCRIPPS RES INST.

PI Curtiss LK, Koduri KR, Smith RS, Wiltzium JL, Young SG;

DR WPI: 1993-134378/16.

DR N-PSDB; AAQ40030.

PT Polypeptide mimic of native apo B-100 and native apo A-I - useful

PS in assays for LDL and HDL in plasma samples

XX Claim 19; Pages 105-106; 137pp; English.

CC The inventors claim a portion of the polypeptide contg. apo B-100

CC that immunoreacts with antibodies secreted by the hybridoma MH47

CC having ATCC Accession No. 8746. Polypeptides specifically claimed

CC include residues 217-297, 216-310, 216-331, 216-352, 216-377, 1-377,

CC 205-297, 173-297, 140-297. DNA sequences encoding the polypeptides

CC are also claimed. Also claimed are a fusion polypeptide that

CC coflans: (a) a first amino acid residue sequence up to 250 residues
CC in length that includes residues 120-135 of apo A-I, (b) a second
CC amino acid residue sequence up to 375 residues in length that
CC includes residues 217-297 of apo B-100 and DNA encoding it.
XX
SQ Sequence 267 AA;

Sequence 267 AA;

Query Match	100.0%;	Score 1362;	DB 14;	Length 267;
Best Local Similarity	100.0%;	Pred. No. 1.7e-99;		
Matches 267;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	MAKAVLAVLVLVTSSQARHFMQODEPOSIMPRVMDLATVYVDLKSGRPYVSQFGS	60
Db	1	mkaavltlavvlvtssqarhfmqodeposimprvmdlatvyvdlksgrdpyvsqfsgs	60
Qy	61	ALCKOALNLKLDNMDSYNTSTSKLRLEQDGLGYTOEPMDNLKETEGLRDMSKDLFEYKAK	120
Db	61	alckoalnllkldnmhsyntstsklrleqldgytodepmdnlketeglrqmskdlfeevak	120
Qy	121	VOPYLDDFOFKMQOEMELRYRQVETPLRAELQEOGAROKLHELDEKISPLGEEKRBRARAHV	180
Db	121	vopylddfqkwmqemelyrykvetplraelqegarqkhldeqeklsplgeemrdrarahn	180
Qy	181	DALRTHLAFLYSBELRQLAALFLALKENGARLAELYNAKATHTSLTSEKAPALDELRLQ	240
Db	181	dalrthlapydselrtqlaalflalkengarilaelynakathtsltsekapaledrlq	240
Qy	241	GLDPVLESPKVSFLSALFEYVKRKLNTQ	267
Db	241	glldpvlspkvsflsalsevykkrklntq	267

RESULT	4
AAR72705	
ID	AAR72705 standard; Protein; 267 AA
vv	

AC	AAR72705;	
XX		
XX		
DT	31-OCT-1995	(first entry)
XX		
DE	Human apo A-I including signal and propeptide sequences.	
KW	Apo A-I; LDL cholesterol; low density lipoprotein; lipid	
XX		
AS	Homo sapiens.	

FT	Key	Location/Qualifiers
FT	Peptide	1..18
FT		/label= presignal
FT	Peptide	19..24
FT		/label= propeptide
FT	Peptide	120..135
FT		/label= claimed
FT		/note= "as part of fusion polypeptide"
FT	Peptide	19..240
FT		/label= claimed
FT		/note= "as part of fusion polypeptide"

PN	US5408038-A.
XX	
PD	18-APR-1995.

PF 09-OCT-1991; 91US-0774633.

PR	09-OCT-1991;	91US-0774633
PR	18-JUN-1992;	92US-0901706
PR	08-OCT-1992;	92US-0959946

PA (Scripps Res Inst.)

PI Curtiss LK, Koduri KR, Smith RS, Witztum JL, Young SG, XX

DR MPI: 1995-161146/21.
DR N-PSDB: AAQ89634.
XX
XX
PT New apo:1lipoprotein B-100 peptide(s) and fusion peptide(s) - used
PT in assay systems for detecting LDL and HDL cholesterol levels in
PT body fluids.
XX

PS Claim 10; Fig 2; 41pp; English.
XX

CC
CC AAB963J and AAR72705 depict the AA sequence of human apo A-I and its
CC corresp. cDNA, including presignal residues and propeptide.
CC residues, according to Sellmeier et al., DNA 3(4):309 (1984).
CC A dispersible apo A-I/B-100 fusion polypeptide is included which
CC contains a first AA sequence of apo A-I and that includes at
CC least AA sequence positions 120-135 (see AAT72506) and which reacts
CC with pan anti-apo AI antibodies such as: AI-4 ATCCC HB8744; AI-7
CC ATCC HB 8745; AI-9 ATCC HB 8741; AI-10 ATCC HB 9200; AI-11 ATCC
CC HB 9201; AI-12 ATCC HB 9202; AI-13 ATCC HB 9203; AI-14 ATCC HB
CC 9204; AI-18 ATCC HB 9507.

X

SQ Sequence 267 AA.

Query Match	100.0%;	Score 1362;	DB 16;	Length 267;
Best Local Similarity	100.0%;	Pred. No. 1.7e-99;		
Matches 267;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

OY	I	MKFAVETTLAVLELTSTSSQARHFMODEPPOSMPORVDLATTVVYDVKOSGRPYVSOPFGS	60
Db	1	mkaevatlavlliltsqgrhlhwvgdpeppgsrwatvkdlatlvvdtkasgdrtyvsqfegs	60
OY	61	ALGQQLNKLLDNMDSVTSFSKLREOLGPVTGEFMDNIEKETEGILROEMSKDLSEYKAK	120
Db	61	algqqlnkllldnmwdsytsfsklreqlgyvtgefwdnleketegilrgemskdlseevkak	120
OY	121	VOPYLDDEFOKKQWQEEMELYRQKVPEPLAELOEASARQKLHELOEKLSPLGEEMKRBARAHV	180
Db	121	vopylddfokkqwqeemeelyrkvpeplaeloedearqklheldeklspslgemkrdarahv	180
OY	181	DALRTHLAFLAYSDLEQRLLAARLEALKENGSGARLAEEHNAKATGHLSTLSEKAPALEDLRO	240
Db	181	dalrthlapysdeqrllaarleaalkengsarlaeyhakatehsltlsekapaledrlrq	240
OY	241	GILLPVESFKVSPSLAAEELRYKRNTO	267
Db	241	gillpvestfkvsfslaaleelrykkntg	267

RESULT	5
AAV18675	
ID	AAV18675 standard; Protein; 267 AA

AC AAY186

DT 09-JUL-1999 (first entry)
XY

Human apolipoprotein AI protein sequence

KW gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder;
 KW APOA-I; cardiovascular disease; atherosclerosis; restenosis; LCAT;
 KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase
 XX

05 Homo sapiens.
xx

FN MO9910409-AZ.
XX

LD 00 HFN-1333.
XX

FE 20 SEP-1996; 98W0-0520329;
XX

PR 29-SEP-1997; 97US-0940136.

PA (BUTT/) BUTTNER K.

CC (AFTI). These fragments are selected from an 18 kD N-terminal fragment
 CC (amino acids 25-194), a 13 kD N-terminal fragment (amino acids 25-144)
 CC and a 13 kD C-terminal fragment (amino acids 156-267). The AFTI
 CC polypeptides and polynucleotides are useful for regulating T-cell
 CC mediated activation of monocytes and for treating, diagnosing,
 CC ameliorating diseases associated with IL-1 and/or TNF activity.
 CC The diseases are acute pancreatitis, Alzheimer's disease, asthma,
 CC cancer, fever, inflammatory bowel disease, ischemia, multiple
 CC sclerosis, osteoporosis, Parkinson's disease or psoriasis. Numerous
 CC examples of other diseases are given in the specification.
 CC The AFTI nucleic acids are useful as hybridization probes in diagnostic
 CC assays to test for the presence of an AFTI or Apo-A-I DNA in mammalian
 CC tissue or bodily fluid samples.

XX Sequence 267 AA:

Query Match 100.0%; Score 1362; DB 22; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1,7e-99;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAAYTLTAVLFTGSAARHFMQDEPPQSPMDRVKDLATVYVDVLDKSGRDVYSQFEGS 60
 DB 1 mkaavtlavllftgsgarhfwgqdeppspmdrvkdlatvyyvdvldksgrdyvsqfegs 60
 QY 61 ALGKOLMLKLDNWDVSTFESKLRQGLCVTQEFWDNLEKTEGLRQMSKDLSEVYKAK 120
 DB 61 algkqlnklldnwdsvstfskltreqlgrvtqefwdnleketeglrgemskdleevkak 120
 QY 121 VQPYLDLDFQKKQOEEMELYRQKEPRLAELOEGARQKLEHLOEKLSPIGEEMRDARAHV 180
 DB 121 vqpyldldfqqkqoeemelyrqkveprlaelqegarklhelqeklspiqgeemrdrarahv 180
 QY 181 DALRTHLAPYSDLRQRLAARLEALKENGARLAAYHAKATENHLSLSEKAPALDRLQ 240
 DB 181 dalrthlapysdelrqrlaarlealkengarlaeayhakatehslslsekakpaledrlq 240
 QY 241 GLPVLSEKVSFSLAEYTKKLNTO 267
 DB 241 glpvlsefkvsflsaeeytkklnq 267

RESULT 7
 ID AAM08602 standard; protein: 267 AA.
 AC AAM08602;
 XX
 DT 04-SEP-1997 (first entry)

DE Human apolipoprotein A-1 variant "Paris" protein sequence.
 XX
 KW Human; apolipoprotein A-1; variant; mutation; serum lipid; cholesterol;
 KW high density lipoprotein; triglyceride; symptom; cardiovascular disease;
 KW atherosclerosis; restenosis; myocardial infarct; angina; death; stroke;
 KW cardiac decompensation; metabolic deficit.

XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /note= "prepro peptide"
 FT Region 172..178
 FT /note= "this sequence which contains the mutated amino
 FT MISC-difference 175 acid residue is claimed - claim 2"
 FT /note= "changed from Arg residue in wild type protein,
 FT due to a C to T transition mutation"

PN M09637608-A1.
 XX
 PD 28-NOV-1996.
 XX

PF 20-MAY-1996; 96WO-FR00747.
 XX
 PR 22-MAY-1995; 95FR-0006061.
 XX
 PA (INSP) INST PASTEUR LILLE.
 PA (RHON) RHONE-POULENC RORER SA.
 PA (UYPA-) UNIV CURIE PARIS VI P & M.

PI Benoit P, Bruckert E, Deneffe P, Duverger N, Fruchart J;
 PI Luc G, Turping, Assmann G, Funke H;
 DR WPI; 1997-021218/02.
 DR N-PSDB; AAT43691.

PT New variant of human apoA-1 with Cys at position 151 - has
 PT anti-atherogenic activity for treatment and prevention of
 PT cardiovascular disease
 PS
 PS Claim 2; Page -: 58pp; French.

CC This is the amino acid sequence of a human apolipoprotein A-1 variant
 CC designated the "Paris" variant which has a Cys replacing the Arg residue
 CC at position 151. The substitution is generated by a mutation of
 CC the C nucleotide at position 523 in the wild type gene to a T residue,
 CC changing the encoded residue from an Arg to a Cys. The gene was isolated
 CC from a patient with an unusual pattern of serum lipids i.e. low levels of
 CC apoA-1 and high density lipoprotein (HDL)-cholesterol and high
 CC triglycerides, but showing symptoms of atherosclerosis. The new variant
 CC protein has anti-atherogenic activity so is useful for treatment and
 CC prevention of cardiovascular diseases such as atherosclerosis,
 CC restenosis, myocardial infarct, angina, sudden death, stroke and cardiac
 CC decompensation, or more generally any condition involving genetic or
 CC metabolic deficit of apoA-1.
 CC Note: this sequence is not given in the specification but is generated
 CC from the wild type apoA-1 gene disclosed in the specification and has
 CC the appropriate amino acid changed.

XX Sequence 267 AA:

Query Match 99.4%; Score 1354; DB 18; Length 267;
 Best Local Similarity 99.6%; Pred. No. 7.3e-99;
 Matches 266; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKAAYTLTAVLFTGSAARHFMQDEPPQSPMDRVKDLATVYVDVLDKSGRDVYSQFEGS 60
 DB 1 mkaavtlavllftgsgarhfwgqdeppspmdrvkdlatvyyvdvldksgrdyvsqfegs 60
 QY 61 ALGKOLMLKLDNWDVSTFESKLRQGLCVTQEFWDNLEKTEGLRQMSKDLSEVYKAK 120
 DB 61 algkqlnklldnwdsvstfskltreqlgrvtqefwdnleketeglrgemskdleevkak 120
 QY 121 VQPYLDLDFQKKQOEEMELYRQKEPRLAELOEGARQKLEHLOEKLSPIGEEMRDARAHV 180
 DB 121 vqpyldldfqqkqoeemelyrqkveprlaelqegarklhelqeklspiqgeemrdrarahv 180
 QY 181 DALRTHLAPYSDLRQRLAARLEALKENGARLAAYHAKATENHLSLSEKAPALDRLQ 240
 DB 181 dalrthlapysdelrqrlaarlealkengarlaeayhakatehslslsekakpaledrlq 240
 QY 241 GLPVLSEKVSFSLAEYTKKLNTO 267
 DB 241 glpvlsefkvsflsaeeytkklnq 267

RESULT 8
 ID AAP80668 standard; protein: 268 AA.
 AC AAP80668;
 XX
 DT 24-OCT-1990 (first entry)

XX
 XX
 XX
 XX

DE Recombinant human preproapoprotein A1.
 XX human preproapoprotein A1; high density lipoprotein deficiency; ss.
 KW
 XX
 OS synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT Peptide /label=precursor
 FT Peptide 19..25
 FT Peptide /label=proprotein
 FT Protein 26..268
 FT /label=mature apoprotein A1
 FT
 XX EP293357-A.
 XX
 XX 30-NOV-1988.
 PD
 XX 24-MAY-1988; 88EP-0870095.
 PP
 XX 28-MAY-1987; 87GB-0012540.
 PR
 XX (UNIO) UCB SA.
 PA
 XX Bollen A, Gobert J, Wulfert E;
 PI
 XX WPI; 1988-339891/48.
 DR
 XX N-PSDB; AAN81258.
 PT
 PT New DNA encoding human preproapoprotein A1 -
 PT modified to eliminate hairpin structures
 XX
 XX Claim 1: Page 12; 25pp; French.
 PS
 XX Met at posn 19 is inserted as an extra amino acid c.f. wild-type
 CC protein.
 CC The DNA fragment used to replace the wild-type sequence encoding
 CC amino acids -6 to +14 (= Arg 20 to Leu 39) modifies codons
 CC corresponding to wild-type amino acids -6, -1, 1, 3, 4, 5, 6, 7,
 CC 10, 11 and 14. The changed codons still encode the same amino acids
 CC as in the wild-type protein but reduce formation of secondary
 CC structures in mRNA.
 CC See also AAN82064.
 CC
 CC Sequence 268 AA:
 SO
 Query Match 99.2%; Score 1351.5; DB 9; Length 268;
 Best Local Similarity 99.6%; Pred. No. 1.2e-98;
 Matches 267; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MKAVALTLAVLFLTGSQA-RHFMOODEPPQSPMDRVKDLATVYVDVLDKSGRDYVSQFEG 59
 DB 1 mkaavltlavflitgsqamhfwqdeppspmdrvkdlatvvydvldksgrdyvsqfeg 60
 QY 60 SALGKQLNLKLDNMDSVTSFESKIREQLGPTQGEFWNLEKETGLRQESKDLSEYKA 119
 DB 1 mkaavltlavflitgsqamhfwqdeppspmdrvkdlatvvydvldksgrdyvsqfeg 60
 QY 61 salgkqlnlkldnmdsvtsfeskireqlgptqgefwndleketglrqemskdlseevka 120
 DB 61 salgkqlnlkldnmdsvtsfeskireqlgptqgefwndleketglrqemskdlseevka 120
 QY 120 KVPYIDDFQKKQWEMELXKQKVEPLRAELOEGARQKLTNHEOELSPGCEMRBARAH 179
 DB 121 kvpylddfqkkwgemelyrqkveplraelqegarqklhelqeklsplgeemrdrarh 180
 QY 121 kvpylddfqkkwgemelyrqkveplraelqegarqklhelqeklsplgeemrdrarh 180
 DB 121 kvpylddfqkkwgemelyrqkveplraelqegarqklhelqeklsplgeemrdrarh 180
 QY 180 VDLRTHLAPYSDLRQRLAARLEALKENGARLAELAHAKATEHLSLSEKAKPALLEDLR 239
 DB 181 vdlrthlapysdelrqrlaarlealkengarlarlaehahakatehlsstlsekapaledlr 240
 QY 240 OGILLPVLESFKVSLSEALEEYTKKLNTQ 267
 DB 241 qgilpvlsefkvsfslaleeytkklntq 268

AAU33170
 ID AAU33170 standard; Protein; 299 AA.
 XX
 XX AAU33170;
 AC
 XX 18-DEC-2001 (first entry)
 DT
 XX Novel human secreted protein #3661.
 DE
 XX Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 KW
 XX Homo sapiens.
 OS
 XX WO200179449-A2.
 PN
 XX 25-OCT-2001.
 PD
 XX 16-APR-2001; 2001WO-US08656.
 PP
 XX 18-APR-2000; 2000US-0552929.
 PR
 XX 26-JAN-2001; 2001US-0770160.
 PA
 XX (HYSE-) HYSEQ INC.
 PI
 XX Tang YT, Liu C, Drmanac RT;
 PT
 PT WPI; 2001-611725/70.
 DR
 XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 PT
 XX Claim 20: Page 718; 765pp; English.
 PS
 XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 CC
 CC Sequence 299 AA:
 SO
 Query Match 97.5%; Score 1328; DB 22; Length 299;
 Best Local Similarity 97.0%; Pred. No. 9.4e-97;
 Matches 259; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MKAVALTLAVLFLTGSQA-RHFMOODEPPQSPMDRVKDLATVYVDVLDKSGRDYVSQFEG 60
 DB 33 mkaavltlavflitgsqamhfwqdeppspmdrvkdlatvvydvldksgrdyvsqfegs 92
 QY 61 ALGKQLNLKLDNMDSVTSFESKIREQLGPTQGEFWNLEKETGLRQESKDLSEYKA 120
 DB 93 algkqlnlkldnmdsvtsfeskireqlgptqgefwndleketglrqemskdlseevka 152
 QY 121 KVPYIDDFQKKQWEMELXKQKVEPLRAELOEGARQKLTNHEOELSPGCEMRBARAH 180
 DB 153 kvpylddfqkkwgemelyrqkveplraelqegarqklhelqeklsplgeemrdrarh 212
 QY 181 DALRTHLAPYSDLRQRLAARLEALKENGARLAELAHAKATEHLSLSEKAKPALLEDLRQ 240

Db 213 daltlrlhapysgdlrqlgallgallrengsarmgynahatehstlsekakpaledlrg 272
 QY 241 GLPLVLESEFKVSFLSALEEYTKRLNTQ 267
 Db 273 glplvlesfkvsflsaaeeytkrlntq 299

RESULT 10

AAP81082 standard; protein; 243 AA.

AC AAP81082;

DT 14-JAN-1991 (first entry)

DE Sequence of mature human apolipoprotein AI (apoAI).

KW Atherosclerosis; therapy; cardiovascular disease.

OS Homo sapiens.

PN W08803166-A.

PD 05-MAY-1988.

PF 21-OCT-1987; 87WO-EP00621.

PR 23-OCT-1986; 86GB-0025435.

PA (FARM) FARMITALIA C ERBA SPA.

PI Lorenzetti R, Monaco L, Soria M, Palomba R, Isacchi A, Sarmientos P;

DR WPI; 1988-133240/19.

DR N-PSDB; AAN80243.

PT Recombinant human apo:lipoprotein AI -
 used to lower plasma cholesterol and/or tri glyceride levels and
 to combat atherosclerosis and cardiovascular diseases

PS Disclosure; Fig 1; 51pp; English.

CC The protein comprising apo AI genetic variants may be used to lower
 CC plasma cholesterol and/or triglyceride levels. They may also be used to
 CC combat atherosclerosis and cardiovascular diseases such as coronary
 CC heart disease. Preid. proteins are Met-apo AI, Met-apo AI-T6, Met-apo
 CC AI-MI and Met-apo AI-T6/MI.

SO Sequence 243 AA:

Query Match 91.1%; Score 1241; DB 9; Length 243;
 Best Local Similarity 100.0%; Pred. No. 5.2e-90;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 DEPPSPMDRVKDLNVTYVDVKDSGRDYVSQESASLGKQNLKLDNMDSVSTFSKL 84
 Db 1 deppspmdrvkdlntvtdvdkdsgrdyvsqesalqkqnlkldnmwdsvtstfskl 60
 QY 85 RBQLGPVTOEFWNLKETEGLRQEMSKDLEEVKAKVOPYLDDFOKKQOEEMELYRQKVE 144
 Db 61 reglqpvtfwefwlnleketeglrqemskdleevkakvpylddfkqkwqeemelyrqkve 120
 QY 145 PLRALGEGARQKHLHLOEKLSPLGEEKMDRRAHVDALRTHLAYSDELRLAARLEA 204
 Db 121 plraelgegarqkhlhelqeklsplgeemdrarahvdalrthlapydselrqlaartlea 180
 QY 205 LKENGARLAETVHAKEATHLSTLSEKAKPALDEDLROGLPLLESFKVSFLSALEEYTKL 264
 Db 181 lkengarlaetvhaekathlslstlsekakpaledlrglpllesfkvsflsaaeeytkl 240
 QY 265 NTQ 267

Db 241 ntq 243

RESULT 11

AAR56863 standard; protein; 264 AA.

AC AAR56863;

DT 26-JAN-1995 (first entry)

DE Apo-lipoprotein AI-M.

KW Apo-lipoprotein AI-M; Apo AI-M; Escherichia coli; plasmid pKP683;

KW vector; atherosclerosis; cardiovascular disease.

OS Homo sapiens.

PN W09413819-A.

PD 23-JUN-1994.

PF 09-DEC-1993; 93WO-SE01061.

PR 11-DEC-1992; 92SE-0003753.

PA (KABI) KABI PHARMACIA AB.

PI Abrahamson L, Holmgren E, Kalderen C, Lake M, Mikaelsson A;

DR Seglitz T;

DR WPI; 1994-217892/26.

DR N-PSDB; AAQ68357.

PT Expression vector for extracellular prodn of apo-lipoprotein AI-M
 in E. coli - includes inducible promoter and signal peptide
 PT sequences providing improved yield, useful in treating
 PT atherosclerosis and cardiovascular disease.

PS Disclosure; Fig. 3; 33pp; English.

CC Plasmid pKP683 encodes human apo-lipoprotein AI-M in E. coli. The
 CC NotI-HindIII segment of pKP683 and the deduced amino acid sequence
 CC of the translated Apo AI-M protein were determined. The plasmid
 CC provides high yields of extracellular Apo AI-M.

SO Sequence 264 AA:

Query Match 90.9%; Score 1237.5; DB 15; Length 264;
 Best Local Similarity 91.9%; Pred. No. 1.1e-89;

Matches 248; Conservative 4; Mismatches 9; Indels 9; Gaps 2;

QY 1 MKAAYLTAVL--FLTGSQARHFWQDEPPSPMDRVKDLATVYVDVKDSGRDYVSOF 57
 Db 1 mkaayltavlagfatvana-----deppspmdrvkdlavtyvdvdkdsgrdyvsqf 54
 QY 58 EGSALGKQNLKLDNMDSVSTFSKLREOLGPVTOEFWNLKETEGLRQEMSKDLEEV 117
 Db 55 egsalqkqnlkldnmwdsvtstfsklreglqpvtfwefwlnleketeglrqemskdleev 114
 QY 118 KAKVOPYLDDFOKKQOEEMELYRQKVEPLRAELQEGARQKHLHLOEKLSPLGEEKMDRRA 177
 Db 115 kakvpylddfqkqkwqeemelyrqkveplraelqegarqkhlhelqeklsplgeemdrar 174
 QY 178 AHVDALRTHLAYSDELRLAARLEALKENGARLAETVHAKEATHLSTLSEKAKPALD 237
 Db 175 ahvdalrthlapydselrqlaarlalengkengarlaetvhaekathlslstlsekakpaled 234
 QY 238 IROGLPLVLESEFKVSFLSALEEYTKRLNTQ 267
 Db 235 lrglplvlesfkvsflsaaeeytkrlntq 264

CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (1) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC anabolic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAU28020-AAU28395 represent novel human secreted protein
 CC amino acid sequences of the invention.
 SQ Sequence 244 AA;

Query Match 89.3%; Score 1216.5; DB 22; Length 244;
 Best Local Similarity 91.0%; Pred. No. 4.4e-88;
 Matches 243; Conservative 1; Mismatches 0; Indels 23; Gaps 1;

QY 1 MKAALVLTAVLEFLNGSQARHFWODEPPQSPMDRVKDLATVYVDVLDKSGRDYVSQFEGS 60
 DB 1 mkaavltlavlfllgsgarhfwqdeppspmdrvkdlatvyvdlksgk----- 51
 QY 61 ALGKQNLKLLDNMDSVTSFESKLEQDLPVTOEFMNLKETEGLROEMSKDLEEVKAK 120
 DB -----dsytsfkskireqlgpytqgefwnlekeeglrqemskaleevkak 97
 QY 121 VQPYLDPFQKKWOEMELRYRQKVEPLRAELQEGARQKLEHLOEKLSPGEMRRAAHV 180
 DB 98 vqpylddfqkwwgeemelyrqkveplraelqegarklhelgeklspdgeemdrarahv 157
 QY 181 DALRTHLAPYSDELQRRLAARLEALKENGARLAELYHAKATEHLSTLSKAPALEDLMO 240
 DB 158 dalrthlapysdelrqrarlaarlealkengarilaelyhakatehlstlskapaledlmo 217
 QY 241 GLPLVESFVSFLSALEETKKLNTQ 267
 DB 218 glplvesfvsflsalleetkklnq 244

RESULT 14

AAU29835
 ID AAU29835 standard; Protein; 221 AA.
 AC AAU29835;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #326.

KW Human: vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-611725/70.

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 PS Claim 20; Page 199; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemia. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 SQ Sequence 221 AA;

Query Match 74.1%; Score 1009; DB 22; Length 221;
 Best Local Similarity 87.9%; Pred. No. 8.6e-72;
 Matches 203; Conservative 2; Mismatches 2; Indels 24; Gaps 2;

QY 1 MKAALVLTAVLEFLNGSQARHFWODEPPQSPMDRVKDLATVYVDVLDKSGRDYVSQFEG 59
 DB 14 mkaavltlavlfllgsgarhfwqdeppspmdrvkdlatvyvdlksgk----- 65
 QY 60 SALGKQNLKLLDNMDSVTSFESKLEQDLPVTOEFMNLKETEGLROEMSKDLEEVKA 119
 DB 66 -----dsytsfkskireqlgpytqgefwnlekeeglrqemskaleevka 110
 QY 120 KVOPLYDDPFQKKWOEMELRYRQKVEPLRAELQEGARQKLEHLOEKLSPGEMRRAAHV 179
 DB 111 kvoplydddfqkwwgeemelyrqkveplraelqegarklhelgeklspdgeemdrarahv 170
 QY 180 VDALTHTLAPYSDELQRRLAARLEALKENGARLAELYHAKATEHLSTLSK 230
 DB 171 vdalrthlapysdelrqrarlaarlealkengarilaelyhakatehlstlsk 221

RESULT 15

AAU30268
 ID AAU30268 standard; Protein; 318 AA.
 AC AAU30268;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #759.

KW Human: vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-611725/70.

XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX

PS Claim 20; Page 270; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.

XX
 SQ Sequence 318 AA:

67.0%; Score 912.5; DB 22; Length 318;

Query Match Best Local Similarity 73.9%; Pred. No. 5.4e-64;
 Matches 207; Conservative 17; Mismatches 43; Indels 13; Gaps 13;

QY 1 MKAALVLAFLVLTNGSQARHFWQ-QDEPPQSPMDRVKDLAT-VYVDYLNDSGRD-VYSGF 57
 DB 14 mkaavltlavltflgsgarhfwgqxprraawdrvkdlatrvpwtvltkeqrteyvsqf 73
 QY 58 EGSALGK-QLMKTLLDNW-DSVTSTFS-KLRBOIGPYTOEFMDNLEKETGLROEMSKDL 114
 DB 74 eglrlgensxtklklidwqgrxstfqpscakqipitgfwynleketegfrqemskdl 133
 QY 115 EYVKAQVOPV-LDDFOKK-WQEMELYRQKVEPL-RAELQEGAR-QKLHFL-QEKLSPLG 169
 DB 134 eevkavqpyrllddqtgerswqemelyrkvpeplarknfgearpeslhelarrslspig 193
 QY 170 EEM-RDRAHVAIDARTILAPYSDELNRQLA-ARLEALKENGARLAELYHAKATEHLSTL 227
 DB 194 eavsrprairpmwdalrthlapysdeampalgraplgalrengarmgynaqatenstl 253
 QY 228 SEKAPALEDLROGLLPVLESEKVSFLSALEEYTKKLNTQ 267
 DB 254 sekakpaledlrqglpvlsefksflsaleeyckklnq 293

Search completed: September 22, 2002, 12:05:15
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:06:29 ; Search time 66.91 Seconds

(Without alignments)
127.813 Million cell updates/sec

Title: US-09-803-918a-2_COPY_25_113

Perfect score: 468

Sequence: 1 DEPPQSPMDRVRKDLATVYD.....EFMDLKEKTEGLRQEMSD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

283138

Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	468	100.0	267 1 LPHUAI	apolipoprotein A-I
2	443	94.7	267 1 A26529	apolipoprotein A-I
3	443	94.7	267 2 JS0079	apolipoprotein A-I
4	407	87.0	266 1 LPDCAI	apolipoprotein A-I
5	405	86.5	264 2 S31394	apolipoprotein A-I
6	405	86.5	265 2 A46018	apolipoprotein A-I
7	393	84.0	265 2 JT0672	apolipoprotein A-I
8	383	81.8	265 1 LPR81B	apolipoprotein A-I
9	383	81.8	265 1 A56858	apolipoprotein A-I
10	383	81.8	266 1 LPR81Z	apolipoprotein A-I
11	378.5	80.9	241 2 A24998	apolipoprotein A-I
12	359	76.7	259 2 A24700	apolipoprotein A-I
13	355	75.9	231 2 JC0704	apolipoprotein A-I
14	343	73.3	262 2 JC1237	apolipoprotein A-I
15	343	73.3	264 2 S22420	apolipoprotein A-I
16	223	47.6	264 1 LPHUAI	apolipoprotein A-I
17	223	47.6	264 1 JCS456	apolipoprotein A-I
18	220	47.0	246 2 A61448	apolipoprotein A-I
19	106	22.6	34 2 S67972	apolipoprotein A-I
20	106	22.6	36 2 A56866	apolipoprotein A-I
21	101	21.6	20 2 A05313	apolipoprotein A-I
22	92	19.7	396 1 LPHUAI	apolipoprotein A-I
23	90	19.2	391 1 LPRMA4	apolipoprotein A-I
24	90	19.2	429 1 S29565	apolipoprotein A-I
25	86	18.4	401 2 A47141	apolipoprotein A-I
26	83	17.7	312 1 LPRTE	apolipoprotein A-I
27	81	17.3	365 2 D71559	apolipoprotein A-I
28	81	17.3	391 2 B40892	apolipoprotein A-I
29	81	17.3	394 2 A25281	apolipoprotein A-I

ALIGNMENTS

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30      81      17.3      395      2      A40892      apolipoprotein A-I
31      81      17.3      399      2      C40892      apolipoprotein A-I
32      78.5      16.8      2697      2      T25444      hypothetical prote
33      78      16.7      311      2      JU0036      apolipoprotein E p
34      76.5      16.3      207      2      S56209      probable membrane
35      73      15.6      491      2      T27661      hypothetical prote
36      72.5      15.5      164      2      B37842      hypothetical prote
37      72.5      15.5      192      2      A81987      hypothetical prote
38      71.5      15.3      625      2      G90570      hypothetical prote
39      70      15.0      453      2      A84167      UDP-glucose 4-epim
40      70      15.0      453      2      A49022      tryptophanase (EC
41      70      15.0      453      2      B49022      tryptophanase (EC
42      69      14.7      926      2      H84415      DNA-directed RNA p
43      68.5      14.6      1560      2      T09202      probable tail comp
44      68.5      14.6      865      2      AC1966      hypothetical prote
45      68.5      14.6      4725      1      A44357      dynein heavy chain

RESULT      1
LPHUAI
apolipoprotein A-I precursor [validated] - human
N:Alternate names: apoa-I-2; apoa-I-4; preproapoa-I; prostacyclin stabilizing factor
C:Species: Homo sapiens (man)
C>Date: 14-Nov-1983 #sequence:revision 14-Nov-1983 #text-change 08-Dec-2000
C:Accession: A90947; B90947; S02373; A93465; A21147; A93519; B93519; A93472; A94010;
6197
R:Seilhamer, J.J.; Protter, A.A.; Frossard, P.; Levy-Wilson, B.
DNA 3, 309-317, 1984
A:Title: Isolation and DNA sequence of full-length cDNA and of the entire gene for hu
A:Reference number: A90947; MUID:85026665
A:Accession: A90947
A:Molecule type: DNA
A:Residues: 1-267 <SEI>
A:Cross-references: GB:X01038; NID:928769; PIDN:CAA25519.1; PID:9296635
A:Accession: B90947
A:Molecule type: mRNA
A:Residues: 1-267 <SE2>
A:Cross-references: GB:X01038; NID:928769; PIDN:CAA25519.1; PID:9296635
R:Markides, S.C.; Ruiz-Opazo, N.; Hayden, M.; Nussbaum, A.L.; Breslow, J.L.; Zannis,
Eur. J. Biochem. 173, 465-471, 1988
A:Title: Sequence and expression of Tangier apoa-I gene.
A:Reference number: S02373; MUID:88196137
A:Accession: S02373
A:Molecule type: DNA
A:Residues: 1-267 <MAK>
A:Cross-references: EMBL:X07496; NID:928774; PIDN:CAA30377.1; PID:9296729
R:Shoulders, C.C.; Kornblith, A.R.; Munro, B.S.; Baralle, F.E.
Nucleic Acids Res. 11, 2827-2837, 1983
A:Title: Gene structure of human apolipoprotein AI.
A:Reference number: A93465; MUID:83220822
A:Accession: A93465
A:Molecule type: DNA
A:Residues: 1-267 <SHO>
A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518;
R:Karathanasis, S.K.; Zannis, V.I.; Breslow, J.L.
Proc. Natl. Acad. Sci. U.S.A. 80, 6147-6151, 1983
A:Title: Isolation and characterization of the human apolipoprotein A-I gene.
A:Reference number: A21147; MUID:84016011
A:Accession: A21147
A:Molecule type: DNA
A:Residues: 1-267 <KAR>
A:Cross-references: GB:J00098; GB:J03222; NID:9178765; PIDN:AA859514.1; PID:9178768
Nucleic Acids Res. 12, 3917-3932, 1984
A:Title: Human apolipoproteins AI, AII, CII and CIIT. cDNA sequences and mRNA abundan
A:Reference number: A93519; MUID:84221405
A:Accession: A93519
A:Molecule type: mRNA
A:Residues: 1-267 <SHA>
A:Cross-references: GB:X00566; NID:928765; PIDN:CAA25232.1; PID:9732753

```

A:Accession: B93519
 A:Molecule type: DNA
 A:Residues: 1-24 <SH2>
 R:Chenry, P.; Chan, L.
 Nucleic Acids Res. 11, 3703-3715, 1983
 A:Title: Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.
 A:Reference number: A93472; MUID:83220772
 A:Accession: A93472
 A:Molecule type: mRNA
 A:Residues: 1-267 <CHE>
 A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GB:R:Law, S.W.; Brewer Jr., H.B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 66-70, 1984
 A:Title: Nucleotide sequence and the encoded amino acids of human apolipoprotein A-I mRNA
 A:Reference number: A94010; MUID:84119404
 A:Accession: A94010
 A:Molecule type: mRNA
 A:Residues: 1-267 <LAW>
 A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GB:R:Zannis-Vassiliou, V.I.; Karathanasis, S.K.; Keutmann, H.T.; Goldberger, G.; Breslow, J.L.
 Proc. Natl. Acad. Sci. U.S.A. 80, 2574-2578, 1983
 A:Title: Intracellular and extracellular processing of human apolipoprotein A-I: secreted
 A:Reference number: A21118; MUID:83195100
 A:Accession: A21118
 A:Molecule type: mRNA
 A:Residues: 1-24 <ZAN>
 R:Brewer Jr., H.B.; Fairwell, T.; Kay, L.; Meng, M.; Roman, R.; Law, S.; Light, J.A.
 Biochem. Biophys. Res. Commun. 113, 626-632, 1983
 A:Title: Human plasma proapo-A-I: isolation and amino-terminal sequence.
 A:Reference number: A90112; MUID:83256553
 A:Accession: A90112
 A:Molecule type: protein
 A:Residues: 19-27 <BRE>
 R:Brewer Jr., H.B.; Fairwell, T.; LaBue, A.; Roman, R.; Houser, A.; Bronzert, T.J.
 Biochem. Biophys. Res. Commun. 80, 623-630, 1978
 A:Title: The amino acid sequence of human APOA-I, an apolipoprotein isolated from high density lipoproteins
 A:Reference number: A90209; MUID:78123731
 A:Accession: A90209
 A:Molecule type: protein
 A:Residues: 25-57, 'Q', '59-169', 'Q', '172-267' <BR2>
 R:Yui, Y.; Aoyama, T.; Morishita, H.; Takahashi, M.; Takatsu, Y.; Kawai, C.
 J. Clin. Invest. 82, 803-807, 1988
 A:Title: Serum proapoA-I stabilizing factor is identical to apolipoprotein A-I (Apo A-I)
 A:Reference number: A30516; MUID:88331387
 A:Accession: A30516
 A:Molecule type: protein
 A:Residues: 25-56 <YUI>
 R:Nichols, W.C.; Dwalet, F.E.; Liepnieks, J.; Benson, M.D.
 Biochem. Biophys. Res. Commun. 156, 762-768, 1988
 A:Title: Variant apolipoprotein AI as a major constituent of a human hereditary amyloid.
 A:Reference number: A31582; MUID:89050104
 A:Accession: A31582
 A:Molecule type: protein
 A:Residues: 25-49, 'R', '51-85', 'D', '87-107' <NIC>
 A:Note: variant sequence from patient with familial amyloidotic polyneuropathy type III
 R:Manjunath, P.; Marcel, Y.L.; Ume, J.; Seidah, N.G.; Chretien, M.; Chapdelaine, A.
 J. Biol. Chem. 264, 16853-16857, 1989
 A:Title: Apolipoprotein A-I binds to a family of bovine seminal plasma proteins.
 A:Reference number: A34409; MUID:89380318
 A:Accession: A34409
 A:Molecule type: protein
 A:Residues: 25-48 <MAN>
 R:Stoffel, W.; Binczek, E.
 Biol. Chem. Hoppe-Seyler 369, 1055-1063, 1988
 A:Title: Structural requirements of human preproapolipoprotein AI for translocation and secretion
 A:Reference number: S02737; MUID:89149957
 A:Accession: S02737
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-6, 'AV', '9', 'LV', '12-29' <STO>
 A:Note: part of this sequence, including the amino end of the mature protein, was confirmed by Stoffel, W.; Binczek, E.
 Biol. Chem. Hoppe-Seyler 372, 481-488, 1991

A:Title: Transient expression of wild type and mutant human apolipoprotein AI in COS cells
 A:Reference number: S16197; MUID:92029676
 A:Contents: annotation; extension of studies in reference S02737
 R:Stoffel, W.; Kruger, E.; Deutzmann, R.
 Hoppe-Seyler's Z. Physiol. Chem. 364, 227-237, 1983
 A:Title: Cell-free translation of human liver apolipoprotein AI and AII mRNA processes
 A:Reference number: A19913; MUID:83236195
 A:Accession: B19913
 A:Molecule type: protein
 A:Residues: 1-6, 'X', '8-13', 'XXX', '17-18', 'XX', '21', 'X', '23-25', 'X', '27-29' <ST2>
 R:Enholm, C.; Bozas, S.E.; Tenkaten, H.; Kirsbaum, L.; Metso, J.; Murphy, B.; Walke
 Biochim. Biophys. Acta 1086, 255-260, 1991
 A:Title: The apolipoprotein A-I binding protein of placenta and the SP-40,40 protein
 A:Reference number: A56815; MUID:92075698
 A:Accession: A56815
 A:Molecule type: protein
 A:Residues: 25-31, 'P', '33' <EHN>
 A:Experimental source: serum
 A:Note: sequence extracted from NCBI backbone (NCBI:69759)
 A:Note: 32-Trp was also found
 R:Knittke, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
 Biochemistry 33, 1988-1993, 1994
 A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipoproteins
 A:Reference number: A54223; MUID:94162201
 A:Accession: A54223
 A:Molecule type: protein
 A:Residues: 25-39 <KUN>
 R:Mouglievsky, N.; Roobol, C.; Loriau, R.; Guillaume, J.P.; Jacobs, P.; Cravador, A.; Dina, B.; 429-436, 1989
 A:Title: Production of human recombinant proapolipoprotein A-I in Escherichia coli: p
 A:Reference number: 139476; MUID:89377481
 A:Accession: 139476
 A:Molecule type: mRNA
 A:Residues: 19-267 <RES>
 A:Cross-references: GB:M29068; NID:9178774; PID:AA51747.1; PID:9178775
 R:Higuchi, K.; Law, S.W.; Hoeg, J.M.; Schumacher, U.K.; Meglin, N.; Brewer, H.B.
 J. Biol. Chem. 263, 18530-18536, 1988
 A:Title: Tissue-specific expression of apolipoprotein A-I (ApoA-I) is regulated by the
 A:Reference number: 139475; MUID:89034040
 A:Accession: 139475
 A:Molecule type: DNA
 A:Residues: 1-14 <RE2>
 A:Cross-references: GB:J04066; NID:9178763; PID:AA51746.1; PID:9553183
 R:Breslow, J.L.
 Annu. Rev. Biochem. 54, 699-727, 1985
 A:Title: Human apolipoprotein molecular biology and genetic variation.
 A:Reference number: A90042; MUID:85278004
 A:Contents: annotation; review of sequences, variants and gene location
 R:Hoeg, J.M.; Meng, M.S.; Roman, R.; Fairwell, T.; Brewer Jr., H.B.
 J. Biol. Chem. 261, 3911-3914, 1986
 A:Title: Human apolipoprotein A-I. Post-translational modification by fatty acid acyl
 A:Reference number: A92577; MUID:86140194
 A:Contents: annotation; acylation with palmitate
 A:Note: an undetermined serine or threonine is acylated by fatty acid; the acylating
 R:Law, S.W.; Brewer, H.B.
 J. Biol. Chem. 260, 12810-12814, 1985
 A:Title: Tangier disease: The complete mRNA sequence encoding for preproapo-A-I.
 A:Reference number: 155236; MUID:86008382
 A:Accession: 155236
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-143, 'D', '145-267' <RE3>
 A:Cross-references: GB:M11791; NID:9178776; PID:AA53545.1; PID:9178777
 C:Comment: Apolipoprotein A-I precursor is synthesized in the liver and small intestine
 A:Gene: GDB:APOA1
 A:Cross-references: GDB:119684; OMIM:107680
 A:Map position: 11q23.3-11q23.3
 A:Introns: 15/1; 67/2
 C:Function: participates in the reverse transport of cholesterol from tissues to the liver
 A:Description: participates in the reverse transport of cholesterol from tissues to the liver
 A:sterol acyltransferase (LCAT); noncovalently binds and stabilizes prostacyclin (PGI-2)

C:Superfamily: apolipoprotein A-I
 C:Keywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid binding; lipid
 F:1-18/Domain: signal sequence #status experimental <SIG>
 F:19-24/Domain: propeptide #status experimental <PRO>
 F:25-267/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 100.0%; Score 468; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2,9e-38;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPMDRVKDLATVYVDYLDKSGRDYVSQFEGSALGKQLNLKLDNMDSVTSTFSKL 60
 |||||||
 Db 25 DEPPQSPMDRVKDLATVYVDYLDKSGRDYVSQFEGSALGKQLNLKLDNMDSVTSTFSKL 84
 QY 61 REQLGPVTOEFMDNLEKETEGGLROEMSKD 89
 |||||||
 Db 85 REQLGPVTOEFMDNLEKETEGGLROEMSKD 113

RESULT 2

A26529
 A:apolipoprotein A-I precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 30-Sep-1989 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999
 C:Accession: A26529; A26627; S23135; A57766
 R:Herbert, P.N.; Bausserman, L.L.; Lynch, K.M.; Saritelli, A.L.; Kantor, M.A.; Nicotoli,
 R:Polites, H.G.; Melchior, G.W.; Castle, C.K.; Marottil, K.R.
 Gene 49, 103-110, 1986
 A:Title: The primary structure of cynomolgus monkey apolipoprotein A-I deduced from the
 A:Accession: A26529; MUID:87191989

A:Molecule type: mRNA
 A:Residues: 1-267 <POL>
 A:Cross-references: GB:M5411; NID:g342074; PIDN:AAA36834.1; PID:g342075
 Biochemstry 26, 1457-1463, 1987
 A:Title: Homologues of the human C and A apolipoproteins in the Macaca fascicularis (cyt
 A:Reference number: A26627; MUID:87185451
 A:Accession: A26627

A:Molecule type: protein
 A:Residues: 25-48 <HER>
 R:Murray, R.W.; Marottil, K.R.
 Biochim. Biophys. Acta 1131, 207-210, 1992
 A:Title: Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene and corres
 A:Reference number: S23135; MUID:92305062
 A:Accession: S23135

A:Molecule type: DNA
 A:Residues: 1-12, 'L', '14-267 <MUR>
 A:Cross-references: GB:M83242; NID:g342070; PIDN:AAA36832.1; PID:g342071
 R:Sorci-Thomas, M.; Kearns, M.W.
 J. Biol. Chem. 266, 18045-18050, 1991
 A:Title: Transcriptional regulation of the apolipoprotein A-I gene.
 A:Reference number: A57766; MUID:92011532
 A:Accession: A57766

A:Molecule type: DNA
 A:Residues: 1-10 <RES>
 A:Cross-references: GB:M69223; NID:g342066; PIDN:AAA36831.1; PID:g553820
 C:Comment: The precursor is synthesized in the liver and small intestine. The propeptide
 C:Comment: ApoA-I makes up about 70% of the protein of the high density lipoproteins (HDL
 Y Promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin
 C:Genetics:
 A:Introns: 15/1; 67/2

C:Superfamily: apolipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem repe
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PRO>
 F:25-267/Product: apolipoprotein A-I #status predicted <MAT>

Query Match 94.7%; Score 443; DB 1; Length 267;
 Best Local Similarity 93.3%; Pred. No. 8e-36;
 Matches 83; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEPPQSPMDRVKDLATVYVDYLDKSGRDYVSQFEGSALGKQLNLKLDNMDSVTSTFSKL 60
 |||||||
 Db 25 DEPPQSPMDRVKDLATVYVDYLDKSGRDYVSQFEGSALGKQLNLKLDNMDSVTSTFSKL 84
 QY 61 REQLGPVTOEFMDNLEKETEGGLROEMSKD 89
 |||||||
 Db 85 REQLGPVTOEFMDNLEKETEGGLROEMSKD 113

RESULT 3

JS0079
 A:apolipoprotein A-I precursor - baboon
 C:Species: Papio sp. (baboon)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Jun-1997
 C:Accession: JS0079
 R:Hixon, J.E.; Borenstein, S.; Cox, L.A.; Rainwater, D.L.; Vandenberg, J.L.
 Gene 74, 483-490, 1988
 A:Title: The baboon gene for apolipoprotein A-I: characterization of a cDNA clone and
 A:Reference number: JS0079; MUID:89232739
 A:Accession: JS0079

A:Molecule type: mRNA
 A:Residues: 1-267 <HIX>
 A:Experimental source: liver
 C:Comment: This protein serves as a cofactor for lecithin cholesterol acyltransferase
 C:Comment: This protein serves as a cofactor for repeated amino acids which form amphipat
 C:Genetics:
 A:Gene: APOAI
 C:Superfamily: apolipoprotein A-I
 C:Keywords: HDL; lipid binding; lipoprotein
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-267/Product: apolipoprotein A-I #status predicted <LAI>
 F:123-144,145-166,167-188,189-210,211-232,233-254/Region: tandem repeats

Query Match 94.7%; Score 443; DB 2; Length 267;
 Best Local Similarity 93.3%; Pred. No. 8e-36;
 Matches 83; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEPPQSPMDRVKDLATVYVDYLDKSGRDYVSQFEGSALGKQLNLKLDNMDSVTSTFSKL 60
 |||||||
 Db 25 DEPPQSPMDRVKDLATVYVDYLDKSGRDYVSQFEGSALGKQLNLKLDNMDSVTSTFSKL 84
 QY 61 REQLGPVTOEFMDNLEKETEGGLROEMSKD 89
 |||||||
 Db 85 REQLGPVTOEFMDNLEKETEGGLROEMSKD 113

RESULT 4

LPDGA1
 A:apolipoprotein A-I precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 17-Dec-1982 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
 C:Accession: A60940; A03092; A61418
 R:Luo, G.C.; Li, W.H.; Chan, L.
 J. Lipid Res. 30, 1735-1746, 1989
 A:Title: Structure and expression of dog apolipoprotein A-I, E, and C-I mRNAs: implic
 A:Reference number: A60940; MUID:90132271
 A:Accession: A60940

A:Molecule type: mRNA
 A:Residues: 1-266 <LUO>
 R:Chung, H.; Randolph, A.; Reardon, I.; Heinrikson, R.L.
 J. Biol. Chem. 257, 2961-2967, 1982
 A:Title: The covalent structure of apolipoprotein A-I from canine high density lipoprot
 A:Reference number: A03092; MUID:82142425
 A:Accession: A03092

A:Molecule type: protein
 A:Residues: 25-167, 'G', '169-201, 'Q', '203-234, 'Q', '236-266 <CHU>
 R:Nakai, T.; Whayne, T.F.; Tang, J.
 FEBS Lett. 64, 409-411, 1976
 A:Title: The amino- and carboxyl-terminal sequences of canine apolipoprotein A-I.
 A:Reference number: A61418; MUID:76210910
 A:Accession: A61418


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QY      62 EQLGPTQEFWDNLEKETEGLRQEMSKD 89  
        |||  
Db      60 EQLGPTQEFWDNLEKETEGLRQEMNKD 87
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RESULT 12

A:apolipoprotein A-I precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1998 #sequence_revision 30-Jun-1988 #text_change 13-Aug-1999
 C:Accession: A24700; S00298; A05314
 R:Hadad, I.A.; Otdovos, J.M.; Fitzpatrick, T.; Karathanasis, S.K.
 J. Biol. Chem. 261, 13260-13277, 1986
 A>Title: Linkage, evolution, and expression of the rat apolipoprotein A-I, C-III, and A-IV
 A:Reference number: A92558; MUID:87008540
 A:Accession: A24700
 A:Molecule type: DNA
 A:Residues: 1-259 <HAD>
 A:Cross-references: EMBL:J02597; NID:g202935; PIDN:AAA40745.1; PID:g202939
 R:Ponclun, J.E.; Martial, J.A.; Gielen, J.E.
 Eur. J. Biochem. 140, 493-498, 1984
 A>Title: Cloning and structure analysis of the rat apolipoprotein A-I cDNA.
 A:Reference number: S00298; MUID:84207987
 A:Accession: S00298
 A:Molecule type: mRNA
 A:Residues: 1-259 <PON>
 A:Cross-references: GB:M00001; EMBL:X00558; NID:g202944; PIDN:AAA40749.1; PID:g202945
 R:Gordon, J.I.; Smith, D.P.; Andy, R.; Alpers, D.H.; Schonfeld, G.; Strauss, A.W.
 J. Biol. Chem. 257, 971-978, 1982
 A>Title: The primary translation product of rat intestinal apolipoprotein A-I mRNA is an
 A:Reference number: A05314; MUID:82098162
 A:Accession: A05314
 A:Molecule type: Protein
 A:Residues: 1-18, 'X', 20-21, 'X', 23-28, 'X', 30-38, 'X', 40-41, 'X', 43-45 <GOR>
 C:Comment: This protein is synthesized in the liver and small intestine. The propeptide
 C:Comment: This protein is a major component of the high density lipoproteins in plasma
 C:Genetics:
 A:Introns: 15/1, 66/2
 C:Superfamily: apolipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipid
 F:1-18/Domain: signal sequence #status experimental <SIG>
 F:19-24/Domain: propeptide #status experimental <PRO>
 F:25-359/Product: apolipoprotein A-I #status experimental <MAT>

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Query Match 76.7%; Score 359; DB 2; Length 259;
Best Local Similarity 76.1%; Pred. No. 1,2e-27;
Matches 67; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Qy      2  EPPOSFMDRVKDATVYDVYDKDSGRDYSOFEGSALGKQLNLKLLDMWDSVTSFSLR 61
      :  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      25  DEQSQMDRVKDEATVYDAVKDSGRDYSOFESSITLGKQLNLNLDMWDTLGSVTEGLQ 84

Qy      62  EOLGPTVQEFWDLLEKTEGLRQEMSKD 89
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      85  EOLGPTVQEFWDLLEKTEGLRQEMSKD 112

RESULT 13
JQ0704
apolipoprotein A-I - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 28-Oct-1994
C/Accession: JQ0704
R;Wellar-quettler, H.; Sommerfeldt, M.; Papandrikopoulou, A.; Mische, U.; Bonltz, D.; F
J.; Neurochem. 54, 444-450, 1990
A;Title: Synthesis of apolipoprotein A-I in pig brain microvascular endothelial cells.
A;Reference number: JQ0704; WUID:90132667
A;Accession: JQ0704
A;Molecule type: mRNA
A;Residues: 1-231 <HEI>
A;Note: the authors translated the codon CAG for residue 124 as His and GAC for residue

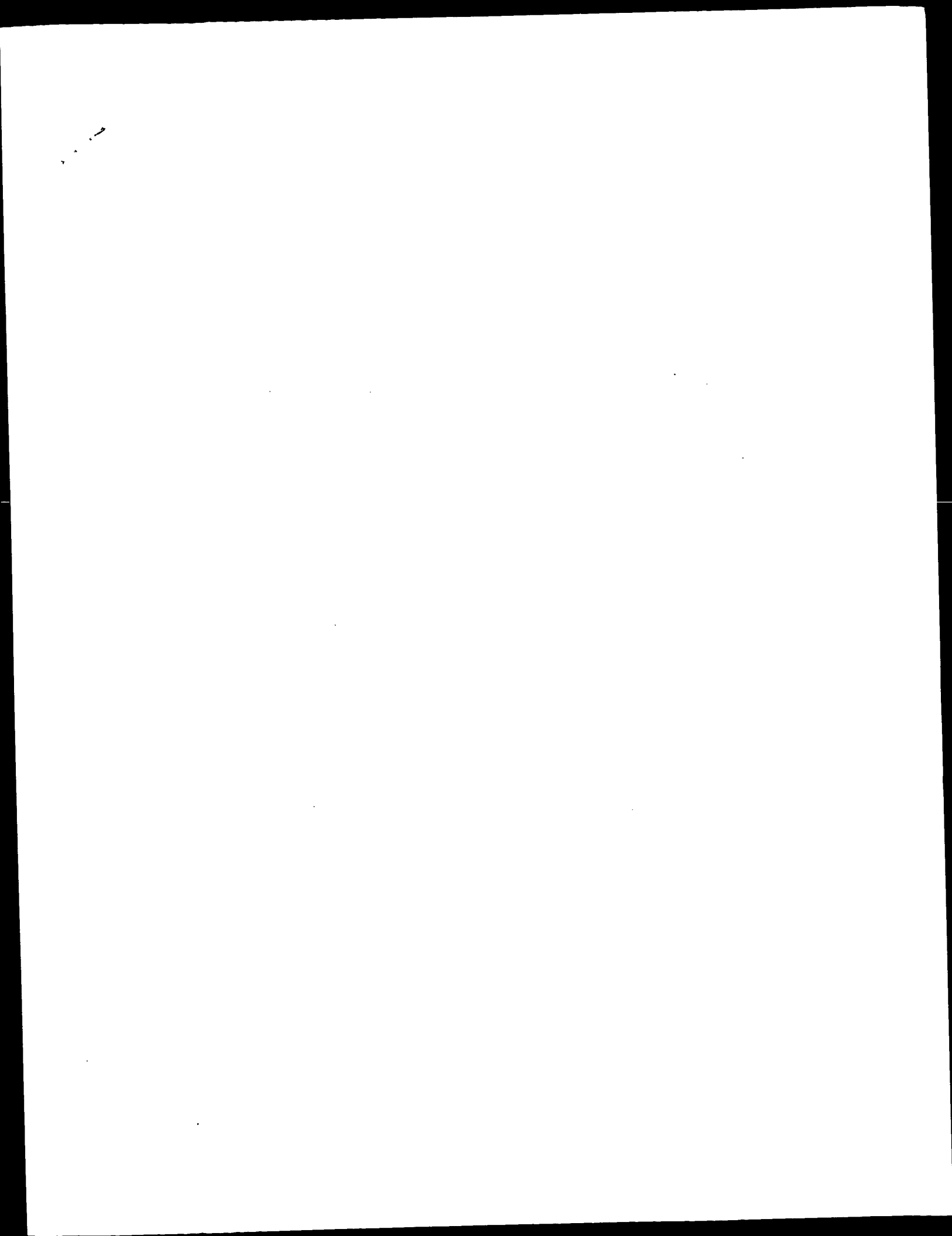
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RESULT 14

Apolipoprotein A-I precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-1993
C:Accession: J01237
R:Boyle, T.P.; Marotti, K.R.
Gene 117, 243-247, 1992
A:Title: Structure of the murine gene encoding apolipoprotein A-I.
A:Reference number: J01237; MUID:92347700
A:Accession: J01237
A:Molecule type: DNA
A:Residues: 1-262 <BOX>
A:Cross-references: GB:M77801
C:Genetics:
A:Gene: ApoA-I
A:Introns: 15/1; 66/2
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; 1
E1-24/Domain: signal sequence #status predicted <SIG>
E1-25-262/Product: apolipoprotein A-I #status predicted <MAT>

RESULT 15

apolipoprotein A-I precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 13-Aug-1999
 C:Accession: S22420- S22421: A44364
 R:Stoitel, W.; Mueller, R.; Binczek, E.; Hofmann, K.
 Biol. Chem. Hoppe-Seyler 373, 187-193, 1992
 A:Title: Mouse apolipoprotein AI. cDNA derived primary structure, gene organisation a
 A:Reference number: S22420; MUID:92281682
 A:Accession: S22420
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-264 <ST0>
 A:Cross-references: EMBL:X64262; NID:g50014; PIDN:CAA45560.1; PID:g50015
 A:Accession: S22421
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-264 <ST2>
 A:Cross-references: EMBL:X64263; NID:g50020; PIDN:CAA45561.1; PID:g50021



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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:22:18 ; Search time 35.02 Seconds
(without alignments)
98.402 Million cell updates/sec

Title: US-09-803-918a-2_COPY_25_113

Perfect score: 468
Sequence: 1 DEPPQSPMDRVKDLATVYVD.....EFMDNLEKETEGLEKQEMSKD 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 segs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	468	100.0	267	1	APAI_HUMAN
2	443	94.7	267	1	APAI_MACFA
3	407	87.0	266	1	APAI_CANFA
4	405	86.5	265	1	APAI_PIG
5	383	81.8	265	1	APAI_BOVIN
6	383	81.8	266	1	APAI_RABIT
7	359	76.7	259	1	APAI_RAT
8	343	73.3	264	1	APAI_MOUSE
9	341	72.9	265	1	APAI_TURGB
10	223	47.6	264	1	APAI_CHICK
11	223	47.6	264	1	APAI_COTUA
12	220	47.0	264	1	APAI_ANAPL
13	101	21.6	20	1	APAI_ERYPA
14	92	19.2	396	1	APAA_HUMAN
15	90	19.2	391	1	APAA_RAT
16	90	19.2	429	1	APAA_MACFA
17	86	18.4	401	1	APAA_PAPAN
18	84	17.9	281	1	APB_BRARE
19	83	17.7	312	1	APB_RAT
20	82	17.5	382	1	APAA_PIG
21	81	17.3	365	1	RECF_CHLTR
22	81	17.3	395	1	APAA_MOUSE
23	78	16.7	311	1	APB_MOUSE
24	76.5	16.3	207	1	YFEB_YEAST
25	72.5	15.5	192	1	YF49_ANASP
26	70.5	15.1	707	1	HS88_NEUCR
27	70	15.0	452	1	TNA2_STYTH
28	70	15.0	453	1	TNA1_STYTH
29	69.5	14.9	759	1	GIR2_HUMAN
30	69	14.7	2033	1	EVPL_HUMAN
31	68.5	14.6	1453	1	MLH3_HUMAN
32	68.5	14.6	4725	1	DYHC_DICDI
33	67.5	14.4	686	1	MEPD_RAT

ALIGNMENTS

RESULT	1	APAI_HUMAN	STANDARD:	PRT:	267 AA.
AC	APAI_HUMAN	P02647:			
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Apolipoprotein A-I precursor (Apo-AI).				
GN	APOA1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84221405; PubMed=6328445;				
RA	Shapoe C.R., Sidoli A., Shelley C.S., Lucero M.A., Shoulders C.C.,				
RA	Baralle F.E.;				
RT	"Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA				
RT	abundance.";				
RL	Nucleic Acids Res. 12:3917-3932(1984).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8502665; PubMed=6207999;				
RA	Seilhamer J.D., Procter A.A., Frossard P., Levy-Wilson B.;				
RT	"Isolation and DNA sequence of full-length cDNA and of the entire				
RT	gene for human apolipoprotein AI -- discovery of a new genetic				
RT	polymorphism in the apo AI gene.";				
RL	DNA 3:309-317(1984).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83220822; PubMed=6406984;				
RA	Shoulders C.C., Kornblith A.R., Munro B.S., Baralle F.E.;				
RT	"Gene structure of human apolipoprotein AI.";				
RL	Nucleic Acids Res. 11:2827-2837(1983).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83220772; PubMed=6304641;				
RA	Cheung P., Chan L.;				
RT	"Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.";				
RL	Nucleic Acids Res. 11:3703-3715(1983).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84119464; PubMed=6198645;				
RA	Law S.W., Brewer H.B. Jr.;				
RT	"Nucleotide sequence and the encoded amino acids of human				
RT	apolipoprotein A-I mRNA.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 81:66-70(1984).				
RN	[6]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=86008382; PubMed=2995392;				
RA	Law S.W., Brewer H.B. Jr.;				
RT	"Ranger disease. The complete mRNA sequence encoding for				
RT	preproapo A-I.";				
RL	J. Biol. Chem. 260:12810-12814(1985).				
RN	[7]				

34 66.5 14.2 185 1 GERD_BACSU
35 66.5 14.2 459 1 FVL_MOUSE
36 66 14.1 210 1 YG21_YEAST
37 66 14.1 298 1 APE_CAVPO
38 66 14.1 317 1 APE_PIG
39 66 14.1 365 1 RECF_CHLMU
40 66 14.1 1051 1 CARB_SULSO
41 65.5 14.0 261 1 HB23_HUMAN
42 65.5 14.0 550 1 G6PI_SCHPO
43 65 13.9 294 1 G6PI_BLAGO
44 65 13.9 294 1 CPPM_STRHY
45 64.5 13.8 747 1 AT12_HSVDB

P16450 bacillus su
P70213 mus musculu
P33251 saccharomyc
P23529 cavia porce
P18650 sus scrofa
O9PKW5 chlamydia m
O59569 sulfolobus
P05537 homo sapien
P78917 schizosacch
O18398 diatella 9
P1435 streptomyc
P28937 equine herp

- RP SEQUENCE FROM N.A.
 RX MEDLINE=84016011; PubMed=6413973;
 RA Karathanasis S.K., Zannis V.I., Breslow J.L.;
 RT "Isolation and characterization of the human apolipoprotein A-I
 RT gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:6147-6151(1983).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89377481; PubMed=2673706;
 RA Mogullevsky N., Roobol C., Loriau R., Guillaume J.P., Jacobs P.,
 RA Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,
 RA Holmquist L., Carlson L.A., Bollen A.;
 RT "Production of human recombinant proapolipoprotein A-I in *Escherichia*
 RT coli: purification and biochemical characterization.";
 RL DNA 8:429-436(1989).
 RN [9]
 RP SEQUENCE FROM N.A. (VARIANT TANGIER).
 RX MEDLINE=88196137; PubMed=3129297;
 RA Makrides S.C., Ruiz-Opazo N., Hayden M., Nusbaum A.L., Breslow J.L.,
 RA Zannis V.I.;
 RT "Sequence and expression of Tangier apoa-I gene.";
 RL Eur. J. Biochem. 173:465-471(1988).
 RN [10]
 RP SEQUENCE OF 118-267 FROM N.A.
 RX MEDLINE=83091059; PubMed=6294659;
 RA Breslow J.L., Ross D., McPherson J., Williams H.W., Kurnit D.,
 RA Nusbaum A.L., Karathanasis S.K., Zannis V.I.;
 RT "Isolation and characterization of cDNA clones for human
 RT apolipoprotein A-I.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6861-6865(1982).
 RN [11]
 RP SEQUENCE OF 19-27.
 RX MEDLINE=83256553; PubMed=6409108;
 RA Brewer H.B. Jr., Fairwell T., Kay L., Meng M., Roman R., Law S.,
 RA Light J.A.;
 RT "Human plasma proapoA-I: isolation and amino-terminal sequence.";
 RL Biochem. Biophys. Res. Commun. 113:626-632(1983).
 RN [12]
 RP SEQUENCE OF 25-267.
 RX MEDLINE=78123731; PubMed=204308;
 RA Brewer H.B. Jr., Fairwell T., Larue A., Roman R., Houser A.,
 RA Bronzert T.J.;
 RT "The amino acid sequence of human APOA-I, an apolipoprotein isolated
 RT from high density lipoproteins.";
 RL J. Biol. Chem. 250:2725-2738(1975).
 RN [13]
 RP SEQUENCE OF 25-267.
 RX MEDLINE=75133493; PubMed=164450;
 RA Baker H.N., Gotto A.M. Jr., Jackson R.L.;
 RT "The primary structure of human plasma high density apolipoprotein
 RT glutamine I (ApoA-I). II. The amino acid sequence and alignment of
 RT cyanoogen bromide fragments IV, III, and I.";
 RL J. Biol. Chem. 250:2725-2738(1975).
 RN [14]
 RP SEQUENCE OF 25-56.
 RX MEDLINE=88331387; PubMed=3047170;
 RA Yui Y., Aoyama T., Morishita H., Takahashi M., Takatsu Y., Kawai C.;
 RT "Serum prostaticin stabilizing factor is identical to apolipoprotein
 RT A-I (Apo A-I). A novel function of Apo A-I.";
 RL J. Clin. Invest. 82:803-807(1988).
 RN [15]
 RP SEQUENCE OF 25-48.
 RX MEDLINE=89380318; PubMed=2506184;
 RA Manjunath P., Marcel Y.L., Uma J., Seldah N.G., Chretien M.,
 RA Chadelaine A.;
 RT "Apolipoprotein A-I binds to a family of bovine seminal plasma
 RT proteins.";
 RL J. Biol. Chem. 264:16853-16857(1989).
 RN [16]
 RP SEQUENCE OF 25-43.
 RX MEDLINE=88070603; PubMed=3120314;
 RA Priolo R.P., Ordovas J.M., Rosenberg I., Schaeffer E.J.,
 RA Pereira M.E.A.;
 RT "Similarity of cruzin, an inhibitor of Trypanosoma cruzi
 RT neuraminidase, to high-density lipoprotein.";
 RL Science 238:1417-1419(1987).
 RN [17]
 RP SEQUENCE OF 25-42.
 RC TISSUE-Heart;
 RX MEDLINE=95203287; PubMed=7895732;
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
 RT "The human myocardial two-dimensional gel protein database: update
 RT 1994.";
 RL Electrophoresis 15:1459-1465(1994).
 RN [18]
 RP PALMITOYLATION.
 RX MEDLINE=86140194; PubMed=3005308;
 RA Hoeg J.M., Meng M.S., Roman R., Fairwell T., Brewer H.B. Jr.;
 RT "Human apolipoprotein A-I. Post-translational modification by fatty
 RT acid acylation.";
 RL J. Biol. Chem. 261:3911-3914(1986).
 RN [19]
 RP PROCESSING.
 RX MEDLINE=83195100; PubMed=6405383;
 RA Zannis V.I., Karathanasis S.K., Keutmann H.T., Goldberger G.,
 RA Breslow J.L.;
 RT "Intracellular and extracellular processing of human apolipoprotein
 RT A-I: secreted apolipoprotein A-I isoprotein 2 is a propeptide.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2574-2578(1983).
 RN [20]
 RP STRUCTURE BY NMR OF 190-209.
 RX MEDLINE=96270776; PubMed=8664326;
 RA Wang G., Treleaven W.D., Cushley R.J.;
 RT "Conformation of human serum apolipoprotein A-I(166-185) in the
 RT presence of sodium dodecyl sulfate or dodecylphosphocholine by ¹H-NMR
 RT and CD. Evidence for specific peptide-SDS interactions.";
 RL Biochim. Biophys. Acta 1301:174-184(1996).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (4.0 ANGSTROMS) OF 67-267.
 RX MEDLINE=98024124; PubMed=9356442;
 RA Borhani D.W., Rogers D.P., Engler J.A., Brouillette C.G.;
 RT "Crystal structure of truncated human apolipoprotein A-I suggests a
 RT lipid-bound conformation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12291-12296(1997).
 RN [22]
 RP VARIANT MILANO.
 RX MEDLINE=83109095; PubMed=6401735;
 RA Weisgraber K.H., Rall S.C. Jr., Bersot T.P., Mahley R.W.,
 RA Franceschini G., Sirtori C.R.;
 RT "Apolipoprotein A-I-Milano. Detection of normal A-I in affected
 RT subjects and evidence for a cysteine for arginine substitution in the
 RT variant A-I.";
 RL J. Biol. Chem. 258:2508-2513(1983).
 RN [23]
 RP VARIANT TANGIER.
 RX MEDLINE=83300108; PubMed=6412234;
 RA Schmitz G., Assmann G., Rall S.C. Jr., Mahley R.W.;
 RT "Tangier disease: defective recombination of a high density
 RT apolipoprotein A-I isoform (pro-apo A-I) with high density
 RT lipoproteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:6081-6085(1983).
 RN [24]
 RP VARIANT NORWAY.
 RX MEDLINE=84289383; PubMed=6432779;
 RA Rall S.C. Jr., Weisgraber K.H., Mahley R.W., Ogawa Y., Fielding C.J.,
 RA Olermann G., Haas J., Steinmetz A., Wenzel H.J., Assmann G.;
 RT "Abnormal lecithin:cholesterol acyltransferase activation by a human
 RT apolipoprotein A-I variant in which a single lysine residue is
 RT deleted.";
 RL J. Biol. Chem. 259:10063-10070(1984).
 RN [25]
 RP SEQUENCE OF 25-107 (VARIANT IOWA).
 RX MEDLINE=89050104; PubMed=3142462;
 RA Nichols W.C., Duvel F.E., Liepnieks J., Benson M.D.;
 RT "Variant apolipoprotein AI as a major constituent of a human
 RT hereditary amyloid.";

Query Match 100.0%; Score 468; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3.9e-39;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPOSQWDRVKDLATVYVDLKDSDGRVYVSQFEGSALGKOLNKLNDNDVSTVSFSL 60
 |||||||
 DB 25 DEPOSQWDRVKDLATVYVDLKDSDGRVYVSQFEGSALGKOLNKLNDNDVSTVSFSL 84
 |||||||

OY 61 REQLGPTVTOEFWDNLEKETEGLEGRQEMSKD 89
 |||||||

DB 85 REQLGPTVTOEFWDNLEKETEGLEGRQEMSKD 113
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RESULT 2
 APAL_MACFA STANDARD; PRT; 267 AA.
 ID APAL_MACFA
 AC P1568; P17929;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
 OS Papio hamadryas (Hamadryas baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NC NCBL_TaxID=9541, 9557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=87191989; PubMed=3106152;
 RA Polites H.G., Melchior G.W., Castle C.K., Marotti K.R.;
 RT "The primary structure of cynomolgus monkey apolipoprotein A-I
 RT deduced from the cDNA sequence: comparison to the human sequence.";
 RL Gene 49:103-110(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=92305062; PubMed=1610902;
 RA Murray R.W., Marotti K.R.;
 RT "Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene
 RT and corresponding flanking regions.";
 RL Biochim. Biophys. Acta 1131:207-210(1992).
 RN [3]
 RP SEQUENCE OF 25-48.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=87185451; PubMed=3105581;
 RA Herbert P.N., Bauserman L.L., Lynch K.M., Sartelli A.L.,
 RA Kantor M.A., Nicolosi R.J., Shulman R.S.;
 RT "Homologues of the human C and A apolipoproteins in the Macaca
 RT fascicularis (cynomolgus) monkey.";
 RL Biochemistry 26:1457-1463(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas; TISSUE=liver;
 RX MEDLINE=89232739; PubMed=2907746;
 RA Hixson J.E., Borenstein S., Cox L.A., Rainwater D.L., Vandeberg J.L.;
 RT "The baboon gene for apolipoprotein A-I: characterization of a cDNA
 RT clone and identification of DNA polymorphisms for genetic studies of
 RT cholesterol metabolism.";
 RL Gene 74:483-490(1988).
 RN [5]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC SPECIES=M.fascicularis;
 RA Sorci-Thomas M.;
 RL Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
 CC THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -!- SUBCELLULAR LOCATION: Extracellular.

CC -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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DR EMBL: M15411; AAA36834.1; -;
 DR EMBL: M83242; AAA36832.1; -;
 DR EMBL: M35634; AAA35380.1; -;
 DR EMBL: M69223; AAA36831.1; -;
 DR PIR: A26529; A26529.
 DR PIR: A26627; A26627.
 DR PIR: J50079; J50079.
 DR PIR: S23135; S23135.
 DR HSSP: P02647; IODR.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein, 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 267
 FT DOMAIN 68 267
 FT REPEAT 68 89
 FT REPEAT 90 111
 FT REPEAT 112 122
 FT REPEAT 123 144
 FT REPEAT 145 166
 FT REPEAT 167 188
 FT REPEAT 189 210
 FT REPEAT 211 232
 FT REPEAT 233 243
 FT REPEAT 244 267
 FT CONFLICT 13 13 L->P (IN REF. 1).
 SQ SEQUENCE 267 AA; 30735 MW; 869955C024088E21 CRC64;

Query Match 94.7%; Score 443; DB 1; Length 267;
 Best Local Similarity 93.3%; Pred. No. 1.1e-36;
 Matches 83; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEPOSQWDRVKDLATVYVDLKDSDGRVYVSQFEGSALGKOLNKLNDNDVSTVSFSL 60
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 DB 25 DEPOSQWDRVKDLATVYVDLKDSDGRVYVSQFEGSALGKOLNKLNDNDVSTVSFSL 84
 |||||||

OY 61 REQLGPTVTOEFWDNLEKETEGLEGRQEMSKD 89
 |||||||

DB 85 REQLGPTVTOEFWDNLEKETEGLEGRQEMSKD 113
 |||||||

RESULT 3
 APAL_CANFA STANDARD; PRT; 266 AA.
 ID APAL_CANFA
 AC P02648;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NC NCBL_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=liver;
 RX MEDLINE=90132271; PubMed=2515239;
 RA Luo C.-C., Li W.-H., Chan L.;

[illegible]

ID	APAL_PIG	STANDARD:	PRT:	265 AA.
AC	P18648;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Apolipoprotein A-I precursor (Apo-AI).			
GN	APOA1			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93224154; PubMed=8468059;			
RA	Birchbauer A., Knipping G., Juritsch B., Aschauer H., Zechner R.;			
RT	"Characterization of the apolipoprotein AI and CIII genes in the			
RT	domestic pig.";			
RL	Genomics 15:643-652(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver and Brain;			
RX	MEDLINE=94125128; PubMed=8294940;			
RA	Moockel B., Zinke H., Flach R., Weiss B., Weller-Guettler H.,			
RA	Gassen H.;			
RT	"Expression of apolipoprotein A-I in porcine brain endothelium in			
RT	vitro.";			
RT	J. Neurochem. 62:788-798(1994).			
RL	[3]			
RN	SEQUENCE OF 34-265 FROM N.A.			
RP	TISSUE=Brain;			
RC	MEDLINE=90132667; PubMed=2105375;			
RX	Weller-Guettler H., Sommerfeldt M., Papadikopoulou A., Mischek U.,			
RA	Bonitz D., Frey A., Grube M., Schleerer J., Gassen H.G.;			
RA	"Synthesis of apolipoprotein A-I in pig brain microvascular			
RT	endothelial cells.";			
RT	J. Neurochem. 54:444-450(1990).			
RL	[4]			
RN	SEQUENCE OF 105-265 FROM N.A.			
RP	TISSUE=Liver;			
RC	MEDLINE=93154581; PubMed=8428656;			
RX	Trieu V.N., Hasler-Rapacz J., Rapacz J., Black D.D.;			
RA	"Sequences and expression of the porcine apolipoprotein A-I and C-II			
RT	mRNAs.";			
RT	Gene 123:173-179(1993).			
RL	[5]			
RN	SEQUENCE OF 25-265.			
RP	Hasler-Rapacz J.O., Choudhary R., Chowdhary B.P., Trieu V.N.,			
RA	Jackson K., Gustavsson I., Rapacz J.;			
RL	Submitted (OCT-1995) to the SWISS-PROT data bank.			
RN	[6]			
RP	SEQUENCE OF 25-34.			
RX	MEDLINE=76184721; PubMed=178359;			
RA	Mahey R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;			
RT	"Characterization of the plasma lipoproteins and apoproteins of the			
RT	Erythrocebus patas monkey.";			
RL	Biochemistry 15:1928-1933(1976).			
CC	-1- FUNCTION. APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF			
CC	CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING			
CC	CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR			
CC	THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).			
CC	-1- SUBCELLULAR LOCATION. Extracellular.			
CC	-1- SUBSPECIFICITY. MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN			
CC	CHROMICRONS. SYNTHESIZED PREDOMINANTLY IN THE INTESTINE AND THE			
CC	LIVER.			
CC	-1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.			
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RT      Molecular evolution of apolipoproteins A-I and B-100." ;
RL      Mol. Biol. Evol. 7:327-339(1990).
RN
RP      SEQUENCE OF 19-265.
RX      MEDLINE=92153895; PubMed=1739745;
RA      Sparrow D.A., Lee B.R., Lapland M.P., Auboliron S., Bauchart D.,
RT      Chapman J.M., Gotto A.M. Jr., Yang C.Y., Sparrow J.T. ;
RL      "Plasma lipid transport in the perinatal calf, Bos spp: primary
RT      structure of bovine apolipoprotein A-I".
RL      Biochim. Biophys. Acta 1123:145-150(1992).
RN
RP      [13]
RX      MEDLINE=90147795; PubMed=2105728;
RA      Auboliron S., Sparrow D.A., Beaubatie L., Bauchart D., Sparrow J.T.,
RT      Lapland M.P., Chapman J.M. ;
RL      "Characterization and amino-terminal sequence of apolipoprotein A-I
RT      from plasma high density lipoproteins in the perinatal calf, Bos
RT      spp." ;
RX      Biochem. Biophys. Res. Commun. 166:833-839(1990).
CC      -I- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC      CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC      CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC      THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC      -I- SUBCELLULAR LOCATION: Extracellular.
CC      -I- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC      CHYLOMICRONS.
CC      -I- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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DR      EMBL, M35870; AAA30381.1; -.
DR      PIR, A34649; A34649.
DR      HSSP, P02647; 10DR.
DR      InterPro: IPR000074; Apolipoprotein.
DR      Pfam: PF01442; Apolipoprotein. 1.
KW      Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
FT      SIGNAL 1 18
FT      PROPEP 19 24
FT      CHAIN 25 265
FT      DOMAIN 67 265
FT      REPEAT 67 88
FT      REPEAT 89 110
FT      REPEAT 111 121
FT      REPEAT 122 143
FT      REPEAT 144 165
FT      REPEAT 166 187
FT      REPEAT 188 209
FT      REPEAT 210 230
FT      REPEAT 231 241
FT      REPEAT 242 265
FT      CONFLICT 185 186
FT      FT 186
SQ      SEQUENCE 265 AA; 30276 MW; 06A2681EA2ABA50F CRC64;
OY      Query Match 81.8%; Score 383; DB 1; Length 265;
Ddb      Best Local Similarity 80.7%; Pred. NO. 9, le-31;
Matches 71; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
OY      2 EPPOSMDWRVADLTAVYDVVLKDSGRDVSQFEGSALGKQLNLKLLDWDVSYTFSSKLR 61
      : ||| ||||| ||||| : ||||| ||| ||| ||||| ||||| : ||| |
Ddb      25 DDPOSMDRVADDFATVYVEALIKDSGRDVAQFEGSALGKQLNLKLLDWDVTLASTLSKVR 84
      ||||| ||||| ||||| ||||| ||
OY      62 FQLGPLYDQFWDNLKEKTEGLRQESKD 89
      ||||| ||||| ||||| ||||| ||
Ddb      85 FQLGPLYDQFWDNLKEKTEGLRQESKMD 112

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FT	REPEAT	210	231	8
FT	REPEAT	232	242	9 (HALF-LENGTH).
FT	REPEAT	243	266	10.
FT	CONFLICT	18	18	A -> R (IN REF. 2; CAA29858).
FT	CONFLICT	44	44	MISSING (IN REF. 3).
FT	CONFLICT	45	45	V -> I (IN REF. 2; CAA29858).
FT	CONFLICT	107	107	E -> Q (IN REF. 3).
FT	CONFLICT	123	123	Y -> F (IN REF. 2; CAA29857).
FT	CONFLICT	147	147	A -> V (IN REF. 2; CAA29858 AND REF. 3).
FT	CONFLICT	150	150	R -> G (IN REF. 2; CAA29858 AND CAA29857).
FT	CONFLICT	191	191	N -> Q (IN REF. 3).
FT	CONFLICT	195	195	MISSING (IN REF. 2; CAA29858 AND CAA29857).
FT	CONFLICT	211	211	S -> K (IN REF. 2; CAA29858 AND CAA29857).
FT	CONFLICT	255	256	VL -> LV (IN REF. 3).
FT	CONFLICT	256	256	L -> V (IN REF. 2; CAA29858 AND CAA29857).
SO	SEQUENCE	266 AA;	30591 MW;	0PFDDB386497C7D2 CRC64;
Query Match				
Best Local Similarity 78.4%; Score 383; DB 1; Length 266;				
Matches 69; Conservative 12; Mismatches 7; Indels 0; Gaps				
OY	2	EPPOSFMDRVKDLATVYVDYDKSGDRIVYSQFESALGKOLNKLIDNMVSYSTSKLR	61	
DB	25	DEPRSMWKRIKIDFATVYVDYDKSGDRYVAQFENSAFGKOLNKLIDNMVSYSTSKLR	84	
OY	62	EQLGVTQEFMDNLEKETEGTGLRQEMSRD	89	
DB	85	EQLGVTQEFMDNLEKETEGTGLRQEMSRD	112	
RESULT 7				
APAL_RAT	APAL_RAT	STANDARD;	PRT;	259 AA.
ID	P04639;			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Apolipoprotein A-I precursor (Apo-AI).			
GN	APOL1.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognath; Muridae; Murinae; Rattus.			
OX	NCBI-TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84207987; PubMed=6426956;			
RA	Poncin J.E., Martini J.A., Gielen J.E.;			
RT	"Cloning and structure analysis of the rat apolipoprotein A-I cDNA."			
RL	Eur. J. Biochem. 140:493-498(1984).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87008540; PubMed=3020028;			
RA	Haddad I.A., Ordovas J.M., Fitzpatrick T., Karathanasis S.K.;			
RT	"Linkage, evolution, and expression of the rat apolipoprotein A-I, C-			
RL	III, and A-IV genes."			
RN	J. Biol. Chem. 261:13268-13277(1986).			
RT	[3]			
RP	SEQUENCE OF 1-45.			
RC	STRAIN=SPRAGUE-DAWLEY;			
RX	MEDLINE=82098162; PubMed=6798036;			
RA	Gordon J.T., Smith D.P., Andy R., Alpers D.H., Schonfeld G.,			
RA	Strauss A.W.;			
RT	"The primary translation product of rat intestinal apolipoprotein A-I-			
RL	mRNA is an unusual preprotein."			
CC	J. Biol. Chem. 257:971-978(1982).			
CC	-I- FUNCTION: APOA-I PARTICIPATES IN THE REVERSE TRANSPORT OF			
CC	CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING			
CC	CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR			

```

CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M00001; AAA40749.1; -.
DR EMBL: X00558; CAA25224.1; -.
DR EMBL: J02597; AAA40745.1; -.
DR PIR: A24700; A24700.
DR HSSP: P02647; IAV1.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein; 1.
KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 259
FT DOMAIN 67 259
FT REPEAT 67 88
FT REPEAT 89 110
FT REPEAT 111 121
FT REPEAT 122 143
FT REPEAT 144 161
FT REPEAT 162 183
FT REPEAT 184 203
FT REPEAT 204 225
FT REPEAT 226 236
FT REPEAT 237 259
FT REPEAT 201 201
FT CONFLICT 214 214
FT CONFLICT 218 218
FT CONFLICT 218 218
FT SEQUENCE 259 AA; 30088 MW; 2E8D5EB45FEAE88 CRC64;

Query Match 76.7%; Score 359; DB 1; Length 259;
Best Local Similarity 76.1%; Pred. No. 2e-28;
Matches 67; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 2 EPPQSPMDRVKDLATVYVDYLDKSGRDYVSQFEGSALGKQNLKLDNMDSVTSFSKLR 61
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 25 DEPOSQMDRVKDFATVYVDYLDKSGRDYVSQFEGSSTLGKQNLNLDNMDTLCSTYGRIG 84
QY 62 EOLGPVTOEFMDNLEKETEGLEKROEMSKD 89
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 EOLGPVTOEFMDNLEKETEGLEKROEMSKD 112

RESULT 8
APAL_MOUSE STANDARD; PRT; 264 AA.
AC Q00623;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92281682; PubMed=1596360;
RA Stoffel W., Mueller R., Binczek E., Hofmann K.;
RT "Mouse apolipoprotein A1. cDNA-derived primary structure, gene

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RT organisation and complete nucleotide sequence.";
RL Biol. Chem. Hoppe-Seyler 373:187-193(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93122774; PubMed=1478650;
RA Januzzi J.L., Azrolan N., O'Connell A., Aalto-Setälä K., Breslow J.L.;
RT Characterization of the mouse apolipoprotein ApoA-1/ApoC-3 gene
RT locus: genomic, mRNA, and protein sequences with comparisons to other
RT species.";
RL Genomics 14:1081-1088(1992).
CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X64262; CAA45560.1; -.
DR EMBL: X64263; CAA45561.1; -.
DR EMBL: L04149; -. NOT ANNOTATED_CDS.
DR EMBL: L04151; -. NOT ANNOTATED_CDS.
DR PIR: S22420; S22420.
DR PIR: A44364; A44364.
DR HSSP: P02647; IAV1.
DR SWISS-2DPAGE: Q00623; MOUSE.
DR MGD: MGI:88049; APOA1.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein; 1.
KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 264
FT DOMAIN 67 264
FT REPEAT 67 88
FT REPEAT 89 110
FT REPEAT 111 121
FT REPEAT 122 143
FT REPEAT 144 165
FT REPEAT 166 187
FT REPEAT 188 207
FT REPEAT 208 229
FT REPEAT 230 240
FT REPEAT 241 264
FT SEQUENCE 264 AA; 30587 MW; C453FF2019634AAC CRC64;

Query Match 73.3%; Score 343; DB 1; Length 264;
Best Local Similarity 69.3%; Pred. No. 7.8e-27;
Matches 61; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

QY 2 EPPQSPMDRVKDLATVYVDYLDKSGRDYVSQFEGSALGKQNLKLDNMDSVTSFSKLR 61
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 25 DEPOSQMDRVKDFATVYVDYLDKSGRDYVSQFESSLGLQNLNLDNMDTLCSTYGRIG 84
QY 62 EOLGPVTOEFMDNLEKETEGLEKROEMSKD 89
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 EOLGPVTOEFMDNLEKETEGLEKROEMSKD 112

RESULT 9
APAL_TUPGB STANDARD; PRT; 265 AA.
AC O18759;

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DT	15-JUL-1998 (Rel. 36, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	Apolipoprotein A-I precursor (Apo-A1).
GN	APoA1.
OS	Tupaia glis belangeri (Common tree shrew).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaia.
OX	NCBI_TaxID=9396;
RP	[1]
RC	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RA	Lu X., Chen B., Zhao Y., Wang K., Xue H., Zeng W.;
RL	Submitted (MAY-1997) to the EMBL/Genbank/DBJ databases.
CC	-1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC	-1- SUBCELLULAR LOCATION: Extracellular.
CC	-1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN CHYLOMICRONS (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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CC	-----
DR	EMBL; AF005638; AAB82326.1; -
DR	HSSP; P02647; IAVI.
DR	InterPro: IPR000074; Apolipoprotein.
DR	Pfam: PF01442; Apolipoprotein.1.
KW	Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
FT	SIGNAL 1 18 BY SIMILARITY.
FT	PROPEP 19 24 APOLOPROTEIN A-I.
FT	CHAIN 25 265 APOLIPROTEIN A-I.
FT	DOMAIN 67 265 10 X APPROXIMATE TANDEM REPEATS.
FT	REPEAT 67 88 1.
FT	REPEAT 89 110 2.
FT	REPEAT 111 121 3 (HALF-LENGTH).
FT	REPEAT 122 143 4.
FT	REPEAT 144 165 5.
FT	REPEAT 166 187 6.
FT	REPEAT 188 209 7.
FT	REPEAT 210 231 8.
FT	REPEAT 232 242 9 (HALF-LENGTH).
FT	REPEAT 243 265 10.
SO	SEQUENCE 265 AA; 30332 MW; 60076BC3FAEA165 CRC64;
QY	2 EPPSPQMRVVKOLAVYVDVLDKSGRDVYSQFEGSALGKQLKILDMNDVSTSPFSKLR 61
DB	25 DEPOSQMDVRKLAVYDVAVESGSEIVYSLDASLGRQLNLKLYDMNDITLGSTFGYKH 84
QY	62 EQLGPFVTOEFMDNLKRETEGLRQESMD 89
DB	85 EHLGPVADQEFWEKLEKTEELRRLNKD 112
RESULT	10
APAI_CHICK	STANDARD: PRT; 264 AA.
AC	P08250;
DT	01-AUG-1988 (Rel. 08, Created)
DT	01-OCT-1989 (Rel. 12, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)

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DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88049703; PubMed=3118875;
RA Byrnes L., Luo C.-C., Li W.-H., Yang C.-Y., Chan L.;
RT "Chicken apolipoprotein A-I: cDNA sequence, tissue expression and
RL evolution.";
RN Biochem. Biophys. Res. Commun. 148:485-492(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88152500; PubMed=3126099;
RA Ferrari S., Tarugi P., Drusiani E., Calandra S., Fregni M.;
RT "The complete sequence of chick apolipoprotein AI mRNA and its
RN expression in the developing chick.";
RN Gene 60:39-46(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87222301; PubMed=3108248;
RA Rajavashisth T.B., Dawson P.A., Williams D.L., Shackelford J.E.,
RA Leberer H., Lusis A.J.;
RT "Structure, evolution, and regulation of chicken apolipoprotein A-I.";
RN J. Biol. Chem. 262:7058-7065(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92381402; PubMed=1512510;
RA Lamou-Fava S., Sastre R., Ferrari S., Rajavashisth T.B.,
RA Lusis A.J., Karathanasis S.K.;
RT "Evolutionary distinct mechanisms regulate apolipoprotein A-I gene
RN expression: differences between avian and mammalian apoA-I gene
RN transcription control regions.";
RN J. Lipid Res. 33:831-842(1992).
RN [5]
RP SEQUENCE OF 25-44.
RX MEDLINE=83213468; PubMed=6406496;
RA Shackelford J.E., Leberer H.G.;
RT "Synthesis and secretion of apolipoprotein AI by chick breast
RN muscle.";
RN J. Biol. Chem. 258:7175-7180(1983).
CC -I- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -I- SUBCELLULAR LOCATION: Extracellular.
CC -I- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC -I- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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CC -----
DR EMBL, M17961; AAA48593.1; -
DR EMBL, M18746; AAA48594.1; -
DR EMBL, M25559; AAA48592.1; -
DR EMBL, M96012; AAA48597.1; -
DR PIR, S01453; IPCHA1.
DR PIR, JH0471; JH0471.
DR HSP, P02647; IODR.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein; 1.
KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
FT SIGNAL 1 18
FT PROPEP 19 24

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FT CHAIN 25 264 APOLOPOPROTEIN A-I.
FT DOMAIN 67 264 10 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 67 88 1.
FT REPEAT 89 110 2.
FT REPEAT 111 121 3 (HALF-LENGTH).
FT REPEAT 122 143 4.
FT REPEAT 144 165 5.
FT REPEAT 166 187 6.
FT REPEAT 188 209 7.
FT REPEAT 210 231 8.
FT REPEAT 232 242 9 (HALF-LENGTH).
FT REPEAT 243 264 10.
FT CONFLICT 16 16 T-> I (IN REF. 4).
FT CONFLICT 148 148 E-> K (IN REF. 3).
SQ SEQUENCE 264 AA; 30680 MW; 968320B1E2AC5C2 CRC64;

Query Match 47.6%; Score 223; DB 1; Length 264;
Best Local Similarity 46.6%; Pred. No. 5,1e-15;
Matches 41; Conservative 24; Mismatches 23; Indels 0; Gaps 0;

QY 2 EPPQSPMDRVKDLATVYVDVLDKSGRDYVSQFEGSALGKQNLKILDMNDVSTFSKLR 61
DB 25 DDPQTPFLDRIRMDVYLETYKASGKDAISQFESSAVGKQDLADNLDTLSAAAKLR 84

QY 62 EQLGPVTQGFMDNLEKETEGLRQEMSKD 89
DB 85 EDMAPYKREVMMLKDTREALRAELTKD 112

RESULT 11
APOL_COTJA STANDARD; PRT; 264 AA.
AC P32918;
DT 01-OCT-1993 (Rel. 27, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OC NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97212027; PubMed=9058967;
RA Oku H., Toda T., Nagata J., Ishikawa M., Neyazaki K., Shinjyo C.,
RA Chinen I.;
RT "Apolipoprotein A-I of Japanese quail: cDNA sequence and modulation of
RT tissue expression by cholesterol feeding.";
RL Biosci. Biotechnol. Biochem. 61:286-290(1997).
RN [2]
RP SEQUENCE OF 25-60.
RX MEDLINE=93213845; PubMed=8461329;
RA Oku H., Ishikawa M., Nagata J., Toda T., Chinen I.;
RT "Lipoprotein and apoprotein profile of Japanese quail.";
RL Biochim. Biophys. Acta 1167:22-28(1993).
CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF VLDL, HDL, LDL AND IN
CC CHYLOMICRONS. EXPRESSED IN A NUMBER OF TISSUES INCLUDING LIVER,
CC SMALL INTESTINE, LUNG, KIDNEY, HEART AND MUSCLE WITH HIGHEST
CC EXPRESSION IN LIVER AND SMALL INTESTINE.
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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CC -----
CC DR EMBL; D85133; BAA12729.1; -.
CC DR HSSP; P02647; 1GWA.
CC DR InterPro; IPR000074; Apolipoprotein.
CC Pfam; PF01442; Apolipoprotein; 1.
CC KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
CC FT SIGNAL 1 18
CC FT PROPEP 19 24
CC FT CHAIN 25 264 APOLOPOPROTEIN A-I.
CC FT DOMAIN 67 264 10 X APPROXIMATE TANDEM REPEATS.
CC FT REPEAT 67 88 1.
CC FT REPEAT 89 110 2.
CC FT REPEAT 111 121 3 (HALF-LENGTH).
CC FT REPEAT 122 143 4.
CC FT REPEAT 144 165 5.
CC FT REPEAT 166 187 6.
CC FT REPEAT 188 209 7.
CC FT REPEAT 210 231 8.
CC FT REPEAT 232 242 9 (HALF-LENGTH).
CC FT REPEAT 243 264 10.
SQ SEQUENCE 264 AA; 30753 MW; 8781DE213C3F863F CRC64;

Query Match 47.6%; Score 223; DB 1; Length 264;
Best Local Similarity 47.7%; Pred. No. 5,1e-15;
Matches 42; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

QY 2 EPPQSPMDRVKDLATVYVDVLDKSGRDYVSQFEGSALGKQNLKILDMNDVSTFSKLR 61
DB 25 DDPQTPFLDRIRMDVYLETYKASGKDAISQFESSAVGKQDLADNLDTLSAAAKLR 84

QY 62 EQLGPVTQGFMDNLEKETEGLRQEMSKD 89
DB 85 EDMAPYKREVMMLKDTREALRAELTKD 112

RESULT 12
APOL_ANAPL STANDARD; PRT; 264 AA.
AC O42296;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OC NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEKIN BREED; TISSUE=Liver;
RA Chen B., Lu X., Wang K., Xue H., Zeng W., Zhu D., Chi L.;
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.:
 RT "Genetic polymorphism of human plasma apolipoprotein A-IV is due to
 RT nucleotide substitutions in the apolipoprotein A-IV gene."
 RL J. Biol. Chem. 265:10061-10064(1990).
 RP VARIANTS A-IV*0 AND A-IV*3.
 RX MEDLINE=90324273; PubMed=1973689;
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.:
 RT "Human plasma apolipoproteins A-IV*0 and A-IV*3. Molecular basis for
 RT two rare variants of apolipoprotein A-IV-1."
 RL J. Biol. Chem. 265:12734-12739(1990).
 RN VARIANTS.
 RA MEDLINE=91310615; PubMed=1677358;
 RX Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.:
 RT "Three genetic variants of human plasma apolipoprotein A-IV: apoA-IV-
 RT 1(7H-347->Ser), apoA-IV-0(Lys-167->Glu, Glu-360->His), and apoA-IV-
 RT 3(Glu-165->Lys)."
 RL J. Biol. Chem. 266:13513-13518(1991).
 RN ERRATUM.
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.:
 RL J. Biol. Chem. 266:19866-19866(1991).
 RN VARIANTS MET-13.
 RX MEDLINE=92238494; PubMed=1349197;
 RA von Eckardstein A., Funke H., Schulte M., Erren M., Schulte H.,
 RA Assmann G.:
 RT "Nonsynonymous polymorphic sites in the apolipoprotein (apo) A-IV
 RT gene are associated with changes in the concentration of apo B- and
 RT apo A-I-containing lipoproteins in a normal population."
 RL Am. J. Hum. Genet. 50:1115-1128(1992).
 RN VARIANTS SER-147.
 RX MEDLINE=92144647; PubMed=1737067;
 RA Tenkunen H., Koskinen P., Metso J., Baumann M., Lukka M.,
 RA Kauppinen-Makelin R., Kontula K., Taskinen M.R., Manttari M.,
 RA Manninen V., Ehnholm C.:
 RT "A novel polymorphism of apolipoprotein A-IV is the result of an
 RT asparagine to serine substitution at residue 127."
 RL Biochim. Biophys. Acta 1138:27-33(1992).
 RN VARIANTS A-IV*5.
 RX MEDLINE=93138374; PubMed=1487136;
 RA Kamboh M.I., Williams E.R., Law J.C., Aston C.E., Bunker C.H.,
 RA Ferrell R.E., Pollitzer W.S.:
 RT "Molecular basis of a unique African variant (A-IV 5) of human
 RT apolipoprotein A-IV and its significance in lipid metabolism."
 RL Genet. Epidemiol. 9:379-388(1992).
 RN VARIANTS LYS-44 (BUDAPEST-2); CYS-305 AND SER-367 (BUDAPEST-1).
 RX MEDLINE=95245341; PubMed=7728150;
 RA Menzel H.J., Dieplinger H., Sandholzer C., Karadi I., Utermann G.,
 RA Caszaz A.:
 RT "Apolipoprotein A-IV polymorphism in the Hungarian population: gene
 RT frequencies, effect on lipid levels, and sequence of two new
 RT variants."
 RL Hum. Mutat. 5:58-65(1995).
 RN VARIANTS FCGL SEATTLE SER-161; LEU-178 AND GLN-264.
 RX MEDLINE=97114287; PubMed=8956036;
 RA Deeb S.S., Nevin D.N., Iwasaki L., Brunzell J.D.:
 RT "Two novel apolipoprotein A-IV variants in individuals with familial
 RT combined hyperlipidemia and diminished levels of lipoprotein lipase
 RT activity."
 RL Hum. Mutat. 8:319-325(1996).
 CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
 CC CARBOHYDRATE METABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
 CC LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
 CC COMPONENT OF HDL AND CHYLOMICRONS.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE INTESTINE.
 CC SECRETED IN PLASMA.

CC -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDDEM REPEATS (EACH
 CC 22-MER IS ACTUALLY A TANDDEM ARRAY OF TWO, A AND B, RELATED 11-
 CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
 CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
 CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL
 CC ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
 CC -1- POLYMORPHISM: EIGHT ALLELES HAVE BEEN CHARACTERIZED (APOA-IV*0
 CC TO APOA-IV*7). APOA-IV*1 IS THE MAJOR ALLELE (90%), IV*2 IS ALSO
 CC COMMON (8%), THE OTHERS ARE RARE ALLELES.
 CC -1- DISEASE: DEFECTS IN APOA4 MAY CONTRIBUTE, ALONG WITH DEFECTS IN
 CC OTHER GENES OR ENVIRONMENTAL FACTORS, TO THE DEVELOPMENT OF
 CC FAMILIAL COMBINED HYPERLIPIDEMIA (FCHL).
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC -----
 DR EMBL: M14642; AA51745.1; -;
 DR EMBL: X13629; CA31955.1; -;
 DR EMBL: M14566; AA51748.1; -;
 DR EMBL: J02758; AA96731.1; -;
 DR EMBL: M13654; AA51744.1; -;
 DR PIR: A26481; LPH04.
 DR PIR: A24449; A2449.
 DR PIR: A29330; A29330.
 DR PIR: A26280; A26280.
 DR PIR: S02715; S02715.
 DR HSSP: P02649; INFO.
 DR SWISS-2DPAGE: P06727; HUMAN.
 DR MIM: 107690; -;
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein. 1.
 DR KEGG: Plasma; lipid transport; HDL; Chylomicron; Repeat; Signal;
 DR KEGG: Disease mutation; Polymorphism.
 FT SIGNAL 1 20
 FT CHAIN 21 396
 FT DOMAIN 33 330
 FT REPEAT 33 54
 FT REPEAT 33 81
 FT REPEAT 82 103
 FT REPEAT 115 136
 FT REPEAT 137 158
 FT REPEAT 159 180
 FT REPEAT 181 202
 FT REPEAT 203 224
 FT REPEAT 225 246
 FT REPEAT 247 268
 FT REPEAT 269 286
 FT REPEAT 287 308
 FT REPEAT 309 330
 FT DOMAIN 372 389
 FT VARIANT 13 13
 FT VARIANT 44 44
 FT VARIANT 147 147
 FT VARIANT 161 161

Query Match 19.7%; Score 92; DB 1; Length 396;
 Best Local Similarity 27.2%; Pred. No. 0.065;
 Matches 22; Conservative 19; Mismatches 40; Indels 0; Gaps 0;

09 9 DRVKRLAVYVDVLDKSDRDVYSGEGLGKOLNKLNDWDSVTSTFKRLQGLPVT 68
 DB 25 DQAVTMDYFSQLSNNAKEVHLQKSELTQOLNALFQDLKGEVNTYAGDLQKLVPEA 84

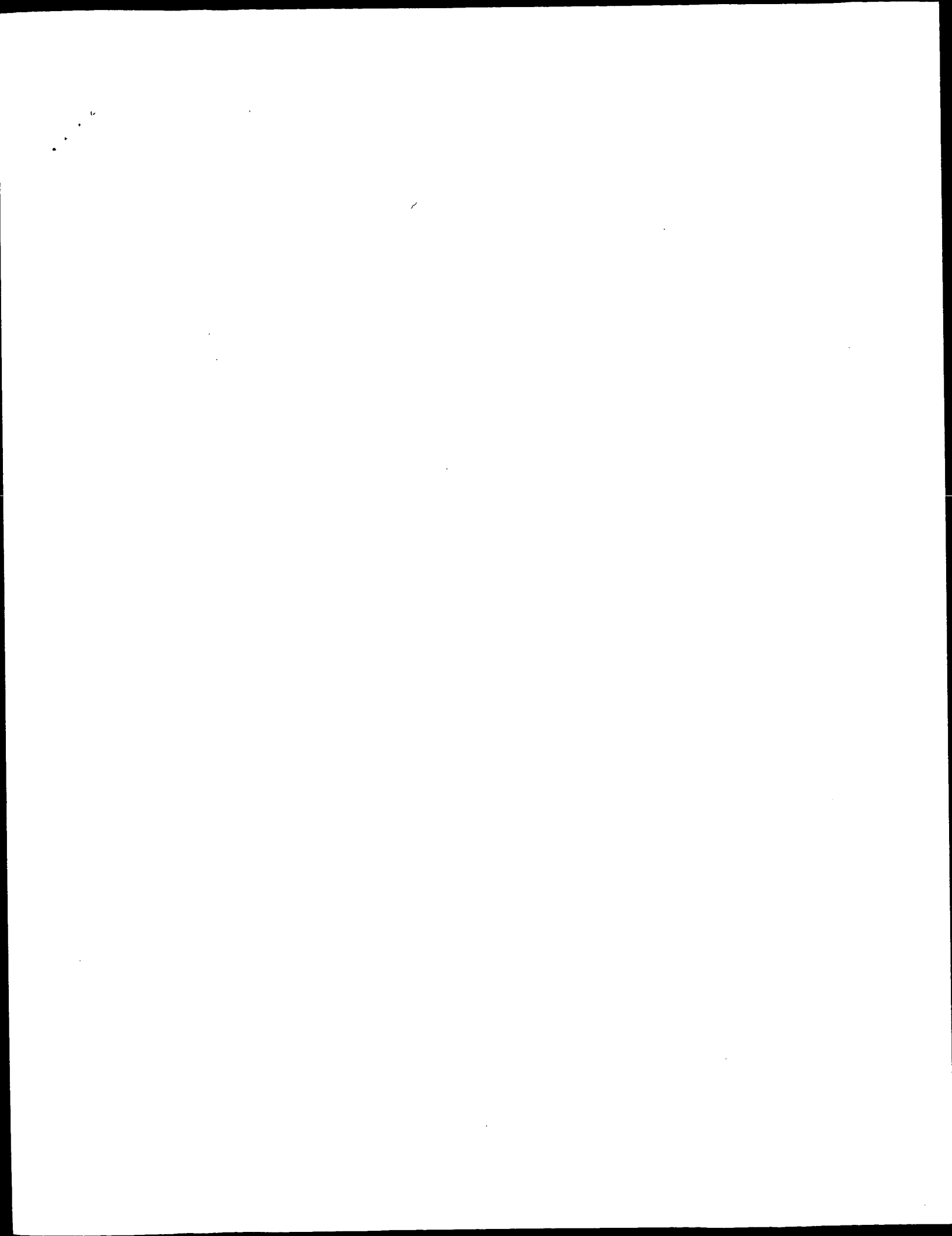
QY 69 QEFWDNLEKETEGLRQEMSKD 89
 DB 85 TELHERLANDESEKKEKEIGKE 105

RESULT 15
 APOA4_RAT
 ID APOA4_RAT STANDARD: PRT: 391 AA.
 AC P02651;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV).
 GN APOA4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86196059; PubMed=3009456;
 RA Boguski M.S., Birkenmeier E.H., Elshourbagy N.A., Taylor J.M.,
 RA Gordon J.I.;
 RT "Evolution of the apolipoproteins. Structure of the rat apo-A-IV gene
 RT and its relationship to the human genes for apo-A-I, C-III, and E.";
 RL J. Biol. Chem. 261:6398-6407(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84298074; PubMed=6591177;
 RA Boguski M.S., Elshourbagy N.A., Taylor J.M., Gordon J.I.;
 RT "Rat apolipoprotein A-IV contains 13 tandem repetitions of a 22-amino
 RT acid segment with amphipathic helical potential.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5021-5025(1984).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87008540; PubMed=3020028;
 RA Haddad I.A., Ordovas J.M., Fitzpatrick T., Karathanasis S.K.;
 RT "Linkage, evolution, and expression of the rat apolipoprotein A-I, C-
 RT III, and A-IV genes.";
 RL J. Biol. Chem. 261:13268-13277(1986).
 CC -I- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
 CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
 CC LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
 CC COMPONENT OF HDL AND CHYLOMICRONS.
 CC -I- SUBCELLULAR LOCATION: Extracellular.
 CC -I- TISSUE SPECIFICITY: SECRETED IN PLASMA.
 CC -I- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
 CC 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
 CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
 CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
 CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL
 CC ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
 CC -I- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----
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 CC -----
 DR EMBL: M00002; AAA85909.1; -;
 DR EMBL: J02588; AAA40747.1; -;
 DR EMBL: M13508; AAA40748.1; -;
 DR PIR: A03095; LPTA4.
 DR PIR: A25214; A25214.
 DR PIR: C24700; C24700.
 DR HSSP: P02671; 1FZB.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein.1.
 KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal.
 FT SIGNAL 1 20

FT CHAIN 21 391 APOLOPOPROTEIN A-IV.
 FT DOMAIN 33 330 13 X 22 AA APPROXIMATE TANDEM REPEATS.
 FT REPEAT 33 54 1.
 FT REPEAT 60 81 2.
 FT REPEAT 82 103 3.
 FT REPEAT 115 136 4.
 FT REPEAT 137 158 5.
 FT REPEAT 159 180 6.
 FT REPEAT 181 202 7.
 FT REPEAT 203 224 8.
 FT REPEAT 225 246 9.
 FT REPEAT 247 268 10.
 FT REPEAT 269 286 11.
 FT REPEAT 287 308 12.
 FT REPEAT 309 330 13.
 FT DOMAIN 374 385 GLU/GLN-RICH.
 FT VARIANT 253 253 Q -> H.
 SQ SEQUENCE 391 AA; 44456 MW; 24095004A809201D CRC64;

Query Match 19.2% Score 90; DB 1; Length 391;
 Best Local Similarity 25.9% Pred No. 0.1; Mismatches 38; Indels 0; Gaps 0;
 Matches 21; Conservative 22;
 QY 9 DRVKDLATVYVDVLDKSGRDYVSQFEGSALGKQLNLKLDNNDVSTPSKLRQGLGPT 68
 DB 25 DQVANVMVDYFTQLSNNAKEAVEQLKTDVTLFDQKLGINTFTYADDLQNKLVPPA 84
 QY 69 QEFWDNLEKETEGLRQEMSKD 89
 DB 85 VOLSGHLTKETERYVERIOKE 105

Search completed: September 22, 2002, 12:22:19
 Job time: 1019 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:21:38 : Search time 111.17 seconds
(without alignments)
138.496 Million cell updates/sec

Title: US-09-803-918a-2_COPY_25_113

Perfect score: 468
Sequence: 1 DEPPSPMDRVKDLATYVVD.....EFMDLKEKETEGLRQEMSKD 89

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	79.1	264	11 092214	092214 mesocricetu
2	344	73.5	258	11 009054	009054 rattus norv
3	344	73.5	258	11 008877	008877 rattus norv
4	343	73.3	263	11 009042	009042 mus musculu
5	343	73.3	263	11 008855	008855 mus musculu
6	292	62.4	241	6 09T549	09T549 erinaceus e
7	217	46.4	82	6 029248	029248 sus scrofa
8	194	41.5	56	6 002762	002762 ovis aries
9	141	30.1	26	4 09UCR8	09UCR8 homo sapien
10	106	22.6	34	13 09PRK6	09PRK6 anser anser
11	101	21.6	30	11 09QV04	09QV04 rattus sp.
12	99	21.2	174	13 09DF03	09DF03 gallinichthys
13	84.5	18.1	366	13 033601	033601 gallus gall
14	81	17.3	435	11 001488	001488 mus musculu
15	78.5	16.8	687	5 095095	095095 caenorhabdi
16	78.5	16.8	2697	5 001438	001438 caenorhabdi

17	77	16.5	395	11 09DBNO	09DBNO mus musculu
18	77	16.5	395	11 091XF8	091XF8 mus musculu
19	74	15.8	313	6 09GLCO	09GLCO tupia glis
20	73	15.6	491	5 045988	045988 caenorhabdi
21	72	15.4	102	6 029258	029258 sus scrofa
22	71.5	15.3	625	16 098095	098095 mycoplasma
23	71.5	15.3	1687	10 09XGN9	09XGN9 oryza sativ
24	71	15.2	562	12 067018	067018 influenza a
25	70.5	15.1	2752	5 09BJYO	09BJYO plasmodium
26	70	15.0	328	17 09HSV1	09HSV1 halobacteri
27	69.5	14.9	452	2 09F1X5	09F1X5 lactobacill
28	69.5	14.9	545	2 096C12	096C12 homo sapien
29	69	14.7	272	4 075663	075663 homo sapien
30	69	14.7	386	10 09LHDO	09LHDO arabidopsis
31	69	14.7	926	17 09HM79	09HM79 halobacteri
32	68.5	14.7	1560	9 064282	064282 streptococc
33	68.5	14.6	160	4 09UP14	09UP14 homo sapien
34	68.5	14.6	329	11 09DA95	09DA95 mus musculu
35	68.5	14.6	391	4 09Y657	09Y657 homo sapien
36	68.5	14.6	633	16 09CN49	09CN49 pasteurella
37	68.5	14.6	1205	5 09VM93	09VM93 drosophila
38	68	14.5	179	11 09DAK6	09DAK6 mus musculu
39	68	14.5	179	11 09WUD8	09WUD8 mus musculu
40	68	14.5	244	4 013784	013784 homo sapien
41	68	14.5	509	5 095SK3	095SK3 drosophila
42	68	14.5	4151	5 096936	096936 drosophila
43	68	14.5	5201	5 09U479	09U479 drosophila
44	68	14.5	5385	5 09V6V3	09V6V3 drosophila
45	68	14.5	5496	5 09V6V2	09V6V2 drosophila

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	264 AA.
092214	092214	01-MAY-1999 (TREMBLrel. 10, Created)		
AC	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	APOLIPOPROTEIN A-I.			
GN	APOLI.			
OS	Mesocricetus auratus (Golden hamster).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC	Mesocricetus.			
OX	NCBI_TaxID=10036;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=GOLDEN SYRIAN; TISSUE=INTESTINE;			
RX	MEDLINE=99061559; PubMed=9843713;			
RA	WU J.Y.J., Reeves S.K., Wang Y.R., Wu Y., Lei P.P., Lei K.Y.;			
RT	"Zinc deficiency decreases plasma level and hepatic mRNA abundance of			
RT	apolipoprotein A-I in rats and hamsters."			
RL	Am. J. Physiol. 275:C1516-C1525(1998).			
DR	EMBL; AF046919; AAC98484.1; -.			
DR	HSSP; P02647; IAV1.			
DR	InterPro; IPR000074; Apolipoprotein.			
DR	Pfam; PF01442; Apolipoprotein; 1.			
KW	lipoprotein.			
SQ	SEQUENCE 264 AA: 30739 MW: 280B22E4C0F0B129 CRC64;			

Query Match 79.1%; Score 370; DB 11; Length 264;

Best Local Similarity 77.3%; Pred. No. 4.1e-31; Matches 68; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY	2	EPPOSPPMDRVKDLATYVVDYKDSGRDYVSQFGSALGKQJLNKLDNDMSVSTFSKUR 61
Db	25	DDPQTMDRVKDFATYVVDYKDSGRDYVSQFETSAIGKQJLNKLDNDMSVSTFSKUR 84
QY	62	EQGLPVTQEFMDNLEKETEGLRQEMSKD 89

```

Db      85  EOLGPVTOEFMDNLEKETEMLRKEMNKD 112
|||||
RESULT  2
AC      009054  PRELIMINARY; PRT; 258 AA.
ID      009054
DT      01-JUL-1997 (TREMBLrel. 04, Created)
DR      01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
OS      Apolipoprotein A-I.
OC      Rattus norvegicus (Rat).
NC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN      NCBI_TaxID=10116;
RP      SEQUENCE FROM N.A.
RC      STRAIN=WKY, AND SHRS; TISSUE=SPLEEN;
RA      Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
RL      Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U79578; AAB58430.1; -
DR      EMBL; U79577; AAB58429.1; -
DR      HSSP; P02647; IAVI.
DR      InterPro: IPR000074; Apolipoprotein.
DR      Pfam; PF01442; Apolipoprotein; 1.
KW      Lipoprotein.
SQ      SEQUENCE 258 AA; 29918 MW; 093B6E2E629CDC8 CRC64;

Query Match 73.5%; Score 344; DB 11; Length 258;
Best Local Similarity 74.2%; Pred. No. 2.2e-28;
Matches 66; Conservative 8; Mismatches 13; Indels 2; Gaps 1;

QY      1 DEPPQSPWDRVKDLATVYVDVKSGRDYVSQFEGSALGKQLNLKLDNMDSVTSFSKL 60
Db      25 DEPSQ--WDRVKDFATVYVDVAVKSGRDYVSQFESSSTLGKQLNLKLDNMDVTSVGR 82
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QY      61 REOLGPVTOEFMDNLEKETEGLRQEMSKD 89
Db      83 OEOLGPVTOEFMDNLEKETDMPREMNKD 111
|||||

RESULT  3
AC      008877  PRELIMINARY; PRT; 258 AA.
ID      008877
DT      01-JUL-1997 (TREMBLrel. 04, Created)
DR      01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
OS      Apolipoprotein A-I.
OC      Rattus norvegicus (Rat).
NC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN      NCBI_TaxID=10116;
RP      SEQUENCE FROM N.A.
RC      STRAIN=SHR; TISSUE=SPLEEN;
RA      MEDLINE=98077648; Pubmed=9415807;
DE      Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
OS      "Repetitive elements in the third intron of murine apolipoprotein A-I
RT      gene."
RL      Biochem. Mol. Biol. Int. 43:989-996(1997).
DR      HSSP; P02647; IAVI.
DR      EMBL; U79576; AAB58428.1; -
DR      InterPro: IPR000074; Apolipoprotein.
DR      Pfam; PF01442; Apolipoprotein; 1.
KW      Lipoprotein.
SQ      SEQUENCE 258 AA; 29831 MW; 093FB502E629CDC8 CRC64;

Query Match 73.5%; Score 344; DB 11; Length 258;
Best Local Similarity 74.2%; Pred. No. 2.2e-28;

```

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Matches 66; Conservative 8; Mismatches 13; Indels 2; Gaps 1;

QY      1 DEPPQSPWDRVKDLATVYVDVKSGRDYVSQFEGSALGKQLNLKLDNMDSVTSFSKL 60
Db      25 DEPSQ--WDRVKDFATVYVDVAVKSGRDYVSQFESSSTLGKQLNLKLDNMDVTSVGR 82
|||||
QY      61 REOLGPVTOEFMDNLEKETEGLRQEMSKD 89
Db      83 OEOLGPVTOEFMDNLEKETDMPREMNKD 111
|||||

RESULT  4
AC      009042  PRELIMINARY; PRT; 263 AA.
ID      009042
DT      01-JUL-1997 (TREMBLrel. 04, Created)
DR      01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
OS      Apolipoprotein A-I.
OC      Mus musculus (Mouse).
NC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      NCBI_TaxID=10090;
RP      SEQUENCE FROM N.A.
RC      STRAIN=ICR AND BALB/C, AND C3H; TISSUE=SPLEEN;
RA      Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
RL      Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U79575; AAB58427.1; -
DR      EMBL; U79572; AAB58424.1; -
DR      EMBL; U79573; AAB58425.1; -
DR      HSSP; P02647; IAVI.
DR      InterPro: IPR000074; Apolipoprotein.
DR      Pfam; PF01442; Apolipoprotein; 1.
KW      Lipoprotein.
SQ      SEQUENCE 263 AA; 30516 MW; E245DF7483A5A0DD CRC64;

Query Match 73.3%; Score 343; DB 11; Length 263;
Best Local Similarity 69.3%; Pred. No. 2.9e-26;
Matches 61; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

QY      2 EPPQSPWDRVKDLATVYVDVKSGRDYVSQFEGSALGKQLNLKLDNMDSVTSFSKL 61
Db      25 DEPSQMDKVKDFANVYVDVAVKSGRDYVSQFESSSTLGKQLNLKLDNMDVTSVGR 84
|||||
QY      62 REOLGPVTOEFMDNLEKETEGLRQEMSKD 89
Db      85 ERLGPLTRDFMDNLEKETDMPREMNKD 112
|||||

RESULT  5
AC      008855  PRELIMINARY; PRT; 263 AA.
ID      008855
DT      01-JUL-1997 (TREMBLrel. 04, Created)
DR      01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
OS      Apolipoprotein A-I.
OC      Mus musculus (Mouse).
NC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      NCBI_TaxID=10090;
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6; TISSUE=SPLEEN;
RA      MEDLINE=98077648; Pubmed=9415807;
DE      Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
OS      "Repetitive elements in the third intron of murine apolipoprotein A-I
RT      gene."
RL      Biochem. Mol. Biol. Int. 43:989-996(1997).
DR      EMBL; U79574; AAB58426.1; -
DR      HSSP; P02647; IAVI.

```

DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 SQ SEQUENCE 263 AA; 30544 MW; 7825DF7483A5B24A CRC64;

Query Match 73.3%; Score 343; DB 11; Length 263;
 Best Local Similarity 69.3%; Pred. No. 2.9e-28;
 Matches 61; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

QY 2 EPPQSPMDRKDLATYVVDYLDKSGRDYVSQFEGSALGKOLNKLNDNDVSTFSKRL 61
 DB 25 DEPOSQMDKVKFANVYVDVAVKSGRDYVSQFESSIGCOLNKLNDNDVSTFSKRL 84
 QY 62 EOLGPVQEFMDLNEKTEGLRQEMSKD 89
 DB 85 ERUGPLRFMDLNEKTEGLRQEMSKD 112

RESULT 6

Q9TS49 PRELIMINARY; PRT; 241 AA.

AC Q9TS49; PRELIMINARY; PRT; 241 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE APOLIPROTEIN A-I, APOA-I-CHOLESTEROL TRANSPORTER.
 OS Etrinecus europaeus (Western European hedgehog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.
 OX NCBI_TaxID=9365;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95294458; PubMed=7775860;
 RA Sparrow D.A., Laplaud P.M., Saboureau M., Zhou G., Dolphin P.J.,
 RA Goto A.M.Jr., Sparrow J.T.;
 RT "Plasma lipid transport in the hedgehog: partial characterization of
 RT structure and function of apolipoprotein A-I.";
 RL J. Lipid Res. 36:485-495(1995).
 DR HSSP: P02647; IAVI.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 SQ SEQUENCE 241 AA; 27630 MW; 2EF00F2B69210535 CRC64;

Query Match 62.4%; Score 292; DB 6; Length 241;
 Best Local Similarity 61.2%; Pred. No. 6.3e-23;
 Matches 52; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

QY 5 QSPMDRKDLATYVVDYLDKSGRDYVSQFEGSALGKOLNKLNDNDVSTFSKRL 64
 DB 4 KSYMDQKMDLTYVVDVAVKSGRDYLSLDTSLGCOLNKLNDNDVSTFSKRL 63
 QY 65 GPVTOEFMDLNEKTEGLRQEMSKD 89
 DB 64 KPIAMEFMDLNEKTEGLRQEMSKD 88

RESULT 7
 Q929248 PRELIMINARY; PRT; 82 AA.
 AC Q929248; PRELIMINARY; PRT; 82 AA.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE APOLIPROTEIN A-I (FRAGMENT).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SMALL INTESTINE;

RX MEDLINE=96327607; PubMed=8672129;
 RA Wintecoe A.K., Fredholm M., Davies W.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 RT library.";
 RL Mamm. Genome 7:509-517(1996).
 DR EMBL: F14858; CAA23298.1; -.
 KW Lipoprotein.
 FT NON_TER
 SQ SEQUENCE 82 AA; 9168 MW; 24625C65CFEED8 CRC64;

Query Match 46.4%; Score 217; DB 6; Length 82;
 Best Local Similarity 70.7%; Pred. No. 1.3e-15;
 Matches 41; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 2 EPPQSPMDRKDLATYVVDYLDKSGRDYVSQFEGSALGKOLNKLNDNDVSTFSKRL 59
 DB 25 DDPXSPMDRKDLATYVVDYLDKSGRDYXQFEGSALGKOLNKLNDNDVSTFSKRL 82

RESULT 8

Q02762 PRELIMINARY; PRT; 56 AA.

AC Q02762; PRELIMINARY; PRT; 56 AA.
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE APOLIPROTEIN A1 (FRAGMENT).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99098454; PubMed=9883985;
 RA Robertson J.A., Bhattacharya S., Ing N.H.;
 RT "Tanoxifen up-regulates oestrogen receptor-alpha, c-fos and
 RT glyceridehydride 3-phosphate-dehydrogenase mRNAs in ovine endometrium.";
 RL J. Steroid Biochem. Mol. Biol. 67:285-292(1998).
 DR EMBL: U94720; MAB57840.1; -.
 DR HSSP: P02647; IAVI.
 DR Lipoprotein.
 KW NON_TER
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 56 AA; 6617 MW; 2AB38E08F1E8F1BC CRC64;

Query Match 41.5%; Score 194; DB 6; Length 56;
 Best Local Similarity 83.7%; Pred. No. 2.1e-13;
 Matches 36; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 47 LNDNDVSTFSKRLRQGLGPVTOEFMDLNEKTEGLRQEMSKD 89
 DB 1 LNDNDVSTFSKRLRQGLGPVTOEFMDLNEKTEGLRQEMSKD 43

RESULT 9
 Q90CT8 PRELIMINARY; PRT; 26 AA.
 AC Q90CT8; PRELIMINARY; PRT; 26 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE SPERM ACTIVATING PROTEIN SUBUNIT I, APOLIPROTEIN A1, SPAP SUBUNIT I.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91369902; PubMed=1909888;
 RA Akerlof E., Jorvall H., Slotte H., Pousette A.;

Sun Sep 22 12:10:21 2002

us-09-803-918a-2_copy_25_113.rspt

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2002, 12:05:16 : Search time 139.03 Seconds
(without alignments)
71.104 Million cell updates/sec

Title: US-09-803-918a-2_COPY_25_113

Perfect score: 468
Sequence: 1 DEPPSPMDRVMKDLATVYVD.....EFWNLKETEGLQEMSKD 89

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT.*
8: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT.*
9: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT.*
10: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT.*
11: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT.*
12: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT.*
13: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT.*
14: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT.*
15: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT.*
16: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT.*
17: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT.*
18: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	468	100.0	243	9 AAP81082	Sequence of mature Apo-IIipoprotein AI
2	468	100.0	264	15 AAR56863	Apo-IIipoprotein AI
3	468	100.0	264	15 AAR56864	Assumed human apol
4	468	100.0	267	7 AAP61079	Entire human prepr
5	468	100.0	267	9 AAP82128	Sequence of apo AI
6	468	100.0	267	14 AAR34032	Human apo A-I incl
7	468	100.0	267	16 AAR72705	Human apolipoprote
8	468	100.0	267	18 AAM08602	Human apolipoprote
9	468	100.0	267	20 AAY18675	Full length Apo-AI
10	468	100.0	267	22 AAB47620	Recombinant human
11	468	100.0	268	9 AAP80668	

12	468	100.0	299	22 AAU33170	Novel human secret
13	415	88.7	154	22 AA012095	Human polypeptide
14	338	72.2	151	22 AA002278	Human polypeptide
15	322.5	68.9	120	22 AAU30267	Novel human secret
16	322.5	68.9	120	22 AAU30469	Novel human secret
17	322.5	68.9	166	22 AAU28372	Novel human secret
18	322.5	68.9	244	22 AAU28184	Novel human secret
19	295	63.0	221	22 AAU29835	Novel human secret
20	247	52.8	119	22 AAU30468	Novel human secret
21	246.5	52.7	318	22 AAU30268	Novel human secret
22	183.5	39.2	359	22 AAU30470	Apo AI epitope. S
23	116	24.8	21	10 AAP90956	Human apolipoprotein
24	95.5	20.4	377	14 AAR39502	Human apolipoprotein
25	92	19.7	183	14 AAR39482	Human apolipoprotein
26	92	19.7	333	14 AAR39481	Human apolipoprotein
27	92	19.7	333	14 AAR39488	Human apolipoprotein
28	92	19.7	333	14 AAR39490	Human apolipoprotein
29	92	19.7	333	14 AAR39495	Human apolipoprotein
30	92	19.7	333	14 AAR39497	Human apolipoprotein
31	92	19.7	337	14 AAR39492	Human apolipoprotein
32	92	19.7	337	14 AAR39494	Human apolipoprotein
33	92	19.7	342	14 AAR39487	Human apolipoprotein
34	92	19.7	342	14 AAR39489	Human apolipoprotein
35	92	19.7	342	14 AAR39491	Human apolipoprotein
36	92	19.7	342	14 AAR39496	Human apolipoprotein
37	92	19.7	342	14 AAR39498	Human apolipoprotein
38	92	19.7	346	14 AAR39493	Human apolipoprotein
39	92	19.7	377	14 AAR39443	Human apolipoprotein
40	92	19.7	377	14 AAR39480	Human apolipoprotein
41	92	19.7	377	14 AAR45242	Human apolipoprotein
42	92	19.7	377	14 AAR45243	Human apolipoprotein
43	92	19.7	377	14 AAR45244	Human apolipoprotein
44	92	19.7	396	22 AAB90664	Human secreted pro
45	91	19.4	16	20 AAY27065	Peptide Seq ID No:

ALIGNMENTS

RESULT	ID	Sequence	Score	Description
1	AAP81082	standard; protein; 243 AA.	468	Sequence of mature human apolipoprotein AI (apoAI).
XX	AC	AAP81082;	468	Atherosclerosis; therapy; cardiovascular disease.
XX	DE	14-JAN-1991 (first entry)	468	Homo sapiens.
XX	XX		468	W08803166-A.
XX	XX		468	05-MAY-1988.
XX	XX		468	21-OCT-1987; 87WO-EP00621.
XX	XX		468	23-OCT-1986; 86GB-0025435.
XX	XX		468	(FARM) FARMITALIA C ERBA SPA.
XX	XX		468	Lorenzetti R, Monaco L, Soria M, Palomba R, Isacchi A, Sarmientos P;
XX	XX		468	WPI: 1988-133240/19.
XX	XX		468	N-PSDB: AAN80243.
XX	XX		468	Recombinant human apo-IIipoprotein AI -
XX	XX		468	used to lower plasma cholesterol and/or tri glyceride levels and
XX	XX		468	to combat atherosclerosis and cardiovascular diseases
XX	XX		468	Disclosure; Fig 1; 51pp; English.

XX The protein comprising apo AI genetic variants may be used to lower
 CC plasma cholesterol and/or triglyceride levels. They may also be used to
 CC combat atherosclerosis and cardiovascular diseases such as coronary
 CC heart disease. Prefd. proteins are Met-apo AI, Met-apo AI-T6, Met-apo
 CC AI-MI and Met-apo AI-T6/MI.

XX Sequence 243 AA;

Query Match 100.0%; Score 468; DB 9; Length 243;
 Best Local Similarity 100.0%; Pred. No. 6.5e-43;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPWDRVKDLATYVYVYLKDSGRDYSQFEGSALGKQLNLKLDNMDSVTSTFSKL 60
 Db 1 deppqspwdrvkdlatyvdyvlkdsgrdyvsqfegsalgkqlnlkldnmdsvtstfskl 60
 QY 61 REQLGPVTQEFWDLNLEKETEGRLROEMSKD 89
 Db 61 reqlgpvtqefwldnleketegrlrgemskd 89

RESULT 2

AAR56863
 ID AAR56863 standard; Protein; 264 AA.

AC AAR56863;

DT 26-JUN-1995 (first entry)

DE Apo-1ipoprotein AI-M.

KW Apo-1ipoprotein AI-M; Apo AI-M; Escherichia coli; plasmid PKP683;
 KM vector; atherosclerosis; cardiovascular disease.

OS Homo sapiens.

PN W09413819-A.

PD 23-JUN-1994.

PF 09-DEC-1993; 93WO-SE01061.

PR 11-DEC-1992; 92SE-0003753.

PA (KABI) KABI PHARMACIA AB.

PI Abrahamsen L, Holmgren E, Kalderen C, Lake M, Mikaelsson A;
 PI Sejlitz T;

DR WPI; 1994-217892/26.

DR N-PSDB; AA068357.

XX Expression vector for extracellular prodn of apo-1ipoprotein AI-M
 PT in E. coli - includes inducible promoter and signal peptide
 PT sequences providing improved yield, useful in treating
 PT atherosclerosis and cardiovascular disease.

PS Disclosure; Fig. 3; 33pp; English.

XX Plasmid PKP683 encodes human apo-1ipoprotein AI-M in E. coli. The
 CC NotI-HindIII segment of PKP683 and the deduced amino acid sequence
 CC of the translated Apo AI-M protein were determined. The plasmid
 CC provides high yields of extracellular Apo AI-M.

XX Sequence 264 AA;

Query Match 100.0%; Score 468; DB 15; Length 264;
 Best Local Similarity 100.0%; Pred. No. 7.2e-43;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPWDRVKDLATYVYVYLKDSGRDYSQFEGSALGKQLNLKLDNMDSVTSTFSKL 60
 Db 22 deppqspwdrvkdlatyvdyvlkdsgrdyvsqfegsalgkqlnlkldnmdsvtstfskl 81
 QY 61 REQLGPVTQEFWDLNLEKETEGRLROEMSKD 89
 Db 82 reqlgpvtqefwldnleketegrlrgemskd 110

RESULT 3

AAR56864
 ID AAR56864 standard; Protein; 264 AA.

AC AAR56864;

DT 26-JAN-1995 (first entry)

DE Apo-1ipoprotein AI-M.

KW Apo-1ipoprotein AI-M; Apo AI-M; Escherichia coli; plasmid PKP764;
 KM vector; atherosclerosis; cardiovascular disease.

OS Homo sapiens.

PN W09413819-A.

PD 23-JUN-1994.

PF 09-DEC-1993; 93WO-SE01061.

PR 11-DEC-1992; 92SE-0003753.

PA (KABI) KABI PHARMACIA AB.

PI Abrahamsen L, Holmgren E, Kalderen C, Lake M, Mikaelsson A;
 PI Sejlitz T;

DR WPI; 1994-217892/26.

DR N-PSDB; AA068358.

XX Expression vector for extracellular prodn of apo-1ipoprotein AI-M
 PT in E. coli - includes inducible promoter and signal peptide
 PT sequences providing improved yield, useful in treating
 PT atherosclerosis and cardiovascular disease.

PS Disclosure; Fig. 4; 33pp; English.

XX Plasmid PKP764 encodes human apo-1ipoprotein AI-M in E. coli. The
 CC NotI-HindIII segment of PKP764 and the deduced amino acid sequence
 CC of the translated Apo AI-M protein were determined. The plasmid
 CC provides high yields of extracellular Apo AI-M.

XX Sequence 264 AA;

Query Match 100.0%; Score 468; DB 15; Length 264;
 Best Local Similarity 100.0%; Pred. No. 7.2e-43;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPQSPWDRVKDLATYVYVYLKDSGRDYSQFEGSALGKQLNLKLDNMDSVTSTFSKL 60
 Db 22 deppqspwdrvkdlatyvdyvlkdsgrdyvsqfegsalgkqlnlkldnmdsvtstfskl 81

QY 61 REQLGPVTQEFWDLNLEKETEGRLROEMSKD 89
 Db 82 reqlgpvtqefwldnleketegrlrgemskd 110

RESULT 4

AAP61079
 ID AAP61079 standard; Protein; 267 AA.

AC AAP61079;

```

XX 07-OCT-1991 (first entry)
DT
XX Assumed human apolipoprotein A-1 derivative gene product.
DE
XX Hyperlipaemia; arteriosclerosis.
KM
XX Homo sapiens.
OS
XX JPI61096998-A.
PN
XX 15-MAY-1986.
PD
XX 16-OCT-1984; 84JP-0216988.
PF
XX 16-OCT-1984; 84JP-0216988.
PR
XX 16-OCT-1984; 84JP-0216988.
PS
XX (MITU ) MITSUBISHI CHEM IND KK.
PA
XX WPI; 1986-165025/26.
DR
XX N-PSDB; AAN60886.
XX
XX Human apo:lipoprotein A-1 (deriv.) prepn. - by providing DNA
PT fragment in cloning site downstream of expression vector promoter
PT and introducing into host microorganism.
XX
XX Disclosure; Fig 2; 9pp; Japanese.
PS
XX
XX The human apolipoprotein may be produced by a suitable transformed
CC host, it is effective in treating hyperlipaemia and arteriosclerosis.
XX
XX Sequence 267 AA;
SQ
Query Match 100.0%; Score 468; DB 7; Length 267;
Best Local Similarity 100.0%; Pred. No. 7.3e-43;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEPPQSPMDRVKDLATVYVDVKDSGRDYSQFEGSALGKQLNKLNDNDSVTSTFSKL 60
DB 25 deppqspmdrvkdlatvyvdvkdsgrdyvsqfegsalsgqlnlkldndsvstfskl 84
QY 61 REOLGPTVOEFMDNLEKETEGSLROEMSKD 89
DB 85 reqlgpvtqefwldnleketegslrqemskd 113
Db
RESULT 5
AAP82128
ID AAP82128 standard; protein; 267 AA.
XX
XX AAP82128;
AC
XX 24-OCT-1990 (first entry)
DT
XX Entire human preproapoprotein A1.
DE
XX
XX human preproapoprotein A1; high density lipoprotein deficiency; ss.
KM
XX
XX synthetic.
OS
XX
XX Key Location/Qualifiers
FH 1..18
FT Peptide /label=precursor
FT 19..24
FT Peptide /label=propeptide
FT 25..267
FT Protein /label=mature apoprotein
XX
XX EP293357-A.
XX
XX 30-NOV-1988.
XX

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PF 24-MAY-1988; 88EP-0870095.
XX
XX 28-MAY-1987; 87GB-0012540.
PR
XX (UNIO ) UCB SA.
PA
XX
XX Bollen A, Gobert J, Wulfert E;
PI
XX WPI; 1988-339891/48.
DR
XX N-PSDB; AAN82064.
DR
XX
XX New DNA encoding human preproapoprotein A1 -
PT modified to eliminate hairpin structures
PT
XX
XX Disclosure; ; p; French.
PS
XX
XX The cDNA 878bp fragment encoding preproapoprotein A1 was detected
CC in clone PUB1609 derived from human liver cells.
CC See also AAN81258.
XX
XX Sequence 267 AA;
SQ
Query Match 100.0%; Score 468; DB 9; Length 267;
Best Local Similarity 100.0%; Pred. No. 7.3e-43;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEPPQSPMDRVKDLATVYVDVKDSGRDYSQFEGSALGKQLNKLNDNDSVTSTFSKL 60
DB 25 deppqspmdrvkdlatvyvdvkdsgrdyvsqfegsalsgqlnlkldndsvstfskl 84
QY 61 REOLGPTVOEFMDNLEKETEGSLROEMSKD 89
DB 85 reqlgpvtqefwldnleketegslrqemskd 113
Db
RESULT 6
AAR34032
ID AAR34032 standard; Protein; 267 AA.
XX
XX AAR34032;
AC
XX 13-AUG-1993 (first entry)
DT
XX
XX Sequence of apo A1.
DE
XX
XX Lipoprotein; apoprotein; B-100; A-I; LDL; HDL; assay.
KM
XX
XX Homo sapiens.
OS
XX
XX WO9307165-A.
PN
XX
XX 15-APR-1993.
PD
XX
XX 09-OCT-1992; 92WO-US08634.
PF
XX
XX 09-OCT-1991; 91US-0774633.
PR
XX 08-OCT-1992; 92US-0555555.
PR 28-JUN-1992; 92US-0901706.
XX
XX (SCRI ) SCRIPPS RES INST.
PA
XX
XX Curtiss LR, Koduri KR, Smith RS, Witzum JL, Young SG;
PI
XX WPI; 1993-134378/16.
DR
XX N-PSDB; AAO40030.
DR
XX
XX Polypeptide mimic of native apo B-100 and native apo A-I - useful
PT in assays for LDL and HDL in plasma samples
PT
XX
XX Claim 19; Pages 105-106; 137pp; English.
PS
XX
XX The inventors claim a portion of the polypeptide contg. apo B-100
CC

```

CC that immunoreacts with antibodies secreted by the hybridoma MB47
 CC having ATCC Accession No. 8746. Polypeptides specifically claimed
 CC include residues 217-297, 216-310, 216-331, 216-352, 216-377, 1-377,
 CC 205-297, 173-297, 140-297. DNA sequences encoding the polypeptides
 CC are also claimed. Also claimed are a fusion polypeptide that
 CC contains (a) a first amino acid residue sequence up to 250 residues
 CC in length that includes residues 120-135 of apo A-I, (b) a second
 CC amino acid residue sequence up to 375 residues in length that
 CC includes residues 217-297 of apo B-100 and DNA encoding it.

XX Sequence 267 AA;

Query Match 100.0%; Score 468; DB 14; Length 267;
 Best Local Similarity 100.0%; Pred. No. 7.3e-43;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPSPMDRYKDLATYVVDYDKSGRDYVSQFESALGKOLNKLIDNMDSVTSFSKL 60
 Db 25 deppspmdrykdlatyvvdylkdsgrdyvsqfegsalgklnklidndsvstfskl 84

QY 61 REOLGPTYQEFWDNLEKETEGSLRQEMSKD 89
 Db 85 reqlgpytqefwdnleketegslrqemskd 113

RESULT 7

AAR72705 standard; Protein: 267 AA.

XX AAR72705;

DT 31-OCT-1995 (first entry)

XX Human apo A-I including signal and propeptide sequences.

DE Apo A-I; LDL cholesterol; low density lipoprotein; lipid.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide /label= presignal

FT Peptide /label= propeptide

FT Peptide /label= claimed

FT Peptide /note= "as part of fusion polypeptide"

FT Peptide /label= claimed

FT Peptide /note= "as part of fusion polypeptide"

XX US5408038-A.

XX 18-APR-1995.

XX 09-OCT-1991; 91US-0774633.

XX 09-OCT-1991; 91US-0774633.

XX 18-JUN-1992; 92US-0901706.

XX 08-OCT-1992; 92US-0959946.

XX (SCRI) SCRIPPS RES INSR.

XX Curtiss LK, Koduri KR, Smith RS, Witzum JL, Young SG;

XX WPI, 1995-161146/21.

XX N-PSDB; AA089634.

XX New apo: lipoprotein B-100 peptide(s) and fusion peptide(s) - used

XX in assay systems for detecting LDL and HDL cholesterol levels in

PS Claim 10; Fig 2; 41pp; English.

XX AAA89634 and AAR72705 depict the AA sequence of human apo A-I and its

XX corresp. cDNA, including presignal residues and propeptide

XX residues, according to Seilhamer et al., DNA 3(4):309 (1984).

XX A dispersible apo A-I/B-100 fusion polypeptide is claimed which

XX contains a first AA sequence of apo A-I and that includes at

XX least AA sequence positions 120-135 (see AAR72606) and which reacts

XX with pan anti-apo A-I antibodies such as: AT-4 ATCC HB8744; AT-7

XX ATCC HB 8745; AT-9 ATCC HB 8741; AT-10 ATCC HB 9200; AT-11 ATCC

XX HB 9201; AT-12 ATCC HB 9202; AT-13 ATCC HB 9203; AT-14 ATCC HB

XX 9204; AT-18 ATCC HB 9507.

XX Sequence 267 AA;

Query Match 100.0%; Score 468; DB 16; Length 267;
 Best Local Similarity 100.0%; Pred. No. 7.3e-43;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPSPMDRYKDLATYVVDYDKSGRDYVSQFESALGKOLNKLIDNMDSVTSFSKL 60
 Db 25 deppspmdrykdlatyvvdylkdsgrdyvsqfegsalgklnklidndsvstfskl 84

QY 61 REOLGPTYQEFWDNLEKETEGSLRQEMSKD 89
 Db 85 reqlgpytqefwdnleketegslrqemskd 113

RESULT 8
 AAM08602 standard; Protein: 267 AA.

XX AAM08602;

DT 04-SEP-1997 (first entry)

XX Human apolipoprotein A-I variant "Paris" protein sequence.

DE Human: apolipoprotein A-I; variant; mutation; serum lipid; cholesterol;

XX high density lipoprotein; triglyceride; symptom; cardiovascular disease;

XX atherosclerosis; restenosis; myocardial infarct; angina; death; stroke;

XX cardiac decompensation; metabolic deficit.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide /label= "prepro peptide"

FT Region /note= "this sequence which contains the mutated amino

FT Region /note= "acid residue is claimed - claim 2"

FT Misc-difference 175 /note= "changed from Arg residue in wild type protein,

FT due to a C to T transition mutation"

XX WO9637608-A1.

XX 28-NOV-1996.

XX 20-MAY-1996; 96WO-FR00747.

XX 22-MAY-1995; 95FR-0006061.

XX (INSP) INST PASTEUR LILLE.

XX (RHON) RHONE-POULENC ROBER SA.

XX (UTPA-) UNIV CURIE PARIS VI P & M.

XX Benoit P, Bruckert E, Deneffe P, Duverger N, Fruchart J;

XX Luc G, Turpin, Assmann G, Funke H;

XX WPI, 1997-021218/02.

XX N-PSDB; AAT43691.

Claim 2; Page -; 58pp; French.

50 Sequence 267 AA;

Query Match	100.0%;	Score 468;	DB 18;	Length 267;
Best Local Similarity	100.0%;	Pred. No. 7.3e-43;		
Matches 89;	Conservative 0;	Mismatches 0;	Indels 0	

```

1 DEPPSPWMDRYKDLATVYVDVLKDSGRDYVSQFEGSALGKOLNLKLDMDWDSVTSFESKL 60
  |||
25 deppspwdrvkdlatyvdvlkdsgrdyvsqfegsaigkqnlkldmdwsvtsfstfsl 84

```

```

61 REQIGPVTQEFWMDNLEKETEGRLQEMSKD 89
    |||||
85 reqigpvtqefwmdnleketegrlqemskd 113

```

RESULT 9
AA18675
AA18675 standard; Protein; 267 AA.

AAV18675;
09-JUL-1999 (first entry)

Human apolipoprotein AI protein sequence.

Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder; ApoA-I; cardiovascular disease; atherosclerosis; restenosis; LCAT; hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase

Homo sapiens.

W09916409-A2.

08-APR-1999.

28-SEP-1998; 98WO-US20329.

29-SEP-1997; 97US-0940136.

(BUTT/) BUTNER K.

(DASS/) DASSEUX J.

(METZ/) METZ G.

(SEKU/) SEKUL R.

Buttner K, Cornut I, Dasseux J, Metz G, Sekul R;

XX	WPI; 1999-254921/21
DR	
DR	N-PSDB; AAX55971.
XX	

PT	Nucleic acid encoding apolipoprotein A-I agonist peptides
XX	
PS	Example; Fig 1; 232pp; English.
XX	

CC The present invention describes a nucleic acid (A) encoding an
 CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,
 CC which forms an amphipathic alpha-helix in presence of lipids. (A'),
 CC optionally as a complex with lipids, and host cells that contain (A'),
 CC are useful for gene therapy, or prevention, of diseases associated with
 CC dyslipidaemia, specifically hypercholesterolaemia, cardiovascular disease,
 CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I
 CC deficiency, hypertriglyceridaemia and metabolic syndrome, also to treat
 CC endotoxaemia (septic shock). Host cells containing (A) can also be used
 CC to study the role of apoA-I in lipid metabolism. (B) can be used
 CC diagnostically, e.g. to measure serum HDL (particularly its
 CC subpopulation involved in retrograde cholesterol transport) and for
 CC imaging the circulatory system or HDL accumulations at fatty streaks.
 CC The present sequence represents human apoA-I.
 CC

50 Sequence 267 AA;

Query Match	100.0%;	Score 468;	DB 20;	Length 267;
Best Local Similarity	100.0%;	Pred. No. 7.3e-43;		
Matches 89; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

Dd 25 deppqspwdrkdlatyvdvlkdsgrdyvsqfegsalgkqlnlklldnwdsvstfskl 84

```

QY      61 REQLGPTVQEEFWNDLLEKETEGLRQEMSKD 89
          |||||
Db      85 reqlgptvqefwndlleketeglrqemskd 113

```

RESULT	10
AAB47620	
ID	AAB47620 standard; Protein; 267 AA
XY	

AC	AAAB47020;
XX	
DT	21-JAN-2002 (first entry)
XY	

	FULL length Apo-A1.
DE	
xy	

NM Apoptinoprotein; Apo-AL; Apo-A1-Irrelevant T-cell activation inhibitor;
NM APT1; monocytic IL-1; interleukin-1; TNF; tumour necrosis factor;
KM acute pancreatitis; Alzheimer's disease; asthma; cancer; fever;
NM inflammatory bowel disease; ischaemia; multiple sclerosis; osteoporosis;
KM Parkinson's disease; psoriasis; probe.

OS Homo sapiens

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
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11	11	11
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93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

/label= Helical lipid binding domain

/label= Helical lipid binding domain

FT /note= "Involved in lipoprotein-mediated cholesterol

FT	Binding-site	149..219	CELLS FROM MONOCYTES

FT	Domain	FT	Domain
99.120	7xaver-receptor binding domain		

FT	Domain	Label	major antigenic epitope domain
99...143			

FT	Domain	Label = hinged domain
66..120		

FT
/label= Phylogenetically conserved domain

FT Domain 90..111 /note="Involved in lectin-cholesterol acyltransferase activity"

FT Domain 44..65 /label= Amphipathic helix

FT Domain 66..98 /label= Amphipathic helix

FT Domain 99..120 /label= Amphipathic helix

FT Domain 121..142 /label= Amphipathic helix

FT Domain 143..164 /label= Amphipathic helix

FT Domain 165..208 /label= Amphipathic helix

FT Domain 209..219 /label= Amphipathic helix

FT Domain 220..241 /label= Amphipathic helix

FT Peptide 25..194 /label= AFTI

FT Peptide /note="18 kD N-terminal fragment"

FT Peptide 25..144 /label= AFTI

FT Peptide /note="13 kD N-terminal fragment"

FT Peptide 156..267 /label= AFTI

FT Peptide /note="13 kD C-terminal fragment"

PN W0200168852-A2.

PD 20-SEP-2001.

PD 13-MAR-2001; 2001WO-0507826.

PE 13-MAR-2000; 2000US-189008P.

PR (AMGE-) AMGEN INC.

PA Edwards CK, Burger D, Dayer J, Kohno T;

PI WPI; 2001-596908/67.

DR N-PSDB; AAH43623.

XX Apo-A-I fragment T-cell activation inhibitor (AFTI) polynucleotides, useful for treating, diagnosing, ameliorating diseases associated with IL-1 and/or TNF activity, e.g. acute pancreatitis, Alzheimer's disease and asthma.

XX Claim 1; Fig 1A; 132pp; English.

XX This sequence shows full length apolipoprotein (Apo-AI). Fragments of Apo-AI may be used as Apo-A-I fragment T-cell activation inhibitors (AFTI). These fragments are selected from an 18 kD N-terminal fragment (amino acids 25-194), a 13 kD N-terminal fragment (amino acids 25-144) and a 13 kD C-terminal fragment (amino acids 156-267). The AFTI polypeptides and polynucleotides are useful for regulating T-cell mediated activation of monocytes and for treating, diagnosing, ameliorating diseases associated with IL-1 and/or TNF activity. The diseases are acute pancreatitis, Alzheimer's disease, asthma, cancer, fever, inflammatory bowel disease, ischemia, multiple sclerosis, osteoporosis, Parkinson's disease or psoriasis. Numerous examples of other diseases are given in the specification. The AFTI nucleic acids are useful as hybridization probes in diagnostic assays to test for the presence of an AFTI or Apo-A-I DNA in mammalian tissue or bodily fluid samples.

XX Sequence 267 AA;

Query Match 100.0%; Score 468; DB 22; Length 267;
 Best Local Similarity 100.0%; Pred. NO. 7.3e-43;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DEPPQSPWDRVKDLATYVVDVYKDSGRDYSQPEGSALGKOLNKLIDNMDSVTSFSKL 60
 |||||||
 Db 25 deppqspwdrvkdlatvyvdvdkdsgrdyvsgfegsalgkqlkildnmdsvtsfsl 84
 |||||||
 Oy 61 REOLGPVTOEFWDNLEKETEGGLROEMSKD 89
 |||||||
 Db 85 reqlgpvrtgefwdnleketegglrgemskd 113
 |||||||

RESULT 11
 AAP80668
 ID AAP80668 standard; protein; 268 AA.
 AC AAP80668;
 AC 24-OCT-1990 (first entry)
 DT Recombinant human preproapoprotein A1.
 DE human preproapoprotein A1; high density lipoprotein deficiency; ss.
 KW synthetic.
 OS Key Location/Qualifiers
 FH 1..18 /label=precursor
 FT 19..25 /label=protein
 FT 26..268 /label-mature apoprotein A1

EP293357-A.
 PD 30-NOV-1988.
 PD 24-MAY-1988; 88EP-0870095.
 PF 28-MAY-1987; 87GB-0012540.
 PR (UNTO) UCB SA.
 XX Bolten A, Gobert J, Wulfert E;
 PI WPI; 1988-339891/48.
 DR N-PSDB; AAN81258.
 XX New DNA encoding human preproapoprotein A1 - modified to eliminate hairpin structures

XX Claim 1; Page 12; 25pp; French.

XX Met at posn 19 is inserted as an extra amino acid c.f. wild-type protein.
 CC The DNA fragment used to replace the wild-type sequence encoding amino acids -6 to +14 (= Arg 20 to Leu 39) modifies codons corresponding to wild-type amino acids -6, -1, 1, 3, 4, 5, 6, 7, 10, 11 and 14. The changed codons still encode the same amino acids as in the wild-type protein but reduce formation of secondary structures in mRNA.
 CC See also AAN82064.

XX Sequence 268 AA;

Query Match 100.0%; Score 468; DB 9; Length 268;
 Best Local Similarity 100.0%; Pred. NO. 7.3e-43;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DEPPQSPWDRVKDLATYVVDVYKDSGRDYSQPEGSALGKOLNKLIDNMDSVTSFSKL 60
 |||||||
 Db 26 deppqspwdrvkdlatvyvdvdkdsgrdyvsgfegsalgkqlkildnmdsvtsfsl 85
 |||||||

QY 61 REQLGPTVTOEFWDLNLEKETEGRLROEMSKD 89
 |||||
 Db 86 reqlgpvtgelfwlnleketeglrqemskd 114

RESULT 12

AAU33170
 ID AAU33170 standard; Protein; 299 AA.
 XX
 AC AAU33170;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #3661.

KW Human; Vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-611725/70.

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -

XX Claim 20; Page 718; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemia. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.

XX Sequence 299 AA;

Query Match 100.0%; Score 468; DB 22; Length 299;
 Best Local Similarity 100.0%; Pred. No. 8.4e-43;

Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPOSPMDRYKDLATYVVDVLDKSDGRDYVSQFEGSALGKQLNKLDMNDVSTSTFSL 60
 |||||

Db 57 deppgspwdrwmdlatayvvdvldksgdyvsqfegsalyqnlklmdwsvstfsl 116
 |||||

QY 61 REQLGPTVTOEFWDLNLEKETEGRLROEMSKD 89
 |||||

Db 117 reqlgpvtgelfwlnleketeglrqemskd 145
 |||||

RESULT 13

AAO12095
 ID AAO12095 standard; Protein; 154 AA.

XX
 AC AAO12095;

XX 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 25987.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

OS

PN WO200164835-A2.

PD 07-SEP-2001.

PF 26-FEB-2001; 2001WO-US04927.

PR 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-514838/56.

DR N-PSDB; AA192026.

PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

XX Claim 20; SEQ ID NO 25987; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 154 AA;

Query Match 88.7%; Score 415; DB 22; Length 154;
 Best Local Similarity 88.8%; Pred. No. 2.1e-37;

Matches 79; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 DEPOSPMDRYKDLATYVVDVLDKSDGRDYVSQFEGSALGKQLNKLDMNDVSTSTFSL 60
 |||||

Db 33 deppgspwdrwmdlatayvvdvldksgdyvsqfegsalyqnlklmdwsvstfsl 92
 |||||

QY 61 REQLGPTVTOEFWDLNLEKETEGRLROEMSKD 89
 |||||

Db 93 reqlgpvtgelfwlnleketeglrqemskd 121
 |||||

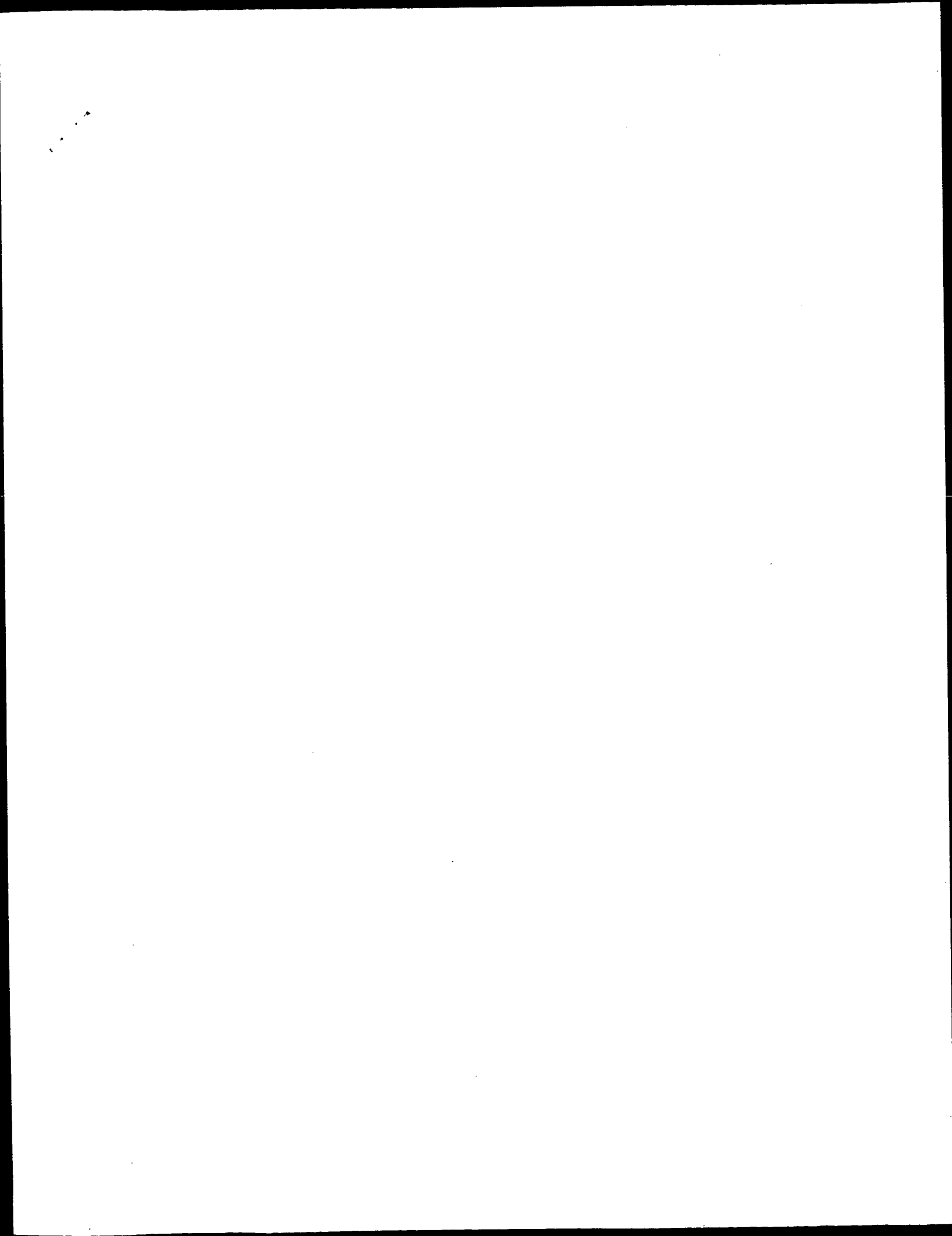
RESULT 14

AA002278
ID AA002278 standard; Protein; 151 AA.
XX
AC AA002278;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 16170.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-514838/56.
DR N-PSDB: AA182209.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 16170; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoietic regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 151 AA:
XX
Query Match 72.2%; Score 338; DB 22; Length 151;
Best Local Similarity 95.6%; Pred. No. 5e-29;
Matches 65; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 22 LKDSGRDYVSQFESGALGKQLNLKLLDNDWDSVTSTFSLRQLRGVYQFNDNEKEEG 81
DB 1 LKdsgrdyvsqfegcalsglnklldndwdsstfslrqlrgvptqetfwnlekdeg 60
QY 82 LRQEMSKD 89
DB 61 LRqemskd 68

RESULT 15
AAU30267
ID AAU30267 standard; Protein; 120 AA.
XX

AC AAU30267;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #758.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US08656.
XX
PR 18-APR-2000; 2000US-0552929.
PR 26-JAN-2001; 2001US-0770160.
XX
PA (HYSE-) HYSEQ INC.
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -
XX
PS Claim 20; Page 270; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX
SQ Sequence 120 AA:
XX
Query Match 68.9%; Score 322.5; DB 22; Length 120;
Best Local Similarity 73.0%; Pred. No. 1.8e-27;
Matches 65; Conservative 1; Mismatches 0; Indels 23; Gaps 1;
QY 1 DEPPQSPMDRVRKRLAIVYVDVNLKDSGRDYVSQFESGALGKQLNLKLLDNDWDSVTSTFSLR 60
DB 25 deppspmdrvrkrlaivyvdvnlkdsgk-----dsvtstfslr 61
QY 61 REQLGPTQGFMDNLEKETEGSLRQEMSKD 89
DB 62 reqlgptqgfmdnleketegslrqemskd 90

Search completed: September 22, 2002, 12:05:16
Job time: 291 sec



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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:02:52 : Search time 51.49 Seconds
(without alignments)
42.219 Million cell updates/sec

Title: US-09-803-918A-2_COPY_25_113

Perfect score: 468
Sequence: 1 DEPPQSPMDRVKDLATVYVD.....EFWDNLEKETEGLEGQEMSKD 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued_Patents_AA:*

1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
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4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	468	100.0	264	1	US-08-448-606-6
2	468	100.0	267	1	US-07-959-946-3
3	468	100.0	267	1	US-08-333-577-3
4	468	100.0	267	4	US-08-952-796-2
5	468	100.0	267	5	PCT-US92-08634-3
6	241	51.5	200	4	US-08-952-796-15
7	66.5	14.2	105	1	US-08-241-853-11
8	66.5	14.2	105	2	US-08-850-917-11
9	66.5	14.2	180	4	US-09-153-586-24
10	66.5	14.2	317	4	US-08-949-155-6
11	65	13.9	200	2	US-08-698-805-6
12	63.5	13.6	174	2	US-08-768-964-13
13	63.5	13.6	174	3	US-09-005-299-13
14	63.5	13.6	174	4	US-09-515-431-13
15	63.5	13.6	199	4	US-08-768-964-12
16	63.5	13.6	199	3	US-09-005-299-12
17	63.5	13.6	199	4	US-09-515-431-12
18	63.5	13.6	238	2	US-08-768-964-7
19	63.5	13.6	238	3	US-09-005-299-7
20	63.5	13.6	238	4	US-09-515-431-7
21	63.5	13.6	263	2	US-08-768-964-2
22	63.5	13.6	263	3	US-09-005-299-2
23	63.5	13.6	263	4	US-09-515-431-2
24	63	13.5	348	1	US-08-229-781-50
25	63	13.5	348	1	US-08-630-918-50
26	63	13.5	348	4	US-09-004-422-50
27	63	13.5	491	2	US-08-687-916-23

28	63	13.5	491	4	US-09-138-614-23	Sequence 23, Appl
29	63	13.5	495	2	US-08-687-916-22	Sequence 22, Appl
30	63	13.5	495	3	US-09-138-614-22	Sequence 22, Appl
31	62.5	13.4	649	3	US-08-996-441B-109	Sequence 109, App
32	62.5	13.4	649	3	US-08-993-722A-109	Sequence 109, App
33	62.5	13.4	649	3	US-08-993-170A-109	Sequence 109, App
34	62.5	13.4	649	3	US-08-993-775B-109	Sequence 109, App
35	62	13.2	796	4	US-08-961-083-56	Sequence 56, Appl
36	61.5	13.1	98	2	US-08-479-078-7	Sequence 7, Appl
37	61.5	13.1	505	4	US-08-426-509A-17	Sequence 17, Appl
38	61.5	13.1	505	5	PCT-US95-05008-17	Sequence 17, Appl
39	60	12.8	620	4	US-09-269-731-6	Sequence 6, Appl
40	60	12.8	729	1	US-08-070-165F-6	Sequence 6, Appl
41	60	12.8	729	2	US-08-885-418-6	Sequence 6, Appl
42	60	12.8	731	1	US-08-070-165F-10	Sequence 10, Appl
43	60	12.8	731	2	US-08-885-418-10	Sequence 10, Appl
44	59.5	12.7	372	3	US-08-918-249-2	Sequence 2, Appl
45	59.5	12.7	372	3	US-08-918-249-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-448-606-6
; Sequence 6, Application US/08448606
; Patent No. 5721114
; GENERAL INFORMATION:
; APPLICANT: Adrahams n, Lars
; APPLICANT: Holmgren, Erik
; APPLICANT: Kalder n, Christina
; APPLICANT: Lake, Mats
; APPLICANT: Mikaelsson, sa
; APPLICANT: Sejlitz, torsten
; TITLE OF INVENTION: Expression System For Producing
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pollock, Vande Sande & Priddy
; STREET: 1990 M Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,606
; FILING DATE: 25-AUG-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SE93/01061
; FILING DATE: 09-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9203753-0
; FILING DATE: 11-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Amerinick, Burton A.
; REGISTRATION NUMBER: 24,852
; REFERENCE/DOCKET NUMBER: 0151/00121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)331-7111
; TELEFAX: (202)293-6229
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-448-606-6

Query Match 100.0%; Score 468; DB 1; Length 264;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPSPMDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDVSTSFESKL 60
|||||
DB 22 DEPPSPMDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDVSTSFESKL 81

QY 61 REOLGPVTOEFMDLKEKETEGLRQEMSKD 89
|||||
DB 82 REOLGPVTOEFMDLKEKETEGLRQEMSKD 110

RESULT 2

US-07-959-946-3
; Sequence 3, Application US/07959946
; Patent No. 5408038
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Wiltum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Suther &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 No. 5408038th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959, 946
; FILING DATE: 19921008
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,706
; FILING DATE: 18-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamsen, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-959-946-3

Query Match 100.0%; Score 468; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPSPMDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDVSTSFESKL 60
|||||
DB 25 DEPPSPMDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDVSTSFESKL 84

QY 61 REOLGPVTOEFMDLKEKETEGLRQEMSKD 89

DB 85 REOLGPVTOEFMDLKEKETEGLRQEMSKD 113
|||||

RESULT 3

US-08-333-577-3
; Sequence 3, Application US/08333577
; Patent No. 5786206
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Wiltum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Suther &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 No. 5786206th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,577
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamsen, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: SCRF 234.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-333-577-3

Query Match 100.0%; Score 468; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPSPMDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDVSTSFESKL 60
|||||
DB 25 DEPPSPMDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKQLNLKLLDNWDVSTSFESKL 84

QY 61 REOLGPVTOEFMDLKEKETEGLRQEMSKD 89
|||||
DB 85 REOLGPVTOEFMDLKEKETEGLRQEMSKD 113

RESULT 4

US-08-952-796-2
; Sequence 2, Application US/08952796
; Patent No. 6238596
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: BRUCKERT, Eric
; APPLICANT: DENEPIE, Patrice
; APPLICANT: DUBERGER, Nicolas
; APPLICANT: FRUCHART, Jean-Charles

APPLICANT: LUC, Gerald
APPLICANT: TURPIN, Gerard
APPLICANT: ASSMANN, Gerd
APPLICANT: FUNKE, Harald
TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPROTEIN A-I
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3c43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,796
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/06061
FILING DATE: 22-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/00747
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fehlner Esq., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: ST95031-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-952-796-2

Query Match 100.0%; Score 468; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPSPMDRVKDLATVYVDVLDKSGRDYVSQFEGSALGKQLNLKLDNMDSVTSFSKL 60
DB 25 DEPPSPMDRVKDLATVYVDVLDKSGRDYVSQFEGSALGKQLNLKLDNMDSVTSFSKL 84
QY 61 REQLGPGVTQEFWDNLEKETEGGLRQEMSKD 89
DB 85 REQLGPGVTQEFWDNLEKETEGGLRQEMSKD 113

RESULT 5
PCT-US92-08634-3
Sequence 3, Application PC/TUS9208634
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Wiltzium, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutter &
ADDRESS: Milnamov, Ltd.
STREET: 180 North Stetson, Suite 4700

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08634
FILING DATE: 19921009
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5400
TELEFAX: (312) 616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-08634-3

Query Match 100.0%; Score 468; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEPPSPMDRVKDLATVYVDVLDKSGRDYVSQFEGSALGKQLNLKLDNMDSVTSFSKL 60
DB 25 DEPPSPMDRVKDLATVYVDVLDKSGRDYVSQFEGSALGKQLNLKLDNMDSVTSFSKL 84
QY 61 REQLGPGVTQEFWDNLEKETEGGLRQEMSKD 89
DB 85 REQLGPGVTQEFWDNLEKETEGGLRQEMSKD 113

RESULT 6
US-08-952-796-15
Sequence 15, Application US/08952796
Patent No. 6258596
GENERAL INFORMATION:
APPLICANT: BENNETT, Patrick
APPLICANT: BRUCKERT, Eric
APPLICANT: DENEFLE, Patrice
APPLICANT: DOBERGER, Nicolas
APPLICANT: FRUCHART, Jean-Charles
APPLICANT: LUC, Gerald
APPLICANT: TURPIN, Gerard
APPLICANT: ASSMANN, Gerd
APPLICANT: FUNKE, Harald
TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPROTEIN A-I
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3c43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952.796
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/06061
FILING DATE: 22-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/00747
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fehner Esq., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: ST95031-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-952-796-15

```

```

Query Match      51.5%; Score 241; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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OY 44 LKLDNDVSTSTFSKRLRDLGPTQEFWNLKKEFEGLRQESKD 89
Db 1 LKLDNDVSTSTFSKRLRDLGPTQEFWNLKKEFEGLRQESKD 46

```

```

RESULT 7
US-08-241-853-11
Sequence 11, Application US/08241853
Patent No. 5693488
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
APPLICANT: Hanafusa, Hidesaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241.853
FILING DATE: 12-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid

```

```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-241-853-11

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```

Query Match      14.2%; Score 66.5; DB 1; Length 105;
Best Local Similarity 27.7%; Pred. No. 1.3;
Matches 26; Conservative 11; Mismatches 28; Indels 29; Gaps 4;

```

```

OY 8 WDRYKDLATVYVDVLKD-----SGRDYVSQFEGS--ALGK 40
Db 12 WQKLDLAFCKKNLQDAENFQFGADDLKAWLQDAHRLISED-VGQDEGATRALGK 70
OY 41 QLNKLDNDVSTSTFSKRLRDLGPTQEFWNL 74
Db 71 K-HKDFLELESRGVMEKLEQQAQGFPEFRDS 103

```

```

RESULT 8
US-08-850-917-11
Sequence 11, Application US/08850917
Patent No. 5854045
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
APPLICANT: Hanafusa, Hidesaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850.917
FILING DATE: 02-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241.853
FILING DATE: 12-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-850-917-11

```

```

Query Match      14.2%; Score 66.5; DB 2; Length 105;
Best Local Similarity 27.7%; Pred. No. 1.3;
Matches 26; Conservative 11; Mismatches 28; Indels 29; Gaps 4;

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[illegible]

RESULT 10
US-08-949-155-6
Sequence 6, Application US/08949155
Patent No. 6271436
GENERAL INFORMATION:
APPLICANT: Piedrahita, Jorge A
APPLICANT: Bazer, Fuller W
TITLE OF INVENTION: Composition and Methods for the
TITLE OF INVENTION: Generation of Transgenic Animal Species
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE AND DURKEE
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,155
FILING DATE: Concurrently Herewith
CLASSIFICATION: 800

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/027,338
 FILING DATE: 11-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/046,094
 FILING DATE: 09-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hbldler, David W.
 REGISTRATION NUMBER: 41,071
 REFERENCE/DOCKET NUMBER: TAMK:177
 TELECOMMUNICATIONS INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (713) 789-2679
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 317 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-949-153-6

```

Query Match      14.2% Score 66.5; DB 4; Length 317;
Best Local Similarity 21.7% Pred. No. 5.6'
Matches 20; Conservative 19; Mismatches 50; Indels 3; Gaps 1

QY      1 DEPP---QSMDDVKRLATVYDVYDKDSRDVYSQFESGALGKLNKLNDNDVSYTSF 57
      :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      33 EEPKMGSSQPMDEALGRFMDILRWYQSLSDVOYDELLSTKVTQELTELIEESKVEKAYR 92
      :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY      58 SKLRDELGPVYQGFNMNLEKETEGTLRQESKSD 89
      :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      93 EELPAGLGFPVYQETQARLSKELDQAQARAGAD 124
      :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

RESULT 11
US-08-698-805-6
; Sequence 6, Application US/08698805
; Patent No. 3869288
; GENERAL INFORMATION:
; APPLICANT: Chapman, Martin
; APPLICANT: Arruda, L. Karla
; TITLE OF INVENTION: Molecular Cloning of Cockroach
; TITLE OF INVENTION: Allergens, Amino Acid and Nucleotide Sequences Therefore
; TITLE OF INVENTION: and Recombinant Expression Thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, Spivak, Mclelland, Maier & Neustadt,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/698,805
; FILING DATE: 16-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,510
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelber, Steven B.
; REGISTRATION NUMBER: 30,073
; REFERENCE/DOCKET NUMBER: 494-203-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 200 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-698-805-6

Query Match 13.9%; Score 65; DB 2; Length 200;
 Best Local Similarity 28.6%; Pred. No. 4.6;
 Matches 24; Conservative 8; Mismatches 26; Indels 26; Gaps 4;

QY 22 LKSS---GRDYVSQFEGSA-----LGRQLNKLIDNW-----DSVTSFSKLRQ 63
 DB 39 LKSSMFGKTPVLEIDKQTHSVASRLRGQFGLSGKDWENLEIDMIVDTISDFRAA 98

QY 64 LGPV-----TQEFWNLKET 79
 DB 99 IANYHYDADENSKKKMDPLKKT 122

RESULT 12
 US-08-768-964-13
 ; Sequence 13, Application US/08768964
 ; Patent No. 5958880
 ; GENERAL INFORMATION:
 ; APPLICANT: Frank, Glenn R.
 ; APPLICANT: Porter James P.
 ; APPLICANT: Rushlow, Keith E.
 ; APPLICANT: Wassom, Donald L.
 ; APPLICANT: Weber, Eric R.
 ; TITLE OF INVENTION: No. 5958880el Feline Fc Epsilon Receptor Alpha
 ; TITLE OF INVENTION: Chain Nucleic Acid Molecules, Proteins
 ; TITLE OF INVENTION: and Uses Thereof
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.
 ; ADDRESS: Heska Corporation
 ; STREET: 1825 Sharp Point Drive
 ; CITY: Fort Collins
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80525
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: Wordperfect for Windows, Version 7.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/768,964
 ; FILING DATE: December 19, 1996
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Verser, Carol Talkington
 ; REGISTRATION NUMBER: 37,459
 ; REFERENCE/DOCKET NUMBER: DI-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 970/493-7272
 ; TELEFAX: 970/493-7272
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 174 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-768-964-13

Query Match 13.6%; Score 63.5; DB 2; Length 174;
 Best Local Similarity 36.6%; Pred. No. 5.7;
 Matches 15; Conservative 10; Mismatches 11; Indels 5; Gaps 2;

QY 14 LATVYVDYLK----DSGRDYVSQFEGSALGKOLNKLIDNW 50
 DB 49 VTTLTLDIVYKAQIRDSG-EYTCQNKSGMLSKPVSLKVPREW 88

RESULT 13
 US-09-005-299-13
 ; Sequence 13, Application US/09005299
 ; Patent No. 6103494

; GENERAL INFORMATION:
 ; APPLICANT: Frank, Glenn R.
 ; APPLICANT: Porter James P.
 ; APPLICANT: Rushlow, Keith E.
 ; APPLICANT: Wassom, Donald L.
 ; APPLICANT: Weber, Eric R.
 ; TITLE OF INVENTION: No. 6103494el Feline Fc Epsilon Receptor Alpha
 ; TITLE OF INVENTION: Chain Nucleic Acid Molecules, Proteins
 ; TITLE OF INVENTION: and Uses Thereof
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.
 ; ADDRESS: Heska Corporation
 ; STREET: 1825 Sharp Point Drive
 ; CITY: Fort Collins
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80525

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: Wordperfect for Windows, Version 7.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/005,299
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/768,964
 ; FILING DATE: December 19, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Verser, Carol Talkington
 ; REGISTRATION NUMBER: 37,459
 ; REFERENCE/DOCKET NUMBER: DI-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 970/493-7272
 ; TELEFAX: 970/493-7333
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 174 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-005-299-13

Query Match 13.6%; Score 63.5; DB 3; Length 174;
 Best Local Similarity 36.6%; Pred. No. 5.7;
 Matches 15; Conservative 10; Mismatches 11; Indels 5; Gaps 2;

QY 14 LATVYVDYLK----DSGRDYVSQFEGSALGKOLNKLIDNW 50
 DB 49 VTTLTLDIVYKAQIRDSG-EYTCQNKSGMLSKPVSLKVPREW 88

RESULT 14
 US-09-515-431-13
 ; Sequence 13, Application US/09515431
 ; Patent No. 6284881
 ; GENERAL INFORMATION:
 ; APPLICANT: Frank, Glenn R.
 ; APPLICANT: Porter James P.
 ; APPLICANT: Rushlow, Keith E.
 ; APPLICANT: Wassom, Donald L.


```

1  APPLICANT:  Weber, Eric R.
2  TITLE OF INVENTION:  No. 6284881el Feline Fc Epsilon Receptor Alpha
3  TITLE OF INVENTION:  Chain Nucleic Acid Molecules, Proteins
4  TITLE OF INVENTION:  and Uses Thereof
5  NUMBER OF SEQUENCES:  16
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE:  Carol Talkington Verser, Ph.D.
8  ADDRESS:  Heeka Corporation
9  STREET:  1825 Sharp Point Drive
10  CITY:  Fort Collins
11  STATE:  Colorado
12  COUNTRY:  USA
13  ZIP:  80525
14  COMPUTER READABLE FORM:
15  MEDIUM TYPE:  Floppy disk
16  COMPUTER:  IBM PC compatible
17  OPERATING SYSTEM:  Windows 95
18  SOFTWARE:  Wordperfect for Windows, Version 7.0
19  CURRENT APPLICATION DATA:
20  APPLICATION NUMBER:  US/09/515.431
21  FILING DATE:
22  CLASSIFICATION:
23  PRIOR APPLICATION DATA:
24  APPLICATION NUMBER:  08/768,964
25  FILING DATE:
26  ATTORNEY/AGENT INFORMATION:
27  NAME:  Verser, Carol Talkington
28  REGISTRATION NUMBER:  37,459
29  REFERENCE/DOCKET NUMBER:  DI-2
30  TELECOMMUNICATION INFORMATION:
31  TELEPHONE:  970/493-7272
32  TELEFAX:  970/493-7333
33  INFORMATION FOR SEQ ID NO:  13:
34  SEQUENCE CHARACTERISTICS:
35  LENGTH:  174 amino acids
36  TYPE:  amino acid
37  TOPOLOGY:  linear
38  MOLECULE TYPE:  protein
39  US-09-515-431-13

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? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
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? SOFTWARE: WordPerfect for Windows, Version 7.0.
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/768,964
? FILING DATE: December 19, 1996
? CLASSIFICATION: 530
? ATTORNEY/AGENT INFORMATION:
? NAME: Verser, Carol Talkington
? REGISTRATION NUMBER: 37,459
? REFERENCE/DOCKET NUMBER: DI-2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 970/493-7272
? TELEFAX: 970/493-7333
? INFORMATION FOR SEQ ID NO: 12:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 199 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
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? US-08-768-964-12

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				Indels 5;
				Gaps 2.
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Search completed: September 22, 2002, 12:02:53
Job time: 253 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:19:45 : Search time 17.64 Seconds
(without alignments)
1454.413 Million cell updates/sec

Title: US-09-803-918a-2

Perfect score: 267

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

PIR_71:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	267	100.0	267	1	LPHUA1
2	69	25.8	267	1	apolipoprotein A-I
3	69	25.8	267	1	apolipoprotein A-I
4	25	9.4	241	2	JS0079
5	22	8.2	265	1	apolipoprotein A-I
6	22	8.2	266	1	LPRB1B
7	22	8.2	266	1	LPRB1Z
8	22	8.2	266	1	apolipoprotein A-I
9	21	7.9	264	2	S31394
10	21	7.9	265	2	apolipoprotein A-I
11	21	7.9	265	2	apolipoprotein A-I
12	21	7.9	265	2	apolipoprotein A-I
13	20	7.5	231	2	UT0672
14	19	7.1	231	2	UT0704
15	19	7.1	231	2	UT0704
16	19	7.1	231	2	UT0704
17	19	7.1	231	2	UT0704
18	19	7.1	231	2	UT0704
19	19	7.1	231	2	UT0704
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ALIGNMENTS

30	7	2.6	67	2	T05224	hypothetical prote
31	7	2.6	101	2	H87207	probable membrane
32	7	2.6	116	2	E71566	probable S16 ribos
33	7	2.6	132	2	C66709	hypothetical prote
34	7	2.6	139	2	G72710	hypothetical prote
35	7	2.6	150	2	T33928	hypothetical prote
36	7	2.6	150	2	E86711	hypothetical prote
37	7	2.6	155	2	AB0918	conserved hypotet
38	7	2.6	161	2	F91222	hypothetical prote
39	7	2.6	161	2	S30747	hypothetical prote
40	7	2.6	161	2	D86069	hypothetical prote
41	7	2.6	199	2	H95871	conserved hypotet
42	7	2.6	205	2	H84357	hypothetical prote
43	7	2.6	216	2	T37221	hypothetical prote
44	7	2.6	218	2	E85021	hypothetical prote
45	7	2.6	219	2	G65089	probable transcript
46	7	2.6	219	2	C91117	probable 2-compone
47	7	2.6	219	2	C85962	probable two-compo
48	7	2.6	219	2	A10888	hypothetical prote
49	7	2.6	219	2	F65018	hypothetical prote
50	7	2.6	219	2	F91042	hypothetical prote
51	7	2.6	219	2	A85887	hypothetical prote
52	7	2.6	219	2	AE0813	ethanolamine utili
53	7	2.6	228	2	F87670	Surf1 family prote
54	7	2.6	231	2	F95267	hypothetical prote
55	7	2.6	244	2	AC3341	precursorin-2 C20-me
56	7	2.6	250	1	A44039	chitinase (EC 3.2
57	7	2.6	265	2	T46013	hypothetical prote
58	7	2.6	265	2	H83008	N-formylglutamate
59	7	2.6	267	2	T37047	probable nitrate r
60	7	2.6	269	2	C90450	signal recognition
61	7	2.6	273	2	S21731	hypothetical prote
62	7	2.6	291	2	AC0907	probable kinase (I
63	7	2.6	296	2	A95408	hypothetical prote
64	7	2.6	301	2	B98211	amidophosphoribosy
65	7	2.6	301	2	AG3075	amidophosphoribosy
66	7	2.6	314	2	E32307	DNA-directed RNA p
67	7	2.6	316	2	D71375	probable ABC trans
68	7	2.6	322	2	G97396	cysteine synthase
69	7	2.6	322	2	AH2614	cysteine synthase
70	7	2.6	330	2	D64526	hypothetical prote
71	7	2.6	330	2	JC5935	exostosin-related p
72	7	2.6	335	2	T29462	hypothetical prote
73	7	2.6	339	2	E82211	conserved hypotet
74	7	2.6	339	2	E97345	oligopeptide ABC t
75	7	2.6	350	2	G01950	hypothetical prote

RESULT 1
LPHUA1
apolipoprotein A-I precursor (validated) - human
N:Alternate names: apoa-I-2; apoa-I-4; preproapoa-I; prostacyclin stabilizing factor
C:Species: Homo sapiens (man)
C:Date: 14-Nov-1983 #sequence, revision 14-Nov-1983 #text, change 08-Dec-2000
C:Accession: A90947; B90947; S02373; A93465; A21147; A93519; B93519; A93472; A94010; 6197
R:Seilhauer, J.J.; Protter, A.A.; Frossard, P.; Levy-Wilson, B.
DNA 3, 309-317, 1984
A:Title: Isolation and DNA sequence of full-length cDNA and of the entire gene for hu
A:Reference number: A90947; MUID:85026655
A:Accession: A90947
A:Molecule type: DNA
A:Residues: 1-267 <SEI>
A:Cross-references: GB:X01038; NID:928769; PIDN:CAA25519.1; PID:9296635
A:Accession: B90947
A:Molecule type: mRNA
A:Residues: 1-267 <SE2>
A:Cross-references: GB:X01038; NID:928769; PIDN:CAA25519.1; PID:9296635
R:Makrides, S.C.; Ruiz-Opazo, N.; Heyden, M.; Nussbaum, A.L.; Breglow, J.L.; Zannis,
Eur. J. Biochem. 173, 465-471, 1988

- A:Title: Sequence and expression of Tangler apoA-I gene.
A:Reference number: S02373; MUID:88196137
A:Accession: S02373
A:Molecule type: DNA
A:Residues: 1-267 <MAX>
A:Cross-references: EMBL:X07496; NID:q28774; PIDN:CAA0377.1; PID:q296729
R:Shoulders, C.C.; Kornblith, A.R.; Munro, B.S.; Baralle, F.E.
Nucleic Acids Res. 11, 2827-2837, 1983
A:Title: Gene structure of human apolipoprotein AI.
A:Reference number: A93465; MUID:83220622
A:Accession: A93465
A:Molecule type: DNA
A:Residues: 1-267 <SHO>
A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GB:K01519; GB:K01520
R:Karthanas, S.K.; Zannis, V.I.; Breslow, J.L.
Proc. Natl. Acad. Sci. U.S.A. 80, 6147-6151, 1983
A:Title: Isolation and characterization of the human apolipoprotein A-I gene.
A:Reference number: A21147; MUID:84016011
A:Accession: A21147
A:Molecule type: DNA
A:Residues: 1-267 <KAR>
A:Cross-references: GB:J00098; GB:J03222; NID:q178765; PIDN:AB59514.1; PID:q178768
R:Shaper, C.R.; Sidoti, A.; Shelley, C.S.; Lucero, M.A.; Shoulders, C.C.; Baralle, F.E.
Nucleic Acids Res. 12, 3917-3932, 1984
A:Title: Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA abundance.
A:Reference number: A93519; MUID:84221405
A:Accession: A93519
A:Molecule type: mRNA
A:Residues: 1-267 <SHA>
A:Cross-references: GB:X00566; NID:q28765; PIDN:CAA5232.1; PID:q732753
A:Accession: B93519
A:Molecule type: DNA
A:Residues: 1-24 <SH2>
R:Cheung, P.; Chan, L.
Nucleic Acids Res. 11, 3703-3715, 1983
A:Title: Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.
A:Reference number: A93472; MUID:83220772
A:Accession: A93472
A:Molecule type: mRNA
A:Residues: 1-267 <CHE>
A:Cross-references: GB:J00098; GB:J00099; GB:J00100; GB:J00101; GB:J03222; GB:K01518; GB:K01519; GB:K01520
R:Law, S.W.; Brewer Jr., H.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 66-70, 1984
A:Title: Nucleotide sequence and the encoded amino acids of human apolipoprotein A-I mRNA
A:Reference number: A94010; MUID:84119464
A:Accession: A94010
A:Molecule type: mRNA
A:Residues: 1-267 <LAM>
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R:Zannis, V.I.; Karathanasis, S.K.; Keutmann, H.T.; Goldberger, G.; Breslow, J.L.
Proc. Natl. Acad. Sci. U.S.A. 80, 2574-2578, 1983
A:Title: Intracellular and extracellular processing of human apolipoprotein A-I: secreted
A:Reference number: A21118; MUID:83195100
A:Accession: A21118
A:Molecule type: mRNA
A:Residues: 1-24 <ZAN>
R:Brewer Jr., H.B.; Fairwell, T.; Kay, L.; Meng, M.; Roman, R.; Law, S.; Light, J.A.
Biochem. Biophys. Res. Commun. 113, 626-632, 1983
A:Title: Human plasma proapoA-I: isolation and amino-terminal sequence.
A:Reference number: A90112; MUID:83256553
A:Accession: A90112
A:Molecule type: protein
A:Residues: 19-27 <BRE>
R:Brewer Jr., H.B.; Fairwell, T.; LaRue, A.; Roman, R.; Houser, A.; Bronzert, T.J.
Biochem. Biophys. Res. Commun. 80, 623-630, 1978
A:Title: The amino acid sequence of human APOA-I, an apolipoprotein isolated from high density lipoproteins
A:Reference number: A90209; MUID:78123731
A:Accession: A90209
A:Molecule type: protein
A:Residues: 25-57, 'Q', '59-169', 'OO', '172-267' <BR2>
R:Yui, Y.; Aoyama, T.; Morishita, H.; Takahashi, M.; Takatsu, Y.; Kawai, C.
J. Clin. Invest. 82, 803-807, 1988
A:Title: Serum prostacyclin stabilizing factor is identical to apolipoprotein A-I (Apo A-I)
- A:Reference number: A30516; MUID:8831387
A:Accession: A30516
A:Molecule type: protein
A:Residues: 25-56 <YUI>
R:Nichols, W.C.; Dwyer, F.E.; Ljepnick, J.; Benson, M.D.
Biochem. Biophys. Res. Commun. 156, 762-768, 1988
A:Title: Variant apolipoprotein AI as a major constituent of a human hereditary amyloid
A:Reference number: A31582; MUID:89050104
A:Accession: A31582
A:Molecule type: protein
A:Residues: 25-49, 'R', '51-85', 'D', '87-107' <NIC>
R:Manjunath, P.; Marcel, Y.L.; Ueda, J.; Seidah, N.G.; Chretien, M.; Chapdelaine, A.
J. Biol. Chem. 264, 16853-16857, 1989
A:Title: Apolipoprotein A-I binds to a family of bovine seminal plasma proteins.
A:Reference number: A34409; MUID:89380318
A:Accession: A34409
A:Molecule type: protein
A:Residues: 25-48 <MAN>
R:Stoffel, W.; Binczek, E.
Biol. Chem. Hoppe-Seyler 369, 1055-1063, 1988
A:Title: Structural requirements of human preproapolipoprotein AI for translocation a
A:Reference number: S02737; MUID:89149957
A:Accession: S02737
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-6, 'AV', '9', 'LV', '12-29' <STO>
R:Stoffel, W.; Binczek, E.
Biol. Chem. Hoppe-Seyler 372, 481-488, 1991
A:Title: Transient expression of wild type and mutant human apolipoprotein AI in COS
A:Reference number: S16197; MUID:92029676
A:Contents: annotation; extension of studies in reference S02737
R:Stoffel, W.; Kruger, E.; Deutzmann, R.
Hoppe-Seyler's Z. Physiol. Chem. 364, 227-237, 1983
A:Title: Cell-free translation of human liver apolipoprotein AI and AII mRNA processes
A:Reference number: A19913; MUID:8326195
A:Accession: B19913
A:Molecule type: protein
A:Residues: 1-6, 'X', '8-13', 'XXX', '17-18', 'XX', '21', 'X', '23-25', 'X', '27-29' <ST2>
R:Einhorn, C.; Bozas, S.E.; Tenkhan, H.; Kirsbaum, L.; Metso, J.; Murphy, B.; Walke
Biochim. Biophys. Acta 1086, 255-260, 1991
A:Title: The apolipoprotein A-I binding protein of placenta and the SP-40,40 protein
A:Reference number: A56815; MUID:92075698
A:Accession: A56815
A:Molecule type: protein
A:Residues: 25-31, 'P', '33' <EBN>
A:Experimental source: serum
A>Note: Sequence extracted from NCBI backbone (NCBIP:69759)
A>Note: 32-TIP was also found
R:Knittke, S.T.; Catill, C.T.; Lau, K.; Potter, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
A:Title: Identification of proteins associated with apolipoprotein A-I-containing lip
A:Reference number: A54223; MUID:94162201
A:Accession: A54223
A:Molecule type: protein
A:Residues: 25-39 <KUN>
R:Mogulievsky, N.; Roobol, C.; Loriau, R.; Guillaume, J.P.; Jacobs, P.; Cravador, A.;
DNA 8, 429-436, 1989
A:Title: Production of human recombinant proapolipoprotein A-I in Escherichia coli: p
A:Reference number: I39476; MUID:89377481
A:Accession: I39476
A:Molecule type: mRNA
A:Residues: 19-267 <RES>
A:Cross-references: GB:M29068; NID:q178774; PIDN:AAA51747.1; PID:q178775
R:Higuchi, K.; Law, S.W.; Hoeg, J.M.; Schumacher, U.K.; Meglin, N.; Brewer, H.B.
J. Biol. Chem. 263, 18530-18536, 1988
A:Title: Tissue-specific expression of apolipoprotein A-I (apoA-I) is regulated by th
A:Reference number: I39475; MUID:89054040
A:Accession: I39475
A:Molecule type: DNA
A:Residues: 1-14 <RED>
A:Cross-references: GB:J04066; NID:q178763; PIDN:AAA51746.1; PID:q553183

R:Breslow, J.L.
 Annu. Rev. Biochem. 54, 699-727, 1985
 A:Title: Human apolipoprotein molecular biology and genetic variation.
 A:Reference number: A90042; MUID:85278004
 A:Contents: annotation; review of sequences, variants and gene location
 R:Hoeg, J.M.; Meng, M.S.; Ronan, R.; Fairwell, T.; Brewer Jr., H.B.
 J. Biol. Chem. 261, 3911-3914, 1986
 A:Title: Human apolipoprotein A-I. Post-translational modification by fatty acid acylation
 A:Reference number: A92577; MUID:86140194
 A:Contents: annotation; acylation with palmitate
 A:Note: an undetermined serine or threonine is acylated by fatty acid; the acylating fat
 R:Law, S.W.; Brewer, H.B.
 J. Biol. Chem. 260, 12810-12814, 1985
 A:Title: Tanager disease: The complete mRNA sequence encoding for preproapo-A-I.
 A:Reference number: I55236; MUID:86008382
 A:Accession: I55236
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-143, 'D', 145-267 <RES>
 A:Cross-references: GB:M11791; NID:q178776; PIDN:AAA35545.1; PID:q178777
 C:Comment: Apolipoprotein A-I precursor is synthesized in the liver and small intestine.
 C:Genetics:
 A:Gene: GDB:APOA1
 A:Cross-references: GDB:119684; OMIM:107680
 A:Map position: 11q23.3-11q23.3
 A:Introns: 15/1; 67/2
 C:Function:
 A:Description: participates in the reverse transport of cholesterol from tissues to the
 sterol acyltransferase (LCAT); noncovalently binds and stabilizes prostacyclin (PGI-2)
 C:Superfamily: apolipoprotein A-I
 C:Keywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid binding; lipid
 F:1-18/Domain: signal sequence #status experimental <SIG>
 F:19-24/Domain: propeptide #status experimental <PRO>
 F:25-267/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 100.0%; Score 267; DB 1; Length 267;
 Best local similarity 100.0%; Pred. No. 1.2e-253;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAELYNAKATEHLSTLSEKAKPALEDLRQ 240
 OY 241 GLPLVLESEFKVSFLSALEETTKLNTQ 267
 DB 241 GLPLVLESEFKVSFLSALEETTKLNTQ 267

RESULT 2
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 A:apolipoprotein A-I precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 30-Sep-1989 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999
 C:Accession: A26529; A26627; S23135; A57766
 R:Polites, H.G.; Melchior, G.W.; Castle, C.K.; Marotli, K.R.
 Gene 49, 103-110, 1986
 A:Title: The primary structure of cynomolgus monkey apolipoprotein A-I deduced from the
 A:Reference number: A26529; MUID:87191989
 A:Accession: A26529

A:Molecule type: mRNA
 A:Residues: 1-267 <POD>
 A:Cross-references: GB:M15411; NID:9342074; PIDN:AAA36834.1; PID:9342075
 R:Herbert, P.N.; Bauseman, L.L.; Lynch, K.M.; Sartelli, A.L.; Kantor, M.A.; Nicolo
 Biochemistry 26, 1457-1463, 1987
 A:Title: Homologues of the human C and A apolipoproteins in the Macaca fascicularis (
 A:Reference number: A26627; MUID:87185451
 A:Accession: A26627
 A:Molecule type: protein
 A:Residues: 25-48 <HER>
 R:Murray, R.W.; Marotli, K.R.
 Biochim. Biophys. Acta 1131, 207-210, 1992
 A:Title: Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene and cor
 A:Reference number: S23135; MUID:92305062
 A:Accession: S23135
 A:Molecule type: DNA
 A:Residues: 1-12, 'L', 14-267 <MUR>
 A:Cross-references: GB:M83242; NID:9342070; PIDN:AAA36832.1; PID:9342071
 R:Scori-Thomas, M.; Kearns, M.W.
 J. Biol. Chem. 266, 18045-18050, 1991
 A:Title: Transcriptional regulation of the apolipoprotein A-I gene.
 A:Reference number: A57766; MUID:92011532
 A:Accession: A57766
 A:Molecule type: DNA
 A:Residues: 1-10 <RES>
 A:Cross-references: GB:M69223; NID:9342066; PIDN:AAA36831.1; PID:9553820
 C:Comment: The precursor is synthesized in the liver and small intestine. The propept
 C:Comment: ApoA-I makes up about 70% of the protein of the high density lipoproteins
 Y promoting cholesterol efflux from tissues and by acting as a cofactor for the leciti
 C:Genetics:
 A:Introns: 15/1; 67/2
 C:Superfamily: apolipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem r
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PRO>
 F:25-267/Product: apolipoprotein A-I #status predicted <MAT>

Query Match 25.8%; Score 69; DB 1; Length 267;
 Best local similarity 100.0%; Pred. No. 1.5e-59;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 SKLREOLGPTQEFWDLNLEKTEGLRQEMSKDLEEVKAKVQPYLDLFQKKQOEMELRYQ 141
 DB 82 SKLREOLGPTQEFWDLNLEKTEGLRQEMSKDLEEVKAKVQPYLDLFQKKQOEMELRYQ 141
 OY 142 KVEPLRAEL 150
 DB 142 KVEPLRAEL 150

RESULT 3
 JS0079
 A:apolipoprotein A-I precursor - baboon
 C:Species: Papio sp. (baboon)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Jun-1997
 C:Accession: JS0079
 R:Hixon, J.E.; Borenstein, S.; Cox, L.A.; Rahnwater, D.L.; Vandenberg, J.L.
 Gene 74, 483-490, 1988
 A:Title: The baboon gene for apolipoprotein A-I: characterization of a cDNA clone and
 A:Reference number: JS0079; MUID:89232739
 A:Accession: JS0079
 A:Molecule type: mRNA
 A:Residues: 1-267 <HIX>
 A:Experimental source: liver
 C:Comment: This protein is the principal protein component of high density lipoprotei
 C:Comment: This protein serves as a cofactor for lecithin cholesterol acyltransferase
 C:Comment: This protein contains a region of repeated amino acids which form amphipat
 C:Genetics:
 A:Gene: apoA1
 C:Superfamily: apolipoprotein A-I
 C:Keywords: HDL; lipid binding; lipoprotein
 F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-267/Product: apolipoprotein A-I #status predicted <LAI>
F:123-144,145-166,167-188,189-210,211-232,233-254/Region: tandem repeats

Query Match 25.8%; Score 69; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.5e-59;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 SKIRBOLGPTQEFMDLNEKETEGRLQEMSKDLEEVKAVQPYLDLDFOKKQEMELTYNQ 141
DB 82 SKIRBOLGPTQEFMDLNEKETEGRLQEMSKDLEEVKAVQPYLDLDFOKKQEMELTYNQ 141

QY 142 KVEPLRAEL 150
DB 142 KVEPLRAEL 150

RESULT 4

A24998 apolipoprotein A-I - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-1993

C:Accession: A24998

R:Yang, C.; Yang, T.; Pownall, H.J.; Gotto Jr., A.M.

Eur. J. Biochem. 160, 427-431, 1986

A:Title: The primary structure of apolipoprotein A-I from rabbit high-density lipoprotein

A:Reference number: A24998; MUID:87030294

A:Accession: A24998

A:Molecule type: protein

A:Residues: 1-241 <YAN>

C:Superfamily: apolipoprotein A-I

C:Keywords: HDL; lipid binding; lipoprotein

Query Match 9.4%; Score 25; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 EQLGPVTQEFMDLNEKETEGRLQEM 110
DB 60 EQLGPVTQEFMDLNEKETEGRLQEM 84

RESULT 5

LPRB1B apolipoprotein A-I precursor (clone pRBA-502) - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999

C:Accession: S00230; S20557

R:Pan, T.C.; Hao, Q.L.; Yamin, T.T.; Dai, P.H.; Chen, B.S.; Chen, S.L.; Kroon, P.A.; Cha

Eur. J. Biochem. 170, 99-104, 1987

A:Title: Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit apolipoprotein A-

A:Reference number: S00230; MUID:88082866

A:Accession: S00230

A:Molecule type: mRNA

A:Residues: 1-265 <PAN>

A:Cross-References: EMBL:X06658; NID:g1461; PIDN:CAA29857.1; PID:g1462

A:Note: the authors translated the codon AGC for residue 174 as Arg

A:Accession: S20557

A:Molecule type: DNA

A:Residues: 1-17, 'R', 19-44, 'T', 46-122, 'Y', 124-146, 'V', 148-265 <PAN2>

A:Cross-References: EMBL:X06659; NID:g1459; PIDN:CAA29858.1; PID:g1460

C:Comment: This protein is synthesized in the small intestine.

C:Comment: This protein is a major component of the high density lipoproteins in plasma.

C:Genetics:

A:Introns: 15/1; 66/2

C:Superfamily: apolipoprotein A-I

C:Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem repe

F:1-18/Domain: signal sequence #status predicted <Sig>

F:19-24/Domain: propeptide #status predicted <PRO>

F:25-265/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 8.2%; Score 22; DB 1; Length 265;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 EQLGPVTQEFMDLNEKETEGRL 107
DB 85 EQLGPVTQEFMDLNEKETEGRL 106

RESULT 6

LPRB1Z apolipoprotein A-I precursor (clone 22ap A1) - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999

C:Accession: S06064

R:Parakevopoulou, T.B.; Kritis, A.; Zannis, V.

submitted to the EMBL Data Library, July 1989

A:Reference number: S06064

A:Accession: S06064

A:Molecule type: mRNA

A:Residues: 1-266 <PAR>

A:Cross-References: EMBL:X15908; NID:g1457; PIDN:CAA34024.1; PID:g1458

C:Comment: This protein is synthesized in the small intestine.

C:Superfamily: apolipoprotein A-I

C:Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem r

F:1-18/Domain: signal sequence #status predicted <Sig>

F:19-24/Domain: propeptide #status predicted <PRO>

F:25-266/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 8.2%; Score 22; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 EQLGPVTQEFMDLNEKETEGRL 107
DB 85 EQLGPVTQEFMDLNEKETEGRL 106

RESULT 7

LPRB1

apolipoprotein A-I precursor - dog

C:Species: Canis lupus familiaris (dog)

C:Date: 17-Dec-1982 #sequence_revision 14-Jul-1994 #text_change 07-May-1999

C:Accession: A60940; A03092; A61418

R:Luo, C.C.; Li, W.H.; Chan, L.

J. Lipid Res. 30, 1735-1746, 1989

A:Title: Structure and expression of dog apolipoprotein A-I, E, and C-I mRNAs: implic

A:Reference number: A60940; MUID:90132271

A:Accession: A60940

A:Molecule type: mRNA

A:Residues: 1-266 <LUO>

R:Chung, H.; Randolph, A.; Reardon, I.; Heinrichson, R.L.

J. Biol. Chem. 257, 2961-2967, 1982

A:Title: The covalent structure of apolipoprotein A-I from canine high density lipopr

A:Reference number: A03092; MUID:82142425

A:Accession: A03092

A:Molecule type: protein

A:Residues: 25-167, 'G', 169-201, 'Q', 203-234, 'Q', 236-266 <CHU>

R:Nakai, T.; Whayne, T.F.; Tang, J.

FEBS Lett. 64, 409-411, 1976

A:Title: The amino- and carboxyl-terminal sequences of canine apolipoprotein A-I.

A:Reference number: A61418; MUID:76210910

A:Accession: A61418

A:Molecule type: protein

A:Residues: 25-56, 'Z', 261-262, 'A' <NAK>

C:Superfamily: apolipoprotein A-I

C:Keywords: atherosclerosis; cholesterol metabolism; HDL; intestine; lipid transport;

F:1-18/Domain: signal sequence #status predicted <Sig>

F:19-24/Domain: propeptide #status predicted <PRO>

F:25-266/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 8.2%; Score 22; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 1.7e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LTLAVLFLTGSOARHFQWOD 27
 |||
 Db 6 LTLAVLFLTGSOARHFQWOD 27

RESULT 8
 S31394

apolipoprotein A-I - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
 C:Accession: S31394
 R:Meichel, B.; Flach, R.; Weiss, B.; Weller-Guetler, H.; Frey, A.; Zinke, H.; Gassen, H.
 submitted to the EMBL Data Library, November 1992
 A:Description: Genomic organization of the porcine apolipoprotein AI gene and study of
 A:Reference number: S31394
 A:Accession: S31394
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-264 <MOE>
 A:Cross-references: EMBL:X69477; NID:q1889; PIDN:CAA9234.1; PID:q1890
 C:Superfamily: apolipoprotein A-I

Query Match 7.9%; Score 21; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 1.6e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VLTAVLFLTGSOARHFQWOD 25
 |||
 Db 5 VLTAVLFLTGSOARHFQWOD 25

RESULT 9
 A46018

apolipoprotein AI - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
 C:Accession: A46018
 R:Birchbauer, A.; Knipping, G.; Juritsch, B.; Aschauer, H.; Zechner, R.
 Genomics 15, 643-652, 1993
 A:Title: Characterization of the apolipoprotein AI and CIII genes in the domestic pig.
 A:Reference number: A46018; MUID:93224154
 A:Accession: A46018
 A:Status: preliminary
 A:Molecule type: DNA; protein
 A:Residues: 1-265 <BIR>
 A:Cross-references: GB:L00626; NID:q164358; PIDN:AAA30992.1; PID:q164359
 A:Note: sequence extracted from NCBI backbone (NCBIN:125509, NCBIPI:125511)
 C:Superfamily: apolipoprotein A-I

Query Match 7.9%; Score 21; DB 2; Length 265;
 Best Local Similarity 100.0%; Pred. No. 1.6e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VLTAVLFLTGSOARHFQWOD 25
 |||
 Db 5 VLTAVLFLTGSOARHFQWOD 25

RESULT 10

A56858
 apolipoprotein A-I precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 05-Jan-1996 #sequence_revision 23-Aug-1997 #text_change 13-Aug-1999
 C:Accession: A56858; A34649
 R:O'Huigin, C.; Chan, L.; Li, W.
 Mol. Biol. Evol. 7, 327-339, 1990

A:Title: Cloning and sequencing of bovine apolipoprotein A-I cDNA and molecular evolu
 A:Reference number: A56858; MUID:90348478

A:Accession: A56858
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-265 <OXH>

A:Cross-references: GB:M35870; NID:q162677; PIDN:AAA30381.1; PID:q162678
 R:Sparrow, D.A.; Lee, B.R.; Laplaud, P.M.; Auboltron, S.; Bauchart, D.; Chapman, M.J.;
 Biochim. Biophys. Acta 1123, 145-150, 1992
 A:Title: Plasma lipid transport in the preparturient calf, Bos spp: primary structure o
 A:Reference number: A56858; MUID:92133895

A:Accession: A56858

A:Status: preliminary

A:Molecule type: protein

A:Residues: 19-184, 'OL', 187-265 <SPA>

A:Experimental source: Friesian-Holstein male calves aged 2-4 weeks

A:Note: sequence extracted from NCBI backbone (NCBIPI:83520)

R:Auboltron, S.; Sparrow, D.A.; Beaudatle, L.; Bauchart, D.; Sparrow, J.T.; Laplaud, P
 Biochem. Biophys. Res. Commun. 166, 833-839, 1990

A:Title: Characterization and amino-terminal sequence of apolipoprotein AI from plasm
 A:Reference number: A34649; MUID:90147795

A:Accession: A34649

A:Molecule type: protein

A:Residues: 25-70 <ADB>

A:Experimental source: Friesian-Holstein male calves aged 2-4 weeks

C:Superfamily: apolipoprotein A-I

C:Keywords: lipid binding; lipoprotein

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-265/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 7.9%; Score 21; DB 2; Length 265;
 Best Local Similarity 100.0%; Pred. No. 1.6e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VLTAVLFLTGSOARHFQWOD 25
 |||
 Db 5 VLTAVLFLTGSOARHFQWOD 25

RESULT 11

JT0672

apolipoprotein A-I - pig

N:Alternate names: apo-A-I

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 11-May-2000

C:Accession: JT0672; PNO471; A05311

R:Trieu, V.N.; Patel, B.; Zhan, R.; Black, D.D.

Gene 134, 267-270, 1993

A:Title: Sequence of the porcine apoA-I gene.

A:Reference number: JT0672; MUID:94085789

A:Accession: JT0672

A:Molecule type: DNA

A:Residues: 1-265 <TRI>

A:Cross-references: EMBL:Z14124; NID:q1893

A:Note: this translation is not annotated in GenBank entry SSAPOAIG, release 111.0; t

R:Trieu, V.N.; Hasler-Rapacz, J.; Rapacz, J.; Black, D.D.

Gene 123, 173-179, 1993

A:Title: Sequences and expression of the porcine apolipoprotein A-I and C-III mRNAs.

A:Reference number: PNO471; MUID:93154581

A:Accession: PNO471

A:Molecule type: mRNA

A:Residues: 105-265 <TR2>

A:Experimental source: liver

R:Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.

Biochemistry 15, 1928-1933, 1976

A:Title: Characterization of the plasma lipoproteins and apoproteins of the Erythroce

A:Reference number: A90395; MUID:76184721

A:Accession: A05311

A:Molecule type: protein

A:Residues: 25-34 <MAH>

A:Comment: This protein is the major apolipoprotein of high-density lipoprotein and s

C:Genetics:

A:Gene: apoa-I
 A:Introns: 15/1: 66/2
 C:Species: apolipoprotein A-I
 C:Superfamily: apolipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid metabolism; lip
 F:99/Region: ochre stop codon

Query Match 7.9%; Score 21; DB 2; Length 265;
 Best Local Similarity 100.0%; Pred. No. 1.6e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VLTAVLELTGSGARHFWOOD 25
 |||||
 DB 5 VLTAVLELTGSGARHFWOOD 25

RESULT 12

J00704
 apolipoprotein A-I - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 28-Oct-1994
 C:Accession: J00704
 R:Weller-Guettler, H.; Sommerfeldt, M.; Papandrikopoulou, A.; Mischek, U.; Bonitz, D.; H
 J. Neurochem. 54, 444-450, 1990
 A:Title: Synthesis of apolipoprotein A-I in pig brain microvascular endothelial cells.
 A:Reference number: J00704; MUID:90132667
 A:Accession: J00704
 A:Molecule type: mRNA
 A:Residues: 1-231 <MET>
 A:Note: the authors translated the codon CAG for residue 124 as His and GAC for residue
 C:Superfamily: apolipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; lipid binding; lipid transport; lipoprotein; pl

Query Match 7.5%; Score 20; DB 2; Length 231;
 Best Local Similarity 100.0%; Pred. No. 1.4e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 85 RBOLGPVTQEFWDLNLEKETE 104
 |||||
 DB 51 RBOLGPVTQEFWDLNLEKETE 70

RESULT 13

S21830
 apolipoprotein A-I - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 20-Feb-1995 #sequence_revision 22-May-1998 #text_change 13-Aug-1999
 C:Accession: S21830
 R:Trileu, V.N.; Rohwer-Nuttler, P.; Black, D.D.
 submitted to the EMBL Data Library, May 1991
 A:Description: Sequence and developmental expression of porcine Apoa-I mRNA.
 A:Reference number: S21830
 A:Accession: S21830
 A:Molecule type: mRNA
 A:Residues: 1-164 <TR>
 A:Cross-references: EMBL:X59414; NID:91891; PIDN:CAA42050.1; PID:g1892
 A:Experimental source: liver
 C:Superfamily: apolipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid metabolism; lip

Query Match 7.1%; Score 19; DB 2; Length 164;
 Best Local Similarity 100.0%; Pred. No. 9.5e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 229 EKAKPALEDLROGLLPVLE 247
 |||||
 DB 126 EKAKPALEDLROGLLPVLE 144

RESULT 14

A24700

apolipoprotein A-I precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 13-Aug-1999
 C:Accession: A24700; S00298; A05314
 R:Madad, I.A.; Ordovas, J.M.; Fitzpatrick, T.; Karathanasis, S.K.
 J. Biol. Chem. 261, 13268-13277, 1986
 A:Title: Linkage, evolution, and expression of the rat apolipoprotein A-I, C-III, and
 A:Reference number: A92558; MUID:87008540
 A:Accession: A24700
 A:Molecule type: DNA
 A:Residues: 1-259 <HAD>

A:Cross-references: EMBL:J02597; NID:g202935; PIDN:AAA0745.1; PID:g202939
 R:Douch, J.E.; Martini, J.A.; Gielen, J.E.
 Eur. J. Biochem. 140, 493-498, 1984

A:Title: Cloning and structure analysis of the rat apolipoprotein A-I cDNA.
 A:Reference number: S00298; MUID:84207987
 A:Accession: S00298

A:Molecule type: mRNA

A:Residues: 1-259 <PON>

A:Cross-references: GB:M00001; EMBL:X00558; NID:g202944; PIDN:AAA0749.1; PID:g202945
 R:Gordon, J.I.; Smith, D.P.; Andy, R.; Alpers, D.H.; Schonfeld, G.; Strauss, A.W.
 J. Biol. Chem. 257, 971-978, 1982

A:Title: The primary translation product of rat intestinal apolipoprotein A-I mRNA is
 A:Reference number: A05314; MUID:82098162
 A:Accession: A05314

A:Molecule type: protein

A:Residues: 1-18, 'X', 20-21, 'X', 23-28, 'X', 30-38, 'X', 40-41, 'X', 43-45 <GOR>

C:Comment: This protein is synthesized in the liver and small intestine. The propepti
 C:Comment: This protein is a major component of the high density lipoproteins in plas

C:Genetics: 15/1: 66/2

A:Introns: 15/1: 66/2

C:Superfamily: apolipoprotein A-I

C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; 1

F:1-18/Domain: signal sequence #status experimental <SIG>

F:19-24/Domain: propeptide #status experimental <PRO>

F:25-259/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 4.5%; Score 12; DB 2; Length 259;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 47 KDSCGRDYVSQFE 58
 |||||

DB 46 KDSCGRDYVSQFE 57

RESULT 15

JC1237
 apolipoprotein A-I precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-1993
 C:Accession: JC1237

R:Boyle, T.P.; Marotti, K.R.

Gene 117, 243-247, 1992

A:Title: Structure of the murine gene encoding apolipoprotein A-I.

A:Reference number: JC1237; MUID:92347700

A:Accession: JC1237

A:Molecule type: DNA

A:Residues: 1-262 <BOY>

A:Cross-references: GB:M77801

C:Genetics:

A:Gene: Apoa-I

A:Introns: 15/1: 66/2

C:Superfamily: apolipoprotein A-I

C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; 1

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-262/Product: apolipoprotein A-I #status predicted <MAT>

Query Match 4.5%; Score 12; DB 2; Length 262;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 KDSGRDYVSQFE 58
 |||||||
 Db 46 KDSGRDYVSQFE 57

RESULT 16
 S22420

apolipoprotein A-I precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
 C:Accession: S22420; S22421; A44364
 R:Stoffel, W.; Mueller, R.; Bincek, E.; Hofmann, K.
 Biol. Chem. Hoppe-Seyler 373, 187-193, 1992
 A:Title: Mouse apolipoprotein AI, cDNA-derived primary structure, gene organisation and
 A:Reference number: S22420; MUID:92281682
 A:Accession: S22420
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-264 <STO>
 A:Cross-references: EMBL:X64262; NID:g50014; PIDN:CAA45560.1; PID:g50015
 A:Accession: S22421
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-264 <ST2>
 A:Cross-references: EMBL:X64263; NID:g50020; PIDN:CAA45561.1; PID:g50021
 R:Janusz, J.L.; Acrolian, N.; O'Connell, A.; Aalto-Setälä, K.; Breslow, J.L.
 Genomics 14, 1081-1088, 1992
 A:Title: Characterization of the mouse apolipoprotein ApoA-1/Apoc-3 gene locus: genomic,
 A:Accession number: A44364; MUID:93122774
 A:Accession: A44364
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-264 <JAN>
 A>Note: sequence extracted from NCBI backbone (NCBIN:122400, NCBIPI:122407)
 C:Genetics:
 A:Introns: 15/1: 66/2
 C:Superfamily: apolipoprotein A-I

Query Match 4.5%; Score 12; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 KDSGRDYVSQFE 58
 |||||||
 Db 46 KDSGRDYVSQFE 57

RESULT 17
 G83132
 hypothetical protein PA4111 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: G83132
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Llm,
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337
 A:Accession: G83132
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-132 <STO>
 A:Cross-references: GB:AE004827; GB:AE004091; NID:g9950306; PIDN:AA607498.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA4111

Query Match 3.7%; Score 10; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 0.052;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 196 ORLAARLEAL 205
 |||||||
 Db 41 ORLAARLEAL 50

RESULT 18
 A61448

apolipoprotein A-I - duck
 C:Species: Anas platyrhynchos (domestic duck)
 C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 17-Mar-1999
 C:Accession: A61448
 R:Gu, Z.W.; Xie, Y.H.; Yang, M.; Sparrow, J.T.; Wang, K.; Li, Y.; Li, W.H.; Gotto Jr.
 J. Protein Chem. 12, 585-591, 1993
 A:Title: Primary structure of Beijing duck apolipoprotein A-1.
 A:Reference number: A61448; MUID:94190456
 A:Accession: A61448
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-246 <GUA>
 A>Note: the source is designated as Beijing duck
 C:Superfamily: apolipoprotein A-I

Query Match 3.7%; Score 10; DB 2; Length 246;
 Best Local Similarity 100.0%; Pred. No. 0.093;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 187 LAPYSDELRLQ 196
 |||||||
 Db 168 LAPYSDELRLQ 177

RESULT 19
 LPCHA1

apolipoprotein A-I precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Mar-1990 #sequence_revision 25-Aug-1995 #text_change 22-Jun-1999
 C:Accession: JH0471; A29657; S01453; S28888; A29616; S00187; S10973; S11023; I50156
 R:Bhattacharyya, N.; Chattopadhyay, R.; Hirsch, A.; Banerjee, D.
 Gene 104, 163-168, 1991
 A:Title: Isolation, characterization and sequencing of the chicken apolipoprotein-AI-
 A:Reference number: JH0471; MUID:92009209
 A:Accession: JH0471
 A:Molecule type: DNA
 A:Residues: 1-264 <BHA>
 R:Byrnes, L.; Luo, C.C.; Li, W.H.; Yang, C.; Chan, L.
 Biochem. Biophys. Res. Commun. 148, 485-492, 1987
 A:Title: Chicken apolipoprotein A-I: cDNA sequence, tissue expression and evolution.
 A:Reference number: A29657; MUID:88049703
 A:Accession: A29657
 A:Molecule type: mRNA
 A:Residues: 1-264 <BYR>
 A:Cross-references: EMBL:M17961; NID:g211147; PIDN:AAA48593.1; PID:g211148
 R:Rajavashisth, T.B.; Dawson, P.A.; Williams, D.L.; Shackelford, J.E.; Leberer, H.; L
 J. Biol. Chem. 262, 7058-7065, 1987
 A:Title: Structure, evolution, and regulation of chicken apolipoprotein A-I.
 A:Reference number: S01453; MUID:87222301
 A:Accession: S01453
 A:Molecule type: mRNA
 A:Residues: 1-15, '1', 17-147, 'K', 149-264 <RAJ>
 A:Cross-references: GB:M25559; EMBL:J02739; NID:g211145; PIDN:AAA48592.1; PID:g211146
 A:Accession: S28888
 A:Molecule type: protein
 A:Residues: 25-44,230-256 <RAJ>
 R:Ferrari, S.; Tarugi, P.; Drusiani, E.; Calandra, S.; Fregni, M.
 Gene 60, 39-46, 1987
 A:Title: The complete sequence of chick apolipoprotein AI mRNA and its expression in
 A:Reference number: A29616; MUID:88152500
 A:Accession: A29616
 A:Molecule type: mRNA
 A:Residues: 1-264 <FER>

A:Cross-references: EMBL:M18746; NID:g211149; PIDN:AAA48594.1; PID:g211150
 R:Yang, C.T.; Gu, Z.W.; Patsch, W.; Weng, S.A.; Kim, T.W.; Chan, L.
 FEBS Lett. 224, 261-266, 1987
 A:Title: The complete amino acid sequence of proapolipoprotein A-I of chicken high density lipoprotein
 A:Reference number: S00187; MUID:88083548
 A:Accession: S00187
 A:Molecule type: protein
 A:Residues: 19-264 <YAN>
 R:Banerjee, D.; Mukherjee, T.K.; Redman, C.M.
 J. Cell Biol. 101, 1219-1226, 1985
 A:Title: Biosynthesis of high density lipoprotein by chicken liver: intracellular transport
 A:Reference number: S10973; MUID:86008443
 A:Accession: S10973
 A:Molecule type: protein
 A:Residues: 19-'H', 21-23, 'Q', 25-44 <BAN>
 A:Note: The sequence from Fig. 4 is inconsistent with that from Table II in having 41-TH
 R:Shackelford, J.E.; Leberer, H.G.
 J. Biol. Chem. 258, 7175-7180, 1983
 A:Title: Synthesis and secretion of apolipoprotein AI by chick breast muscle.
 A:Reference number: S11023; MUID:83213468
 A:Accession: S11023
 A:Molecule type: protein
 A:Residues: 25-44 <SHA>
 R:Lamon-Fava, S.; Sastri, R.; Ferrari, S.; Rajavashisth, T.B.; Lusis, A.J.; Karathanasis
 J. Lipid Res. 33, 831-842, 1992
 A:Title: Evolutionary distinct mechanisms regulate apolipoprotein A-I gene expression: D
 A:Reference number: I50156; MUID:92381402
 A:Accession: I50156
 A:Status: preliminary; translated from GR/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-15, 'I', 17-264 <LAN>
 A:Cross-references: GB:M6012; NID:g211158; PIDN:AAA48597.1; PID:g211159
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipoprotein
 C:Comment: This protein is synthesized only in the liver in mammals, whereas in chicken
 C:Genetics: This protein is a major component of the high density lipoproteins in plasma.
 A:Gene: APOAI
 A:Introns: 15/1: 66/2
 C:Superfamily: apolipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipoprotein
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: signal sequence #status experimental <PRO>
 F:25-264/Product: apolipoprotein A-I #status experimental <MAT>

Query Match 3.7%; Score 10; DB 1; Length 264;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 LAPYSDLRQ 196
 |||||||||
 DB 186 LAPYSDLRQ 195

RESULT 20
 JC5436
 apolipoprotein A-I precursor - Japanese quail
 C:Species: Coturnix coturnix japonica (Japanese quail)
 C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 20-Jun-2000
 C:Accession: JC5436; PCA472
 R:Oku, H.; Toda, T.; Nagata, J.; Ishikawa, M.; Noyazaki, K.; Shinjyo, C.; Chinen, I.
 Biosci. Biotechnol. Biochem. 61, 286-290, 1997
 A:Title: Apolipoprotein A-I of Japanese quail: cDNA sequence and modulation of tissue ex
 A:Reference number: JC5436; MUID:97212027
 A:Accession: JC5436
 A:Molecule type: mRNA
 A:Residues: 1-264 <OKU>
 A:Cross-references: GB:D85133; NID:g1890065; PIDN:BA12729.1; PID:g1890066
 A:Accession: PCA472
 A:Molecule type: protein
 A:Residues: 25-60 <OK2>
 C:Comment: This protein is the major protein moiety of plasma HDL. It functions as a ve
 C:Superfamily: apolipoprotein A-I
 F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-264/Product: apolipoprotein A-I #status predicted <MAT>

Query Match 3.4%; Score 9; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 0.95;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TLAVFLTG 15
 |||||||
 DB 7 TLAVFLTG 15

RESULT 21
 A05313
 apolipoprotein A-I - red guenon (fragment)
 N:Alternate names: apo-A-I
 C:Species: Erythrocebus patas (red guenon, hussar)
 C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 11-May-2000
 C:Accession: A05313
 R:Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.
 Biochemistry 15, 1928-1933, 1976
 A:Title: Characterization of the plasma lipoproteins and apoproteins of the Erythroce
 A:Reference number: A90395; MUID:76184721
 A:Accession: A05313
 A:Molecule type: protein
 A:Residues: 1-20 <MAH>
 C:Superfamily: apolipoprotein A-I
 C:Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; 1

Query Match 3.0%; Score 8; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.81;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 PMDRVKDL 38
 |||||||
 DB 7 PMDRVKDL 14

RESULT 22
 G83100
 hypothetical protein PA4368 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: G83100
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
 Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; L
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A:Reference number: AB2950; MUID:20437337
 A:Accession: G83100
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-300 <STO>
 A:Cross-references: GB:AE004852; GB:AE004091; NID:g9950587; PIDN:AA07756.1; GSPDB:GN
 C:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA4368

Query Match 3.0%; Score 8; DB 2; Length 300;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 RLARLEA 204
 |||||||
 DB 228 RLARLEA 235

RESULT 23
 S33450
 apolipoprotein E - pig

N:Alternate names: apo-E
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Oct-1999
C:Accession: S33450; A05312
R:Przozowska, A.M.; Grimholt, U.; Kulseth, M.A.; Wold, I.; Rogne, S.
Submitted to the EMBL Data Library, May 1993
A:Description: The sequence of porcine apolipoprotein E(APOE) cDNA.
A:Reference number: S33450
A:Accession: S33450
A:Molecule type: mRNA
A:Residues: 1-317

A:Cross-references: EMBL:X72835; NID:g911232; PIDN:CAA51356.1; PID:g911233
R:Weisgraber, K.H.; Troxler, R.F.; Rall, S.C.; Mahley, R.W.
Biochem. Biophys. Res. Commun. 95, 374-380, 1980
A:Reference number: A90221; MUID:81021043
A:Accession: A05312
A:Molecule type: protein
A:Residues: 19-26, 'Q', '28', 'GXL', <WEI>
C:Superfamily: apolipoprotein A-I
C:Keywords: cholesterol; chylomicron; HDL; lipid binding; lipid transport; lipoprotein;

Query Match 3.0%; Score 8; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 87 QLGPTQGE 94
|||||
DB 98 QLGPTQGE 105

RESULT 24
F82692
conserved hypothetical protein XF1359 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: F82692
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: F82692
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <SI>
A:Cross-references: GB:AE003967; GB:AE003849; NID:g9106347; PIDN:AAF84168.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Agencio, M.; Alvarenga, R.; Brlones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carver, H. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fromm, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Klieger, J.E.; Kuramae, E.E.; Laig, chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B. A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Rodrigues, V.; Rosa, A.J.; de M., de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1359

Query Match 3.0%; Score 8; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 AAVLTAV 10
|||||
DB 161 AAVLTAV 168

RESULT 25
B40892
apolipoprotein A-IV precursor - mouse (strain 129)
C:Species: Mus musculus (house mouse)
C>Date: 27-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 13-Aug-1999
C:Accession: B40892
R:Reue, K.; Leete, T.H.
J. Biol. Chem. 266, 12715-12721, 1991
A:Title: Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion
A:Reference number: A40892; MUID:91286309
A:Accession: B40892
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-391 <REU>
A:Cross-references: GB:M64248; NID:g9191884; PIDN:AAA37214.1; PID:g9191885
A>Note: the authors translated the codon CTG for residue 87 as Glu, GAG for residue 2
C:Superfamily: apolipoprotein A-I
C:Keywords: lipid binding; lipoprotein

Query Match 3.0%; Score 8; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KAAVLTAA 9
|||||
DB 4 KAAVLTAA 11

RESULT 26
A25281
apolipoprotein A-IV precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 13-Aug-1999
C:Accession: A25281
R:Williams, S.C.; Bruckheimer, S.M.; Lusis, A.J.; LeBeauf, R.C.; Kinniburgh, A.J.
Mol. Cell. Biol. 6, 3807-3814, 1986
A:Title: Mouse apolipoprotein A-IV gene: nucleotide sequence and induction by a high-
A:Reference number: A25281; MUID:87089722
A:Accession: A25281
A:Molecule type: DNA
A:Residues: 1-394 <WIL>
A:Cross-references: GB:ML3966; NID:g9192006; PIDN:AAA37253.1; PID:g387102
C:Genetics:
A:Insertions: 16/1; 58/2
C:Superfamily: apolipoprotein A-I
C:Keywords: chylomicron; HDL; lipid binding; lipoprotein

Query Match 3.0%; Score 8; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KAAVLTAA 9
|||||
DB 4 KAAVLTAA 11

RESULT 27
A40892
apolipoprotein A-IV precursor - mouse (strain C57BL/6)
C:Species: Mus musculus (house mouse)
C>Date: 27-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 13-Aug-1999
C:Accession: A40892
R:Reue, K.; Leete, T.H.
J. Biol. Chem. 266, 12715-12721, 1991
A:Title: Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion
A:Reference number: A40892; MUID:91286309
A:Accession: A40892
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-395 <RED>
 A:Cross-references: GB:M64249; NID:g191886; PIDN:AA37215.1; PID:g191887
 A:Note: the authors translated the codon CTG for residue 87 as Glu, GAG for residue 207
 C:Superfamily: apolipoprotein A-I
 C:Keywords: lipid binding; lipoprotein

Query Match 3.0%; Score 8; DB 2; Length 395;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KAAVLTIA 9
 |||||
 Db 4 KAAVLTIA 11

RESULT 28

C40892
 apolipoprotein A-IV precursor - mouse
 C:Species: Mus musculus castaneus (southeastern Asian house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Dec-1993
 C:Accession: C40892
 R:Reue, K.; Leete, T.H.
 J. Biol. Chem. 266, 12715-12721, 1991
 A:Title: Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion in
 A:Reference number: A40892; MUID:91286309
 A:Accession: C40892
 A:Molecule type: mRNA
 A:Residues: 1-399 <RED>
 A:Cross-references: GB:M64250
 A:Note: the authors translated the codon CTG for residue 87 as Glu, GAG for residue 207
 C:Superfamily: apolipoprotein A-I
 C:Keywords: chylomicron; duplication; HDL; lipid binding; lipid transport; lipoprotein;

Query Match 3.0%; Score 8; DB 2; Length 399;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KAAVLTIA 9
 |||||
 Db 4 KAAVLTIA 11

RESULT 29

S12332
 ubiquitin--protein ligase (EC 6.3.2.19) - Yeast (Saccharomyces cerevisiae) (strain S288C
 N:Alternate names: protein G7166; protein YGR184c
 C:Species: Saccharomyces cerevisiae
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 20-Jun-2000
 C:Accession: S12332; S64502; S64498
 R:Bartel, B.; Wuenning, I.; Varshavsky, A.
 EMBO J. 9, 3179-3189, 1990
 A:Title: The recognition component of the N-end rule pathway.
 A:Reference number: S12332; MUID:91006011
 A:Accession: S12332
 A:Molecule type: DNA
 A:Residues: 1-1950 <BAR>
 A:Cross-references: EMBL:X53747; NID:g4743; PIDN:CAA37779.1; PID:g4744
 A:Experimental source: strain S288C
 R:Arriyo, J.; Garcia-Gonzalez, M.; Garcia-Saez, M.I.; Sanchez-Perez, M.; Nombela, C.
 submitted to the Protein Sequence Database, May 1996
 A:Reference number: S64499
 A:Accession: S64502
 A:Molecule type: DNA

A:Residues: 1-1950 <ARR>
 A:Cross-references: EMBL:Z72969; NID:g1323325; PIDN:CAA97210.1; PID:g1323326; MIPS:YGR18
 A:Experimental source: strain S288C
 R:Hebling, U.; Hofmann, B.; Delius, H.
 submitted to the Protein Sequence Database, May 1996
 A:Reference number: S64003
 A:Accession: S64498
 A:Molecule type: DNA

A:Residues: 1615-1950 <HEB>
 A:Cross-references: EMBL:Z72969; MIPS:YGR184c
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: SGD:UBR1; PTR1
 A:Cross-references: SGD:S0003416; MIPS:YGR184c
 A:Map position: 7R
 C:Superfamily: ubiquitin--protein ligase
 C:Keywords: ligase; protein degradation

Query Match 3.0%; Score 8; DB 2; Length 1950;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 202 LEALKENG 209
 |||||
 Db 1277 LEALKENG 1284

RESULT 30

T05224
 hypothetical protein F1715.150 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
 C:Accession: T05224
 R:Bevan, M.; Vitale, D.; Liguori, R.; Argiriou, A.; De Simone, V.; Hohelsel, J.; Mewe
 submitted to the Protein Sequence Database, July 1998
 A:Reference number: Z15404
 A:Accession: T05224
 A:Molecule type: DNA
 A:Residues: 1-67 <BEV>
 A:Cross-references: EMBL:AL031032
 A:Experimental source: cultivar Columbia; BAC clone F1715
 C:Genetics:
 A:Map position: 4
 A:Note: F1715.150

Query Match 2.6%; Score 7; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 238 LRQGLLP 244
 |||||
 Db 46 LRQGLLP 52

RESULT 31

H87207
 probable membrane protein [imported] - Mycobacterium leprae
 C:Species: Mycobacterium leprae
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: H87207
 R:Coile, S.T.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
 R.; Davies, R.M.; Devlin, K.; Dutroy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holro
 eam, M.A.; Rutherford, K.M.
 Nature 409, 1007-1011, 2001
 A:Authors: Rutherford, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
 A:Title: Massive gene decay in the leprosy bacillus.
 A:Reference number: A86909; MUID:21128732; PMID:11234002
 A:Accession: H87207
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-101 <STO>
 A:Cross-references: GB:AL450380; NID:g13093975; PIDN:CAC31904.1; GSPDB:GN00147
 C:Genetics:
 A:Gene: ML2388

Query Match 2.6%; Score 7; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VLTLAVL 11
 |||||
 Db 90 VLTLAVL 96

RESULT 32

E71566
 probable S16 ribosomal protein - Chlamydia trachomatis (serotype D, strain UW3/Cx)
 C:Species: Chlamydia trachomatis
 C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
 C:Accession: E71566
 R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
 A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
 A:Reference number: A71570; MUID:99000809
 A:Accession: E71566
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-116 <ARN>
 A:Cross-references: GB:AE001277; GB:AE001273; NID:g3328408; PIDN:AA067616.1; PID:g332841
 A:Experimental source: serotype D, strain UW-3/Cx
 C:Genetics:
 A:Gene: rsl6
 C:Superfamily: Escherichia coli ribosomal protein S16

Query Match 2.6%; Score 7; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 195 RORLAAR 201
 |||||
 Db 103 RORLAAR 109

RESULT 33

C86709
 hypothetical protein y9hc [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C:Accession: C86709
 R:Boitlin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: C86709
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-132 <STO>
 A:Cross-references: GB:AE005176; PID:g12723583; PIDN:AA04773.1; GSPDB:GN00146
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: y9hc

Query Match 2.6%; Score 7; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 207 ENGGAARL 213
 |||||
 Db 122 ENGGAARL 128

RESULT 34

G72710
 hypothetical protein APE1102 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: G72710
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaiawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
 A:Reference number: A72450; MUID:99310339
 A:Accession: G72710
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-139 <RAW>
 A:Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA80087.1; PID:d1043873; PID:g
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE1102

Query Match 2.6%; Score 7; DB 2; Length 139;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 QRLAARL 202
 |||||
 Db 120 QRLAARL 126

RESULT 35

T33928
 hypothetical protein y66H1A.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000
 C:Accession: T33928
 R:Clarke, K.; Wohlmann, P.
 submitted to the EMBL Data Library, February 1999
 A:Description: The sequence of C. elegans cosmid y66H1A.
 A:Reference number: 221440
 A:Accession: T33928
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-150 <CIA>
 A:Cross-references: EMBL:AF125462; PIDN:AD12855.1; GSPDB:GN00022; CESP:y66H1A.3
 A:Experimental source: strain Bristol N2; clone y66H1A
 C:Genetics:
 A:Gene: CESP:y66H1A.3
 A:Map position: 4
 A:Insertions: 17/1; 50/1; 92/3; 124/3
 C:Superfamily: Caenorhabditis elegans hypothetical protein Y66H1A.3

Query Match 2.6%; Score 7; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 195 RORLAAR 201
 |||||
 Db 109 RORLAAR 115

RESULT 36

E86711
 hypothetical protein y9jb [imported] - Lactococcus lactis subsp. lactis (strain IL140
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C:Accession: E86711
 R:Boitlin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehr Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: E86711
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-150 <STO>
 A:Cross-references: GB:AE005176; PID:g12723602; PIDN:AA04791.1; GSPDB:GN00146
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: y9jb

Query Match 2.6%; Score 7; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 232 KPALEDL 238
 Db 136 KPALEDL 142

RESULT 37

AB0918
 conserved hypothetical protein STY3603 [imported] - *Salmonella enterica* subsp. *enterica*
 C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh
 A>Note: this species has also been called *Salmonella typhi*
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
 C:Accession: AB0918
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaara, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhimurium
 A:Reference number: AB0502; PMID:11677608
 A:Accession: AB0918
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-155 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD07936.1; PID:916504481; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY3603

Query Match 2.6%; Score 7; DB 2; Length 155;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 192 DELRQRL 198
 Db 90 DELRQRL 96

RESULT 38

F91222
 hypothetical protein ECs4750 [imported] - *Escherichia coli* (strain O157:H7, substrain R)
 C:Species: *Escherichia coli*
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
 C:Accession: F91222
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genome analysis of a closely related strain
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: F91222
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-161 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BA838173.1; PID:913364226; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RMD 0509952
 C:Genetics:
 A:Gene: ECs4750

Query Match 2.6%; Score 7; DB 2; Length 161;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 192 DELRQRL 198
 Db 96 DELRQRL 102

RESULT 39

S30747
 hypothetical 17.1k protein (rarp-p1da intergenic region) - *Escherichia coli*
 N:Alternate names: hypothetical protein f161
 C:Species: *Escherichia coli*
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999
 C:Accession: S30747; E65186; S30710
 R:Ohmori, H.
 submitted to the EMBL Data Library, January 1993
 A:Description: Physical map of the cora region of the *E.coli* chromosome.
 A:Reference number: S30742
 A:Accession: S30747
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-161 <OHM>

A:Cross-references: EMBL:J02122; NID:9145575; PIDN:AA05042.1; PID:9145581
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.: Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of *Escherichia coli* K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: E65186
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-161 <BLAT>
 A:Cross-references: GB:AE000457; GB:U00096; NID:92367294; PIDN:AA06823.1; PID:923672
 A:Experimental source: strain K-12, substrain MG1655
 R:Daniels, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R.
 Science 257, 771-778, 1992
 A:Title: Analysis of the *Escherichia coli* genome: DNA sequence of the region from 84.
 A:Reference number: S30660; MUID:92358234
 A:Accession: S30710
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-101, 'V', 103-161 <DAN>

A:Cross-references: EMBL:M87049; NID:9836656; PIDN:AA67616.1; PID:9148219
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992
 C:Genetics:
 A:Gene: y1g1

Query Match 2.6%; Score 7; DB 2; Length 161;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 192 DELRQRL 198
 Db 96 DELRQRL 102

RESULT 40

D86069
 hypothetical protein y1g1 [imported] - *Escherichia coli* (strain O157:H7, substrain ED)
 C:Species: *Escherichia coli*
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: D86069
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: D86069
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-161 <STO>
 A:Cross-references: GB:AE005174; NID:912518694; PIDN:AA059016.1; GSPDB:GN00145; UMGCP:
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: y1g1

Query Match 2.6%; Score 7; DB 2; Length 161;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 192 DELRQRL 198
 |||||||
 DB 96 DELRQRL 102

RESULT 41

conserved hypothetical protein [Imported] - *Sinorhizobium meliloti* (strain 1021) magapla
 C:Species: *Sinorhizobium meliloti*
 C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: H95871
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: H95871
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-199 <KUR>
 A:Cross-references: GB:AL591985; PIDN:CA48640.1; PID:q15140112; GSPDB:GN00167
 A:Experimental source: strain 1021, megaplasmid pSymb
 R:Dalbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, J.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Jelaure,
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: Smb20250
 A:Genome: plasmid

Query Match 2.6%; Score 7; DB 2; Length 199;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 196 QRLAARL 202
 |||||||
 DB 38 QRLAARL 44

RESULT 42

hypothetical protein Vng2080c [Imported] - *Halobacterium* sp. NRC-1
 C:Species: *Halobacterium* sp. NRC-1
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: H84357
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
 A:Title: Genome sequence of *Halobacterium* species NRC-1.
 A:Reference number: A84160; MUID:20504483
 A:Accession: H84357
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-205 <STO>
 A:Cross-references: GB:AE004437; MID:910581497; PIDN:AAG20228.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: VNG2080C

Query Match 2.6%; Score 7; DB 2; Length 205;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 177 RAHVADL 183
 |||||||

DB 41 RAHVADL 47

RESULT 43

hypothetical protein SC2H4.05 - *Streptomyces coelicolor*
 C:Species: *Streptomyces coelicolor*
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: J37221
 R:Olliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL data library, September 1998
 A:Reference number: 221615
 A:Accession: J37221
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-216 <OLI>
 A:Cross-references: EMBL:AL031514; PIDN:CA420599.1; GSPDB:GN00070; SCODEB:SC2H4.05
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCODEB:SC2H4.05

Query Match 2.6%; Score 7; DB 2; Length 216;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 241 GLLPVLE 247
 |||||||
 DB 89 GLLPVLE 95

RESULT 44

hypothetical protein AT4g01670 [Imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
 C:Accession: E85021
 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp
 Nature 402, 769-777, 1999
 A:Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.
 A:Reference number: A85001; MUID:20083488
 A:Accession: E85021
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-218 <STO>
 A:Cross-references: GB:NC_001268; MID:97268210; PIDN:CA877737.1; GSPDB:GN00140
 C:Genetics:
 A:Gene: AT4g01670
 A:Map position: 4
 C:Superfamily: Arabidopsis hypothetical protein F14M4.23

Query Match 2.6%; Score 7; DB 2; Length 218;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 113 DLEEVKA 119
 |||||||
 DB 172 DLEEVKA 178

RESULT 45

Probable transcriptional regulatory protein b3025 - *Escherichia coli* (strain K-12)
 C:Species: *Escherichia coli*
 C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 27-Nov-2001
 C:Accession: G65089
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of *Escherichia coli* K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: G65089

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-219 <BLAT>
 A:Cross-references: GB:AE000384; GB:U00096; NID:g2367186; PIDN:AAC76061.1; PID:g1789402;
 A:Experimental source: strain K-12, substrain MG1655
 C:Superfamily: ompR protein; response regulator homology
 C:Keywords: phosphoprotein
 F:3-112/Domain: response regulator homology <RRH>
 F:51/Binding site: phosphate (asp) (covalent) #status predicted

Query Match 2.6%; Score 7; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 199 AARLEAL 205
 |||||
 Db 109 AARLEAL 115

RESULT 46
 C91117
 Probable 2-component transcription regulator [Imported] - Escherichia coli (strain O157:
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
 gasawara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
 A:Reference number: A96629; MUID:21156231; PMID:11258796
 A:Accession: C91117
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-219 <HAT>
 A:Cross-references: GB:BA000007; PIDN:BA837330.1; PID:g13363379; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RMD 0509952
 C:Genetics:
 A:Gene: ECS3907
 C:Superfamily: ompR protein; response regulator homology

Query Match 2.6%; Score 7; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 199 AARLEAL 205
 |||||
 Db 109 AARLEAL 115

RESULT 47
 C85962
 Probable 2-component transcription regulator yxiX [Imported] - Escherichia coli (strain
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: C85962
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: AB5480; MUID:21074935; PMID:11206551
 A:Accession: C85962
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-219 <STO>
 A:Cross-references: GB:AE005174; NID:g12517595; PIDN:AA658159.1; GSPDB:GN00145; UWGP:Z4
 A:Experimental source: strain O157:H7, substrain EDJ933
 C:Genetics:
 A:Gene: YxiX
 C:Superfamily: ompR protein; response regulator homology

Query Match 2.6%; Score 7; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 199 AARLEAL 205
 |||||
 Db 109 AARLEAL 115

RESULT 48
 A10888
 Probable two-component system response regulator. STY3354 [Imported] - Salmonella ent
 C:Species: Salmonella enterica subsp. enterica serovar Typh
 A:Note: This species has also been called Salmonella typh
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
 C:Accession: A10888
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
 , S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
 A:Reference number: AB0502; PMID:11677608
 A:Accession: A10888
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-219 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD03009.1; PID:g16504255; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY3354
 C:Superfamily: ompR protein; response regulator homology

Query Match 2.6%; Score 7; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 199 AARLEAL 205
 |||||
 Db 109 AARLEAL 115

RESULT 49
 F65018
 Hypothetical protein b2439 - Escherichia coli (strain K-12)
 C:Species: Escherichia coli
 C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 04-Mar-2000
 C:Accession: F65018
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 .A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: F65018
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-219 <BLAT>
 A:Cross-references: GB:AE000331; GB:U00096; NID:g1788775; PIDN:AAC75492.1; PID:g17887
 A:Experimental source: strain K-12, substrain MG1655
 C:Superfamily: Escherichia coli hypothetical protein b2439

Query Match 2.6%; Score 7; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

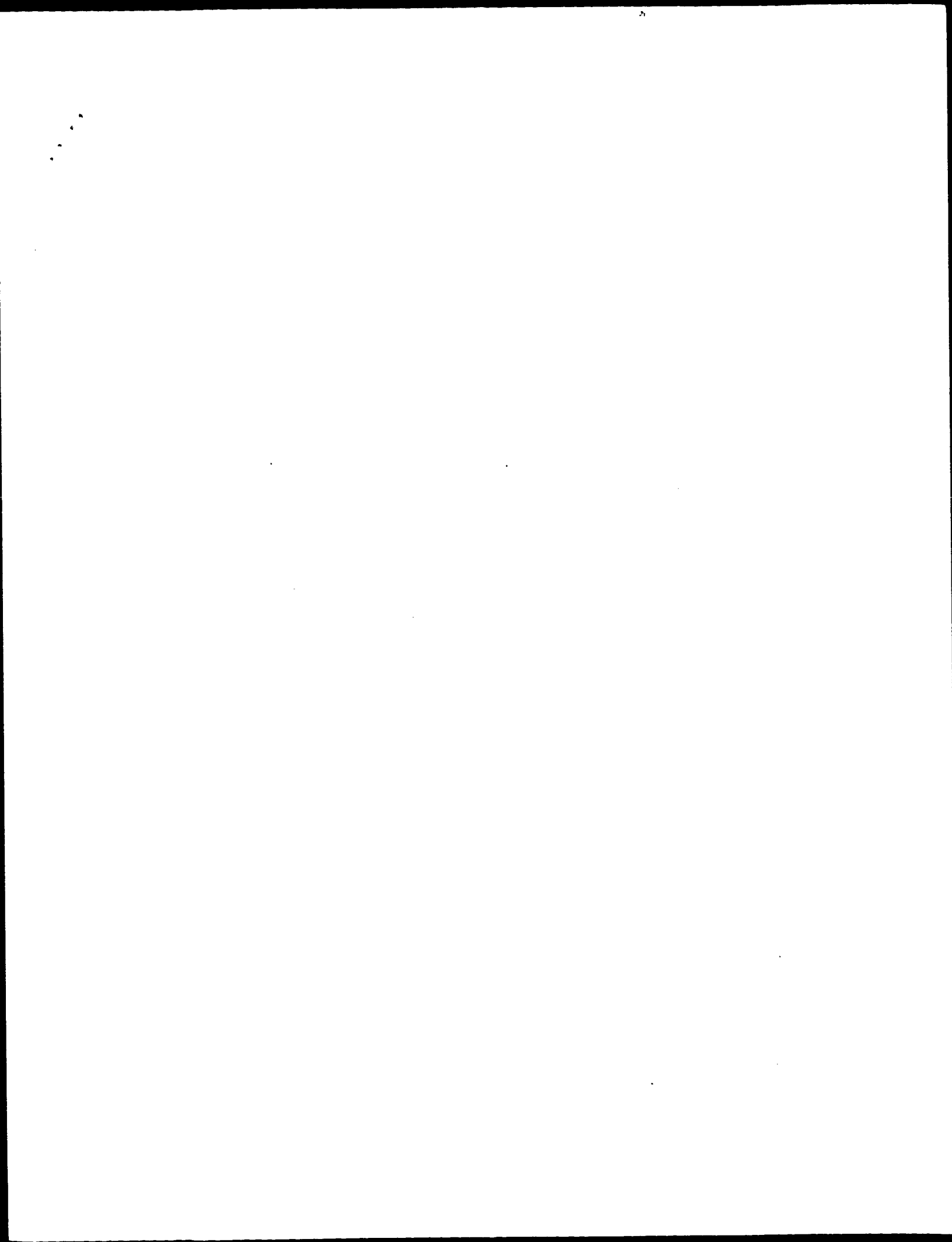
OY 12 FLTGSQA 18
 |||||
 Db 189 FLTGSQA 195

RESULT 50
 F91042

hypothetical protein ECS3310 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: F91042
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91042
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1219 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA036733.1; PID:q13362780; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: ECS3310
C;Superfamily: Escherichia coli hypothetical protein b2439

Query Match	2.6%	Score 7	DB 2	Length 219
Best Local Similarity	100.0%			Pred. No. 73
Matches 7	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 12	FLTGSQA 18			
Db 189	FLTGSQA 195			

Search completed: September 22, 2002, 12:23:38
Job time: 233 sec



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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:23:20 : Search time 11.64 Seconds
(without alignments)
888.155 Million cell updates/sec

Title: US-09-803-918a-2

Sequence: 1 MKAVALTLAVFLTGSQARH.....SFKVSLALEEYTKKINTQ 267

Scoring table: OLIGO
Gapop 60.0, Gapept 60.0

Searched: 105224 seqs, 38719550 residues

Word size: 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	267	100.0	267	1 APAL_HUMAN	P02647 homo sapien
2	69	25.8	267	1 APAL_MACFA	P15568 macaca fasc
3	23	8.6	265	1 APAL_TUPGB	O18759 tupia glis
4	22	8.2	266	1 APAL_CANFA	P02648 canis famli
5	22	8.2	266	1 APAL_RABIT	P09809 oryctolagus
6	21	7.9	265	1 APAL_BOVIN	P15497 bos taurus
7	21	7.9	265	1 APAL_PIG	P18648 sus scrofa
8	12	4.5	259	1 APAL_RAT	P04639 rattus norv
9	12	4.5	264	1 APAL_MOUSE	O00623 mus musculu
10	10	3.7	264	1 APAL_ANAPL	O42296 anas platyr
11	10	3.7	264	1 APAL_CHICK	P08250 gallus gall
12	9	3.4	264	1 APAL_CHICK	P33918 coturnix co
13	8	3.0	20	1 APAL_ERYP	P18647 erythrocybu
14	8	3.0	317	1 APE_PIG	P18650 sus scrofa
15	8	3.0	395	1 APA4_MOUSE	P06728 mus musculu
16	8	3.0	1950	1 UBR1_YEAST	P19812 saccharomyc
17	7	2.6	116	1 R516_CHLAMU	O99113 chlamydia m
18	7	2.6	116	1 R516_CHLAMU	O99113 chlamydia m
19	7	2.6	132	1 TRMA_LACIA	O84029 chlamydia t
20	7	2.6	139	1 YB02_AERPE	O99113 chlamydia t
21	7	2.6	155	1 YIGI_ECOLI	O99113 chlamydia t
22	7	2.6	155	1 YIGI_ECOLI	O99113 chlamydia t
23	7	2.6	207	1 LOLE_ACTAC	O99113 chlamydia t
24	7	2.6	219	1 ERTL_ECOLI	O99113 chlamydia t
25	7	2.6	219	1 ERTL_ECOLI	O99113 chlamydia t
26	7	2.6	219	1 YGIX_ECOLI	O99113 chlamydia t
27	7	2.6	250	1 CHIT_DIOA	P52076 escherichia
28	7	2.6	273	1 SC65_YEAST	P80052 dioscorea j
29	7	2.6	300	1 VATI_HUMAN	P29478 saccharomyc
30	7	2.6	314	1 RPOA_HUMAN	O99536 homo sapien
31	7	2.6	316	1 Y034_TREPA	P20429 bacillus su
32	7	2.6	330	1 EXL2_HUMAN	O83077 treponema p
33	7	2.6	349	1 DIA2_MOUSE	O99566 mus musculu

34	7	2.6	352	1 RPBH_THIRE	P27166 thiobacillu
35	7	2.6	359	1 CILD_MOUSE	O99113 mus musculu
36	7	2.6	366	1 P53_PLAF	O12946 platichthys
37	7	2.6	379	1 YCCZ_ECOLI	P75881 escherichia
38	7	2.6	394	1 DXR_NEIMA	O99113 neisseria m
39	7	2.6	394	1 DXR_NEIMA	O99113 neisseria m
40	7	2.6	394	1 DXR_NEIMA	O99113 neisseria m
41	7	2.6	396	1 HIF1_ALCEU	P45805 alcaligenes
42	7	2.6	401	1 APA4_HUMAN	P06727 homo sapien
43	7	2.6	412	1 AATC_BOVIN	O28758 papio anubi
44	7	2.6	412	1 AATC_BOVIN	P33097 bos taurus
45	7	2.6	412	1 AATC_HORSE	P08906 equus cabal
46	7	2.6	412	1 AATC_MOUSE	P17174 homo sapien
47	7	2.6	412	1 AATC_MOUSE	P05201 mus musculu
48	7	2.6	412	1 AATC_PIG	P00503 sus scrofa
49	7	2.6	429	1 APA4_MACFA	P33621 macaca fasc
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51	7	2.6	473	1 PCC6_MYCTU	O10506 mycobacteri
52	7	2.6	476	1 PCCB_RHOER	O06101 rhodococcus
53	7	2.6	486	1 MYL_DROME	P49283 drosophila
54	7	2.6	504	1 FTSY_SYNY3	P73930 synochocyst
55	7	2.6	530	1 UDB2_RAT	P08541 rattus norv
56	7	2.6	534	1 FM2_ACTNA	O77741 sus scrofa
57	7	2.6	538	1 NRMI_PIG	P54645 rattus norv
58	7	2.6	548	1 AAK1_RAT	O95102 bison bison
59	7	2.6	548	1 NRMI_BISBI	O27981 bos taurus
60	7	2.6	548	1 NRMI_BOVIN	O27981 bos taurus
61	7	2.6	548	1 NRMI_BUBBU	P27946 bubalus bub
62	7	2.6	548	1 NRMI_CEREL	P56436 cervus elap
63	7	2.6	548	1 NRMI_MOUSE	P41251 mus musculu
64	7	2.6	548	1 NRMI_SHEEP	P49279 homo sapien
65	7	2.6	550	1 NRMI_HUMAN	P49282 mus musculu
66	7	2.6	568	1 NRMI_MOUSE	P49281 mus musculu
67	7	2.6	568	1 NRMI_MOUSE	P49282 mus musculu
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69	7	2.6	620	1 GG95_HUMAN	O08379 homo sapien
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71	7	2.6	653	1 CCME_RHOCA	O00500 rhodobacter
72	7	2.6	726	1 PIOL_BOVIN	O77568 bos taurus
73	7	2.6	790	1 SYFB_CHLAMU	O99113 chlamydia m
74	7	2.6	834	1 TFIIB_MOUSE	O62318 mus musculu
75	7	2.6	835	1 TFIIB_HUMAN	O13263 homo sapien

ALIGNMENTS

RESULT 1
APAL_HUMAN STANDARD; PRT; 267 AA.
ID APAL_HUMAN
AC P02647;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
RX MEDLINE=84221405; PubMed=6328445;
RA Sharpe C.R., Sidoli A., Shelley C.S., Lucero M.A., Shoulders C.C.,
RT Baralle F.E.;
RT "Human apolipoproteins AI, AII, CII and CIII. cDNA sequences and mRNA
abundance".
RL Nucleic Acids Res. 12:3917-3932(1984).
[2]
SEQUENCE FROM N.A.
RX MEDLINE=8502665; PubMed=6207999;
RA Sellmeier J.J., Procter A.A., Frossard P., Levy Wilson B.;
RT "Isolation and DNA sequence of full-length cDNA and of the entire

RT gene for human apolipoprotein AI -- discovery of a new genetic
RT polymorphism in the apo AI gene.";
RL DNA 3:309-317(1984).
RN [13]
RP SEQUENCE FROM N.A.
RX MEDLINE=63220822; PubMed=6406984;
RA Shoulters C.C., Kornblith A.R., Munro B.S., Baralle F.E.;
RT "Gene structure of human apolipoprotein AI.";
RL Nucleic Acids Res. 11:2827-2837(1983).
RN [14]
RP SEQUENCE FROM N.A.
RX MEDLINE=83220772; PubMed=6304641;
RA Chung P., Chan L.;
RT "Nucleotide sequence of cloned cDNA of human apolipoprotein A-I.";
RL Nucleic Acids Res. 11:3703-3715(1983).
RN [15]
RP SEQUENCE FROM N.A.
RX MEDLINE=84119464; PubMed=6198645;
RA Law S.W., Brewer H.B. Jr.;
RT "Nucleotide sequence and the encoded amino acids of human
apolipoprotein A-I mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:66-70(1984).
RN [16]
RP SEQUENCE FROM N.A.
RX MEDLINE=86008382; PubMed=2995392;
RA Law S.W., Brewer H.B. Jr.;
RT "Tangier disease. The complete mRNA sequence encoding for
preproapo-A-I.";
RL J. Biol. Chem. 260:12810-12814(1985).
RN [17]
RP SEQUENCE FROM N.A.
RX MEDLINE=84016011; PubMed=6413973;
RA Karathanasis S.K., Zannis V.I., Breslow J.L.;
RT "Isolation and characterization of the human apolipoprotein A-I
gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:6147-6151(1983).
RN [18]
RP SEQUENCE FROM N.A.
RX MEDLINE=89377481; PubMed=2673706;
RA Mogilivsky N., Roobol C., Loriau R., Guillaume J.P., Jacobs P.,
Cravador A., Herzog A., Brouwers L., Scarso A., Gilles P.,
Holmquist U., Carlson L.A., Bollen A.;
RT "Production of human recombinant proapolipoprotein A-I in Escherichia
coli: purification and biochemical characterization.";
RL DNA 8:429-436(1989).
RN [19]
RP SEQUENCE FROM N.A. (VARIANT TANGIER).
RX MEDLINE=88196137; PubMed=3129297;
RA Makrides S.C., Ruiz-Opazo N., Hayden M., Nussbaum A.L., Breslow J.L.,
Zannis V.I.;
RT "Sequence and expression of tangier apoA-I gene.";
RL Eur. J. Biochem. 173:465-471(1988).
RN [10]
RP SEQUENCE OF 118-267 FROM N.A.
RX MEDLINE=83091059; PubMed=6294659;
RA Breslow J.L., Ross D., McPherson J., Williams H.W., Kurnit D.,
Nussbaum A.L., Karathanasis S.K., Zannis V.I.;
RT "Isolation and characterization of cDNA clones for human
apolipoprotein A-I.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6861-6865(1982).
RN [11]
RP SEQUENCE OF 19-27.
RX MEDLINE=83256553; PubMed=6409108;
RA Brewer H.B. Jr., Fairwell T., Kay L., Meng M., Roman R., Law S.,
Light J.A.;
RT "Human plasma proapoA-I: isolation and amino-terminal sequence.";
RL Biochem. Biophys. Res. Commun. 113:626-632(1983).
RN [12]
RP SEQUENCE OF 25-267.
RX MEDLINE=78123731; PubMed=204308;
RA Brewer H.B. Jr., Fairwell T., Larue A., Roman R., Houser A.,
Bronzert T.J.;
RT "The amino acid sequence of human APOA-I, an apolipoprotein isolated

RT from high density lipoproteins.";
RL Biochem. Biophys. Res. Commun. 80:623-630(1978).
RN [13]
RP SEQUENCE OF 25-267.
RX MEDLINE=75133493; PubMed=164450;
RA Baker H.N., Gotto A.M. Jr., Jackson R.L.;
RT "The primary structure of human plasma high density apolipoprotein
glutamine I (APOA-I). II. The amino acid sequence and alignment of
cytogenetic bromide fragments IV, III, and I.";
RL J. Biol. Chem. 250:2725-2738(1975).
RN [14]
RP SEQUENCE OF 25-56.
RX MEDLINE=88331387; PubMed=3047770;
RA Yui Y., Aoyama T., Morishita H., Takahashi M., Takatsu Y., Kawai C.;
RT "Serum prostacyclin stabilizing factor is identical to apolipoprotein
A-I (Apo A-I). A novel function of Apo A-I.";
RL J. Clin. Invest. 82:803-807(1988).
RN [15]
RP SEQUENCE OF 25-48.
RX MEDLINE=89380318; PubMed=2506184;
RA Manjunath P., Marcel Y.L., Uma J., Seidah N.G., Chretien M.,
Chapelaine A.;
RT "Apolipoprotein A-I binds to a family of bovine seminal plasma
proteins.";
RL J. Biol. Chem. 264:16853-16857(1989).
RN [16]
RP SEQUENCE OF 25-43.
RX MEDLINE=88070603; PubMed=3120314;
RA Prioli R.P., Ordovas J.M., Rosenberg I., Schaeffer E.J.,
Perrella M.E.A.;
RT "Similarity of cruzin, an inhibitor of Trypanosoma cruzi
neuraminidase, to high-density lipoprotein.";
RL Science 238:1417-1419(1987).
RN [17]
RP SEQUENCE OF 25-42.
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
1994.";
RL Electrophoresis 15:1459-1465(1994).
RN [18]
RP PALMITOYLATION.
RX MEDLINE=86140194; PubMed=3005308;
RA Hoeg J.M., Meng M.S., Roman R., Fairwell T., Brewer H.B. Jr.;
RT "Human apolipoprotein A-I. Post-translational modification by fatty
acid acylation.";
RL J. Biol. Chem. 261:3911-3914(1986).
RN [19]
RP PROCESSING.
RX MEDLINE=83195100; PubMed=6405383;
RA Zannis V.I., Karathanasis S.K., Keutmann H.T., Goldberger G.,
Breslow J.L.;
RT "Intracellular and extracellular processing of human apolipoprotein
A-I: secreted apolipoprotein A-I isoprotein 2 is a propeptide.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2574-2578(1983).
RN [20]
RP STRUCTURE BY NMR OF 190-209.
RX MEDLINE=96270776; PubMed=8664326;
RA Wang G., Treleaven W.D., Cushley R.J.;
RT "Conformation of human serum apolipoprotein A-I(166-185) in the
presence of sodium dodecyl sulfate or dodecylphosphocholine by 1H-NMR
and CD. Evidence for specific peptide-SDS interactions.";
RL Biochim. Biophys. Acta 1301:174-184(1996).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (4.0 ANGSTROMS) OF 67-267.
RX MEDLINE=98024124; PubMed=9356442;
RA Borhani D.W., Rogers D.P., Engler J.A., Brouillette C.G.;
RT "Crystal structure of truncated human apolipoprotein A-I suggests a
lipid-bound conformation.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12291-12296(1997).
RN [22]
RP VARIANT MILANO.

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RX MEDLINE=83109095; PubMed=6401735;
RA Weisgraber K.H., Rall S.C. Jr., Bersot T.P., Mahley R.W.,
RA Franceschini G., Sirtori C.R.;
RT "Apolipoprotein A-III Milano. Detection of normal A-I in affected
RT subjects and evidence for a cysteine for arginine substitution in the
RT variant A-I."
RL J. Biol. Chem. 258:2508-2513(1983).
RN [23]
RP VARIANT TANGIER.
RX MEDLINE=83300108; PubMed=6412234;
RA Schmitz G., Assmann G., Rall S.C. Jr., Mahley R.W.;
RT "Tangier disease: defective recombination of a specific Tangier
RT apolipoprotein A-I isoform (pro-apo A-I) with high density
RT lipoproteins."
RL Proc. Natl. Acad. Sci. U.S.A. 80:6081-6085(1983).
RN [24]
RP VARIANT NORWAY.
RX MEDLINE=84289383; PubMed=6432779;
RA Rall S.C. Jr., Weisgraber K.H., Mahley R.W., Ogawa Y., Fielding C.J.,
RA Utermann G., Haas J., Steinmetz A., Menzel H.J., Assmann G.;
RT "Abnormal lecithin:cholesterol acyltransferase activation by a human
RT apolipoprotein A-I variant in which a single lysine residue is
RT deleted."
RL J. Biol. Chem. 259:10063-10070(1984).
RN [25]
RP SEQUENCE OF 25-107 (VARIANT IOWA).
RX MEDLINE=89050104; PubMed=3142462;
RA Nichols W.C., Dwyer F.E., Liepnieks J., Benson M.D.;
RT "Variant apolipoprotein AI as a major constituent of a human
RT hereditary amyloid."

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Query Match 100.0%; Score 267; DB 1; Length 267;
 Best Local Similarity 100.0%; Pred. No. 6.8e-251;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MKAAYLTAVLFTGSAHFHMOQDEPPSPMDRVKATVYVDVVKDGRVYVSFEGS 60
DB 1 MKAAYLTAVLFTGSAHFHMOQDEPPSPMDRVKATVYVDVVKDGRVYVSFEGS 60
QY 61 ALGKQNLKLLDNMDSVTSTFSKLRQLQPVYQEFWDNLEKEKEGLRQMSKDLFEVKAK 120
DB 61 ALGKQNLKLLDNMDSVTSTFSKLRQLQPVYQEFWDNLEKEKEGLRQMSKDLFEVKAK 120
QY 121 VQPYLDDFOKKQWEEMLYRQKVEPRALQEGAROKLHELOKSLPGEEMKRRARAHV 180
DB 121 VQPYLDDFOKKQWEEMLYRQKVEPRALQEGAROKLHELOKSLPGEEMKRRARAHV 180
QY 181 DALRTHLAPYSDLRORLAARLEALKENGARLAETFAHAKATHLSTLSKAPALDLRQ 240
DB 181 DALRTHLAPYSDLRORLAARLEALKENGARLAETFAHAKATHLSTLSKAPALDLRQ 240
QY 241 GLLPVLESFVSFLSALFEYTKKLNQ 267
DB 241 GLLPVLESFVSFLSALFEYTKKLNQ 267

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RESULT 2
 APAL_MACFA STANDARD; PRT; 267 AA.

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ID APAL_MACFA P17929;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Macaca fascicularis (Crap eating macaque) (Cynomolgus monkey), and
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541, 9557;
RN [1]
RP SEQUENCE FROM N.A.

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RC SPECIES=M.fascicularis;
RX MEDLINE=87191989; PubMed=3106152;
RA Pollen H.G., Melchior G.W., Castle C.K., Marotti K.R.;
RT "The primary structure of cynomolgus monkey apolipoprotein A-I
RT deduced from the cDNA sequence: comparison to the human sequence."
RL Gene 49:103-110(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.fascicularis;
RX MEDLINE=92305062; PubMed=1610902;
RA Murray R.W., Marotti K.R.;
RT "Nucleotide sequence of the cynomolgus monkey apolipoprotein A-I gene
RT and corresponding flanking regions."
RL Biochim. Biophys. Acta 1131:207-210(1992).
RN [3]
RP SEQUENCE OF 25-48.
RC SPECIES=M.fascicularis;
RX MEDLINE=87185451; PubMed=3105581;
RA Herbert P.N., Bauserman L.L., Lynch K.M., Saritelli A.L.,
RA Kantor M.A., Nicolosi R.J., Shulman R.S.;
RT "Homologues of the human C and A apolipoproteins in the Macaca
RT fascicularis (cynomolgus) monkey."
RL Biochemistry 26:1457-1463(1987).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas; TISSUE=Liver;
RX MEDLINE=89232739; PubMed=2907746;
RA Hixson J.E., Borenstein S., Cox L.A., Rainwater D.L., Vandenberg J.L.;
RT "The baboon gene for apolipoprotein A-I: characterization of a cDNA
RT clone and identification of DNA polymorphisms for genetic studies of
RT cholesterol metabolism."
RL Gene 74:483-490(1988).
RN [5]
RP SEQUENCE OF 1-10 FROM N.A.
RC SPECIES=M.fascicularis;
RA Sorci-Thomas M.;
RL Submitted (OCT-1991) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M15411; AAA36834.1; -
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DR EMBL; M35634; AAA35380.1; -
DR EMBL; M69223; AAA36831.1; -
DR PIR; A26529; A26529.
DR PIR; A26627; A26627.
DR PIR; J50079; J50079.
DR PIR; S23135; S23135.
DR HSSP; P02647; 1ODR.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 267
FT DOMAIN 68 267
FT REPEAT 68 89
FT REPEAT 90 111
FT REPEAT 112 122
FT REPEAT 112 122

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3 (HALF-LENGTH).

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FT REPEAT 145 166 5.
FT REPEAT 167 188 6.
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FT REPEAT 211 232 8.
FT REPEAT 233 243 9 (HALF-LENGTH).
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01-APR-1950 (rel. 14, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 30-MAY-2000 (Rel. 39, Last annotation update)
 Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Bos taurus (Bovine)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
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 RP SEQUENCE FROM N.A.
 RX MEDLINE=90348478; PubMed=2117227;
 RA O'Huigin C., Chan L., Li W.H.;
 RT "Cloning and sequencing of bovine apolipoprotein A-I cDNA and
 RT molecular evolution of apolipoproteins A-I and B-100.";
 RL Mol. Biol. Evol. 7:327-339(1990).
 RN (2)
 RP SEQUENCE OF 19-265.
 RX MEDLINE=92153895; PubMed=1739745;
 RA Sparrow D.A., Lee B.R., Laplaud M.P., Auboliron S., Beauchart D.,
 RA Chapman J.M., Gatto A.M., Jr., Yang C.Y., Sparrow J.T.;
 RT "Plasma lipid transport in the pre-ruminant calf, Bos spp: primary
 RT structure of bovine apolipoprotein A-I";
 RL Biochim. Biophys. Acta 1123:145-150(1992).
 RN (3)
 RP SEQUENCE OF 25-70.
 RX MEDLINE=90147795; PubMed=2105728;
 RA Auboliron S., Sparrow D.A., Beauchart L., Beauchart D., Sparrow J.T.,
 RA Laplaud M.P., Chapman J.M.;
 RT "Characterization and amino-terminal sequence of apolipoprotein AI
 RT from plasma high density lipoproteins in the pre-ruminant calf, Bos
 RT spp.";
 RL Biochim. Biophys. Res. Commun. 166:833-839(1990).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC -----
 DR EMBL: M35870; AAA30381.1; -;
 DR PIR: A34649; A34649.
 DR HSSP: P02647; 10DR.
 DR InterPro: IPR000074; Apolipoprotein.
 DR Pfam: PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 265
 FT DOMAIN 67 265
 FT REPEAT 67 88
 FT REPEAT 89 110
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 FT CONFLICT 265 AA; 30276 MM; 06A2681EA2ABA50F CRC64;
 SQ SEQUENCE

Query Match 7.9%; Score 21; DB 1; Length 265;
 Best local similarity 100.0%; Pred. No. 1e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VLTLAVLFTGSOARHFHFWOOD 25
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 Db 5 VLTLAVLFTGSOARHFHFWOOD 25
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 APAL_PIG STANDARD; PRT; 265 AA.
 ID APAL_PIG
 AC P18648;
 DT 01-NOV-1990 (rel. 16, Created)
 DT 01-FEB-1994 (rel. 28, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
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 RP SEQUENCE FROM N.A.
 RX MEDLINE=93224154; PubMed=8468059;
 RA Birchaauer A., Knipping G., Juritsch B., Aschauer H., Zechner R.;
 RT "Characterization of the apolipoprotein AI and CII genes in the
 RT domestic pig.";
 RL Genomics 15:643-652(1993).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX TISSUE=Liver, and Brain;
 RC MEDLINE=94125128; PubMed=8294940;
 RA Moeckel B., Zinke H., Flach R., Weiss B., Weller-Guettler H.,
 RA Gassen H.;
 RT "Expression of apolipoprotein A-I in porcine brain endothelium in
 RT vitro.";
 RL J. Neurochem. 62:788-798(1994).
 RN (3)
 RP SEQUENCE OF 34-265 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=90132667; PubMed=2105375;
 RA Weller-Guettler H., Sommerfeldt M., Pappadimitrakopoulou A., Mischek U.,
 RA Bonitz D., Frey A., Grupe M., Scherer J., Gassen H.G.;
 RT "Synthesis of apolipoprotein A-I in pig brain microvascular
 RT endothelial cells.";
 RL J. Neurochem. 54:444-450(1990).
 RN (4)
 RP SEQUENCE OF 105-265 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93154581; PubMed=8428656;
 RA Trieu V.N., Hasler-Rapacz J., Rapacz J., Black D.D.;
 RT "Sequences and expression of the porcine apolipoprotein A-I and C-II
 RT mRNAs.";
 RL Gene 123:173-179(1993).
 RN (5)
 RP SEQUENCE OF 25-265.
 RA Hasler-Rapacz J.O., Chaudhary R., Chowdhary B.P., Trieu V.N.,
 RA Jackson K., Gustavsson I., Rapacz J.;
 RL Submitted (OCT-1995) to the SWISS-PROT data bank.
 RN (6)
 RP SEQUENCE OF 25-34.
 RX MEDLINE=76184721; PubMed=178359;
 RA Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B., Jr.;
 RT "Characterization of the plasma lipoproteins and apolipoproteins of the
 RT Erythrocytus patas monkey.";
 RL Biochemistry 15:1928-1933(1976).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS. SYNTHESIZED PREDOMINANTLY IN THE INTESTINE AND THE
 CC LIVER.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----

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 CC or send an email to license@isb-sib.ch).

DR EMBL; L00626; AAA30992.1; -
 DR EMBL; X69477; CAA49234.1; -
 DR EMBL; X17057; -; NOT_ANNOTATED_CDS.
 DR EMBL; X59414; CAA42050.1; -
 DR PIR; J00704; J00704.
 DR PIR; A05311; A05311.
 DR PIR; A46018; A46018.
 DR PIR; S21830; S21830.
 DR PIR; S31394; S31394.
 DR HSSP; P02647; 10DR.
 DR InterPro; IPR000074; Apolipoprotein.
 DR Pfam; PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 265
 FT DOMAIN 67 265
 FT REPEAT 67 265
 FT REPEAT 89 110
 FT REPEAT 111 121
 FT REPEAT 122 142
 FT REPEAT 144 165
 FT REPEAT 166 187
 FT REPEAT 188 209
 FT REPEAT 210 230
 FT REPEAT 231 241
 FT REPEAT 242 265
 FT CONFLICT 108 108
 FT CONFLICT 143 143
 FT CONFLICT 173 173
 FT CONFLICT 180 180
 FT CONFLICT 185 186
 FT CONFLICT 209 209
 FT CONFLICT 224 224
 SQ SEQUENCE 265 AA; 30325 MW; 2C6E578318ECF69C CRC64;

Query Match 7.9%; Score 21; DB 1; Length 265;
 Best Local Similarity 100.0%; Pred. No. 1e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VLTAVLFLTGSQARHFWOOD 25
 DB 5 VLTAVLFLTGSQARHFWOOD 25

RESULT 8
 APAL_RAT STANDARD; PRT; 259 AA.
 AC P04639;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Apolipoprotein A-I precursor (Apo-AI).
 GN APOA1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-84207987; PubMed-6426956;
 RA Poncin J.E., Martial J.A., Gielen J.E.;
 RT "Cloning and structure analysis of the rat apolipoprotein A-I cDNA.";
 RL Eur. J. Biochem. 140:493-498(1984).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87008540; PubMed-3020028;
 RA Haddad I.A., Ordovas J.M., Fitzpatrick T., Karathanasis S.K.;
 RT "Linkage, evolution, and expression of the rat apolipoprotein A-I, C-
 RT I1, and A-IV genes."
 RL J. Biol. Chem. 261:13268-13277(1986).

RN [3]
 RP SEQUENCE OF 1-45.
 RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE-82098162; PubMed-6798036;
 RA Gordon J.I., Smith D.P., Andy R., Alpers D.H., Schonfeld G.,
 RA Strauss A.W.;
 RT "The primary translation product of rat intestinal apolipoprotein A-I
 RT mRNA is an unusual preprotein."
 RL J. Biol. Chem. 257:971-978(1982).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.

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DR EMBL; M00001; AAA40749.1; -
 DR EMBL; X00538; CAA25224.1; -
 DR EMBL; J02597; AAA40745.1; -
 DR PIR; A24700; A24700.
 DR HSSP; P02647; 1AV1.
 DR InterPro; IPR000074; Apolipoprotein.
 DR Pfam; PF01442; Apolipoprotein; 1.
 KW Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 259
 FT DOMAIN 67 259
 FT REPEAT 67 88
 FT REPEAT 89 110
 FT REPEAT 111 121
 FT REPEAT 122 143
 FT REPEAT 144 161
 FT REPEAT 162 183
 FT REPEAT 184 203
 FT REPEAT 204 225
 FT REPEAT 226 237
 FT REPEAT 237 259
 FT CONFLICT 201 201
 FT CONFLICT 214 214
 FT CONFLICT 218 218
 SQ SEQUENCE 259 AA; 30088 MW; 2E8D5B45FEAE88 CRC64;

Query Match 4.5%; Score 12; DB 1; Length 259;
 Best Local Similarity 100.0%; Pred. No. 0.0053;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 47 KDSGRVYSQFE 58
 DB 46 KDSGRVYSQFE 57

RESULT 9
 APAL_MOUSE STANDARD; PRT; 264 AA.
 ID APAL_MOUSE

AC Q00623: (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92281682; PubMed=1596360;
RA Stoffel W., Mueller R., Binček E., Hofmann K.;
RT "Mouse apolipoprotein AI. cDNA-derived primary structure, gene
RT organisation and complete nucleotide sequence.";
RL Biol. Chem. Hoppe-Seyler 373:187-193(1992).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93122774; PubMed=1478650;
RA Tanuzzi J.L., Azrolan N., O'Connell A., Aalto-Setälä K., Breslow J.L.;
RT "Characterization of the mouse apolipoprotein ApoA-1/Apoc-3 gene
RT locus: genomic, mRNA, and protein sequences with comparisons to other
RT species.";
RL Genomics 14:1081-1088(1992).
- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC - SUBCELLULAR LOCATION: Extracellular.
CC - TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
CC CHYLOMICRONS.
CC - SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC -----
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CC -----
DR EMBL: X64262; CAA45560.1; -;
DR EMBL: X64263; CAA45561.1; -;
DR EMBL: L04149; -, NOT_ANNOTATED_CDS.
DR EMBL: L04151; -, NOT_ANNOTATED_CDS.
DR PIR: S22420; S22420.
DR PIR: A44364; A44364.
DR HSSP: P02647; 1AV1.
DR SWISS-2DPAGE: Q00623; MOUSE.
DR MGD: MGI:88049; APOA1.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein; 1.
KW Plasma; Lipid transport; HDL; cholesterol metabolism; Repeat; Signal.
KW STGMAL; 1
FT PROPE 19 24
FT CHAIN 25 264
FT DOMAIN 67 264
FT REPEAT 67 88
FT REPEAT 89 110
FT REPEAT 111 121
FT REPEAT 122 143
FT REPEAT 144 165
FT REPEAT 166 187
FT REPEAT 188 207
FT REPEAT 208 229
FT REPEAT 230 240
FT REPEAT 241 264
FT REPEAT 264 264
SQ SEQUENCE 264 AA; 30587 MW; C45F5F2019634AAC CRC64;

	Matches	12; Conservative	0; Mismatches	0; Indels	0; Gaps
QY	47	KDSGRDYSQFE 58			
Db	46	KDSGRDYSQFE 57			

RESULT	10	
APAL_ANAPL		
ID	APAL_ANAPL	STANDARD;
		PRT;
		264 AA

DT 15 JUN-1998 (Rel. 36, Created)
DT 15-JUN-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).

05 Anas platyrhynchos (domestic duck).
0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
0C Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
0X NCBI_TaxID=8839;

RP SEQUENCE FROM N.A.
RC STRAIN-PEKIN BREED; TISSUE-Liver;
RA Chen B., Lu X., Wang K., Xue H., Zeng W., Zhu D., Chi L.
RL Submitted (JAN-1997) to the ENBL/Genbank/DBD databases.

CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT BY PROMOTING
CC CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR
CC THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC

CC -I- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO
CC CHYLOMICRONS.
CC -I- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY
CC -----
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CC -----
DR EMRL; U86131; AAR64381.1; -.
DR HSSP; P02647; IODR.
DR InterPro; IPR000074; Apolipoprotein.
DR -----

DR	PFam:	APolipoprotein: 1.
KM	Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat.	
FT	SIGNAL	1
FT	PROPEP	19
FT	CHAIN	25
		264
		APOLIPOPROTEIN A-1.

FT	DOMAIN	67	264	10 X APPROXIMATE
FT	REPEAT	67	88	1.
FT	REPEAT	89	110	2.
FT	REPEAT	111	121	3 (HALF-LENGTH)
FT	REPEAT	122	143	4.

FT	REPEAT	144	165	5.
FT	REPEAT	166	187	6.
FT	REPEAT	188	209	7.
FT	REPEAT	210	231	8.
FT	REPEAT	232	242	9 (HALF-LENGTH)

FT	REPEAT	243	264	10.	
SQ	SEQUENCE	264	AA;	30659	MM; 7546F4BAF846500 CRC64,
Query Match		3.7%; Score 10; DB 1; Length			

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Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 187 LAFYSDLRQ 196
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Query Match	4.5%;	Score 12;	DB 1;	Length 264;
Best Local Similarity	100.0%;	Pred. No.	0.00054;	

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RESULT 11
APAL_CHICK STANDARD: PRT: 264 AA.
AC P08250;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88049703; PubMed=3118875;
RA Byrnes L., Luo C.-C., Li W.-H., Yang C.-Y., Chan L.;
RT "Chicken apolipoprotein A-I: cDNA sequence, tissue expression and
RT evolution."
RL Biochem. Biophys. Res. Commun. 148:485-492(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88152500; PubMed=3126099;
RA Ferrari S., Tarugi P., Drusiani E., Calandra S., Fregni M.;
RT "The complete sequence of chick apolipoprotein AI mRNA and its
RT expression in the developing chick."
RL Gene 60:39-46(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87222301; PubMed=3108248;
RA Rajavashisth T.B., Dawson P.A., Williams D.L., Shackelford J.E.,
RA Leberer H., Lusis A.J.;
RT "Structure, evolution, and regulation of chicken apolipoprotein A-I."
RL J. Biol. Chem. 262:7058-7065(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92381402; PubMed=1512510;
RA Lamou Rava S., Sastre R., Ferrari S., Rajavashisth T.B.,
RA Lusis A.J., Karathanasis S.K.;
RT "Evolutionary distinct mechanisms regulate apolipoprotein A-I gene
RT expression: differences between avian and mammalian apoA-I gene
RT transcription control regions."
RL J. Lipid Res. 33:831-842(1992).
RN [5]
RP SEQUENCE OF 25-44.
RX MEDLINE=83213468; PubMed=6406496;
RA Shackelford J.E., Leberer H.G.;
RT "Synthesis and secretion of apolipoprotein AI by chick breast
RT muscle."
RL J. Biol. Chem. 258:7175-7180(1983).
RN [6]
RP FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
RN CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
RN THE EFFLUX OF CHOLESTEROL AND BY ACTING AS A COFACTOR FOR
RN THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
RN [7]
RP SUBCELLULAR LOCATION: Extracellular.
RN [8]
RP TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
RN CHYLOMICRONS.
RN [9]
RP SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
RN [10]
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RN [11]
RN EMBL: M17961; AAA48593.1; -
RN EMBL: M18746; AAA48594.1; -
RN EMBL: M25559; AAA48592.1; -
RN EMBL: M96012; AAA48597.1; -
RN PIR: S01453; LPCHAL.

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DR PIR: JH0471; JH0471.
DR HSSP: P02647; 1ODR.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein: 1.
DR KEGG: Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 264
FT DOMAIN 67 264
FT REPEAT 67 88
FT REPEAT 89 110
FT REPEAT 111 121
FT REPEAT 122 143
FT REPEAT 144 165
FT REPEAT 166 187
FT REPEAT 188 209
FT REPEAT 210 231
FT REPEAT 232 242
FT REPEAT 243 264
FT CONFLICT 16 264
FT CONFLICT 148 148
FT SEQUENCE 264 AA; 30680 MW; 968320E81E2AC5C2 CRC64;

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Query Match 3.7%; Score 10; DB 1; Length 264;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 187 LAPSDELRLQ 196
Db 186 LAPSDELRLQ 195

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RESULT 12
APAL_COTYA STANDARD: PRT: 264 AA.
AC P32918;
DT 01-OCT-1993 (Rel. 27, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN APOA1.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=97212027; PubMed=9058967;
RA Oku H., Toda T., Nagata J., Ishikawa M., Neyazaki K., Shinjyo C.,
RA Chinen I.;
RT "Apolipoprotein A-1 of Japanese quail: cDNA sequence and modulation of
RT tissue expression by cholesterol feeding."
RL Biosci. Biotechnol. Biochem. 61:286-290(1997).
RN [2]
RP SEQUENCE OF 25-60.
RX MEDLINE=93213845; PubMed=8461329;
RA Oku H., Ishikawa M., Nagata J., Toda T., Chinen I.;
RT "Lipoprotein and apoprotein profile of Japanese quail."
RL Biochim. Biophys. Acta 1167:22-28(1993).
RN [3]
RP FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
RN CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
RN THE EFFLUX OF CHOLESTEROL AND BY ACTING AS A COFACTOR FOR
RN THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
RN [4]
RP SUBCELLULAR LOCATION: Extracellular.
RN [5]
RP TISSUE SPECIFICITY: MAJOR PROTEIN OF VLDL, HDL, LDL AND IN
RN CHYLOMICRONS. EXPRESSED IN A NUMBER OF TISSUES INCLUDING LIVER,
RN SMALL INTESTINE, LUNG, KIDNEY, HEART AND MUSCLE WITH HIGHEST
RN EXPRESSION IN LIVER AND SMALL INTESTINE.
RN [6]
RP SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
RN [7]

```

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CC -----
 CC EMBL: D85133; BAA12729.1; -
 CC HSSP: P02647; 1GM4.
 CC InterPro: IPR000074; Apolipoprotein.1.

DR Pfam; PF01442; Apolipoprotein.1.
 DR Plasma; Lipid transport; HDL; Cholesterol metabolism; Repeat; Signal.

FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 264
 FT DOMAIN 67 264
 FT REPEAT 89 110
 FT REPEAT 111 121
 FT REPEAT 122 143
 FT REPEAT 144 165
 FT REPEAT 166 187
 FT REPEAT 188 209
 FT REPEAT 210 231
 FT REPEAT 232 242
 FT REPEAT 243 264
 FT SEQUENCE 264 AA; 30753 MW; 8781DE213C3F863F CRC64;

Query Match 3.4%; Score 9; DB 1; Length 264;
 Best Local Similarity 100.0%; Pred. No. 0.43; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TLAVLELFG 15
 |||||
 DB 7 TLAVLELFG 15

RESULT 13
 ID APAL_ERYPA STANDARD; PRT; 20 AA.
 AC P18647;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Apolipoprotein A-I (Apo-AI) (Fragment).
 GN APOA1.
 OS Erythrocytus patas (Red guenon) (Hussar).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Erythrocytus.
 CC NCBI_TaxID=9538;
 CC [1]
 CC SEQUENCE.
 CC MEDLINE=76184721; PubMed=178359;
 CC Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;
 CC "Characterization of the plasma lipoproteins and apoproteins of the
 CC Erythrocytus patas monkey".
 CC Biochemistry 15:1928-1933(1976).
 CC -1- FUNCTION: APOA-1 PARTICIPATES IN THE REVERSE TRANSPORT OF
 CC CHOLESTEROL EFFLUX FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING
 CC THE LECTININ CHOLESTEROL ACYLTRANSFERASE (LCAT).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN
 CC CHYLOMICRONS.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC PIR: A05313; A05313.
 CC Plasma; Lipid transport; HDL; Cholesterol metabolism.
 FT NON_TER 20 20
 FT SEQUENCE 20 AA; 2387 MW; 9C970997C7FC976A CRC64;

Query Match 3.0%; Score 8; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 PWDVRVKDL 38
 |||||
 DB 7 PWDVRVKDL 14

RESULT 14
 ID APE_PIG STANDARD; PRT; 317 AA.
 AC P18650; O19099;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Apolipoprotein E precursor (Apo-E).
 GN APOE.
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CC NCBI_TaxID=9823;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC TISSUE=Liver;
 CC Brzozowska A.M., Grimholt U., Kulseth M.A., Wold I., Rognes S.;
 CC Submitted (May-1993) to the EMBL/Genbank/DBJ databases.
 CC [2]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=98347372; PubMed=9682450;
 CC Ramascondar J.J., Rucker E.B., Vasquez J.C., Gallagher D.S.,
 CC Grimm D.R., Lunney J.K., Schook L.B., Piedrahita J.A.;
 CC "Isolation and genetic characterization of the porcine apolipoprotein
 CC E gene".
 CC Anim. Genet. 29:43-47(1998).
 CC [3]
 CC PRELIMINARY SEQUENCE OF 19-31.
 CC MEDLINE=81021043; PubMed=7417263;
 CC Weisgraber K.H., Troxler R.F., Rall S.C., Mahley R.W.;
 CC "Comparison of the human, canine and swine E apoproteins".
 CC Biochem. Biophys. Res. Commun. 95:374-380(1980).
 CC -1- FUNCTION: APO-E MEDIATES BINDING, INTERNALIZATION, AND CATABOLISM
 CC OF LIPOPROTEIN PARTICLES. IT CAN SERVE AS A LIGAND FOR THE LDL(APO
 CC B/E) RECEPTOR AND FOR THE SPECIFIC APO-E RECEPTOR (CHYLOMICRON
 CC REMNANT) OF HEPATIC TISSUES.
 CC -1- SUBCELLULAR LOCATION: SECRETED IN PLASMA.
 CC -1- TISSUE SPECIFICITY: SECRETED IN PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----
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FT REPEAT 79 100 1.
 FT REPEAT 101 122 2.
 FT REPEAT 123 144 3.
 FT REPEAT 145 166 4.
 FT REPEAT 167 188 5.
 FT REPEAT 189 210 6.
 FT REPEAT 211 232 7.
 FT REPEAT 233 254 8.
 FT CONFLICT 35 35 S -> P (IN REF. 2).
 FT CONFLICT 160 161 NV -> KL (IN REF. 2).
 FT CONFLICT 166 166 V -> L (IN REF. 2).
 FT CONFLICT 251 252 DE -> EQ (IN REF. 2).
 FT CONFLICT 273 273 A -> G (IN REF. 2).
 FT CONFLICT 275 275 Q -> H (IN REF. 2).
 FT CONFLICT 277 277 R -> L (IN REF. 2).
 FT CONFLICT 289 289 M -> I (IN REF. 2).
 FT CONFLICT 303 303 M -> G (IN REF. 2).
 SO SEQUENCE 317 AA, 36599 MW, 83EF7F51A07785055 CRC64,

Query Match 3.0%; Score 8; DB 1; Length 317;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 87 QGCPYQOE 94
 1111111111
 Db 98 QGCPYQOE 105

RESULT 15
 ID APA_MOUSE STANDARD: PRT: 395 AA.
 AC P06728;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV).
 GN APOA4
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87089722; PubMed=3796595;
 RA Williams S.C., Bruckheimer S.M., Lusis A.J., Leboeuf R.C.,
 RA Kimbrough A.J.,
 RT "Mouse apolipoprotein A-IV gene: nucleotide sequence and induction by
 RT a high-lipid diet.";
 RL Mol. Cell. Biol. 6:3807-3814(1986).
 RN [2]
 RP REVISIONS.
 RA Kimbrough A.J.,
 RL Submitted (DEC-1986) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J, AND 129/T;
 RX MEDLINE=91286309; PubMed=1648102;
 RA Reue K., Leete T.H.,
 RT "Genetic variation in mouse apolipoprotein A-IV due to insertion and
 RT deletion in a region of tandem repeats.";
 RL J. Biol. Chem. 266:12715-12721(1991).
 CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
 CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
 CC LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
 CC COMPONENT OF HDL AND CHYLOMICRONS.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SECRETED IN PLASMA.
 CC -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
 CC 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
 CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
 CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
 CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL

CC ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
 CC -1- POLYMORPHISM: THERE IS A POLYMORPHISM WITHIN A SERIES OF IMPERFECT
 CC REPEATS ENCODING THE SEQUENCE E-Q-[AV]-Q. INSERTIONS OR DELETIONS
 CC OF 12 NUCLEOTIDES HAVE GIVEN RISE TO THREE FORMS CHARACTERIZED BY
 CC THREE (129), FOUR (C57BL/6), OR FIVE (M.CASTANEUS) COPIES OF THE
 CC REPEAT UNIT.
 CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
 CC -----
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 CC -----
 CC DR EMBL: M13966; AAA37253.1; -;
 CC DR EMBL: M64249; AAA37215.1; -;
 CC DR EMBL: M64248; AAA37214.1; -;
 CC DR PIR: A25281; A25281.
 CC DR MGI: 88051; APOA4.
 CC DR InterPro: IPR000074; Apolipoprotein.
 CC DR Pfam: PF01442; Apolipoprotein; 1.
 CC KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal;
 CC KW Polymorphism.
 CC FT SIGNAL 1 20
 CC FT CHAIN 21 395
 CC FT DOMAIN 33 330
 CC FT REPEAT 33 54
 CC FT REPEAT 60 81
 CC FT REPEAT 82 103
 CC FT REPEAT 115 136
 CC FT REPEAT 137 158
 CC FT REPEAT 159 180
 CC FT REPEAT 181 202
 CC FT REPEAT 203 224
 CC FT REPEAT 225 246
 CC FT REPEAT 247 268
 CC FT REPEAT 269 286
 CC FT REPEAT 287 308
 CC FT REPEAT 309 330
 CC FT DOMAIN 366 389
 CC FT VARIANT 382 385
 CC FT CONFLICT 15 15 MISSING (IN SOME STRAINS).
 CC FT CONFLICT 63 63 MISSING (IN REF. 1).
 CC FT CONFLICT 207 207 O -> K (IN REF. 1).
 CC FT CONFLICT 288 288 E -> R (IN REF. 1).
 CC FT CONFLICT 294 295 S -> A (IN REF. 1).
 CC FT CONFLICT 295 295 RQ -> KA (IN REF. 1).
 CC FT CONFLICT 315 316 NK -> GG (IN REF. 1).
 CC SO SEQUENCE 395 AA, 45029 MW, 5FE27D0236226257 CRC64;

Query Match 3.0%; Score 8; DB 1; Length 395;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KAAVLTIA 9
 1111111111
 Db 4 KAAVLTIA 11

RESULT 16
 ID UBR1_YEAST STANDARD: PRT: 1950 AA.
 AC P19812;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE N-end-recognition protein (Ubiquitin-protein ligase E3 component) (N-
 DE recognin).
 GN UBR1 OR PPR1 OR YGR184C OR G7168.
 OS Saccharomyces cerevisiae (baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=5288C / GRP88;
 RA MEDLINE=91006011; PubMed=2209542;
 RA Bartel B., Wuenning I., Varshavsky A.;
 RT "The recognition component of the N-end rule pathway."
 RT EMBO J. 9:3179-3189(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C.
 RC MEDLINE=91279231; PubMed=9133739;
 RA Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez-Perez M.,
 RA Nombela C.;
 RT "DNA sequence analysis of a 23,002 bp DNA fragment of the right arm
 RT of Saccharomyces cerevisiae chromosome VII.";
 RT Yeast 13:357-363(1997).
 RN [3]
 RP SEQUENCE OF 346-1950 FROM N.A.
 RP Hebling U., Hofmann B., Dellus H.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECOGNITION COMPONENT OF THE N-END RULE PATHWAY. BINDS
 CC TO PROTEINS BEARING AMINO-TERMINAL RESIDUES THAT ARE DESTABILIZING
 CC ACCORDING TO THE N-END RULE, BUT DOES NOT BIND TO OTHERWISE
 CC IDENTICAL PROTEINS BEARING STABILIZING AMINO-TERMINAL RESIDUES.
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 CC -----
 DR EMBL: X53747; CAA37779.1; -;
 DR EMBL: X99074; CAA67528.1; -;
 DR EMBL: 272969; CAA97210.1; -;
 DR PIR: S12332; S12332.
 DR SGD: S0003416; UBR1.
 DR InterPro: IPR003126; ZNF-UBR1.
 DR InterPro: IPR001841; Znf-ubrl.
 DR Pfam: PF02207; zf-UBR1; 1.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00396; Znf-UBR1; 1.
 DR LIGase: Ubiquitin conjugation.
 SQ SEQUENCE 1950 AA; 224836 MW; 33FACD3A031AF523 CRC64;

Query Match 3.0%; Score 8; DB 1; Length 1950;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 202 LEALKENG 209
 DB 1277 LEALKENG 1284
 RESULT 17
 RS16_CHLNU STANDARD; PRT; 116 AA.
 ID RS16_CHLNU
 AC Q9PL13;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 30S ribosomal protein S16.
 DE RPS16 OR TC0295.
 GN RPS16 OR TC0295.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=Mopn / N199;

RA MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Uitterbeck T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwin M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
 RT pneumoniae AR39";
 RT Nucleic Acids Res. 28:1397-1406(2000).
 RN [1]
 RP SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 DR EMBL: AE002297; AAF73544.1; -;
 DR TIGR: TC0295; -;
 DR InterPro: IPR000307; Ribosomal_S16.
 DR Pfam: PF00886; Ribosomal_S16; 1.
 DR PROSITE: PS00732; RIBOSOMAL_S16; FALSE_NEG.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 116 AA; 13452 MW; 298132809F2C5011 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 195 RORLAR 201
 DB 103 RORLAR 109
 RESULT 18
 RS16_CHLNU STANDARD; PRT; 116 AA.
 ID RS16_CHLNU
 AC O84029;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 30S ribosomal protein S16.
 DE RPS16 OR RS16 OR CF026.
 GN RPS16 OR RS16 OR CF026.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=D/uv-3/CX;
 RC MEDLINE=99000809; PubMed=9784136;
 RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RT "Genome sequence of an obligate intracellular pathogen of humans:
 RT Chlamydia trachomatis";
 RT Science 282:754-759(1998).
 CC -1- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 DR EMBL: AE001277; AAC67616.1; -;
 DR HSSP: P80379; IEMW.
 DR InterPro: IPR000307; Ribosomal_S16.
 DR Pfam: PF00886; Ribosomal_S16; 1.

DR PROSITE; PS00732; RIBOSOMAL_S16; FALSE_NEG.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 116 AA; 13409 MW; 29813291EB44721 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 195 RORLAAR 201
 |||||
 DB 103 RORLAAR 109

RESULT 19
 TRMA_LACLA STANDARD; PRT; 132 AA.
 AC 09RTA4;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Thermo-resistant insertional mutant protein A.
 GN TRMA OR NRPR OR IL0675.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis), and
 OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Lactococcus.
 RX NCBI_TaxID=1360, 1359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=L.lactis; STRAIN=IL1403;
 RA MEDLINE=21235186; PubMed=11374771;
 RA Boletín A., Wincker P., Manger S., Jallón O., Malarme K.,
 RA Weissbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis ssp. lactis IL1403".
 RL Genome Res. 11:731-753(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=L.l.cremoris; STRAIN=MG1363;
 RX MEDLINE=99157588; PubMed=10048028;
 RA Duwat P., Ehrlich S.D., Gruss A.;
 RT "Effects of metabolic flux on stress response pathways in Lactococcus
 RT lactis".
 RL Mol. Microbiol. 31:845-858(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=L.l.cremoris; STRAIN=MG1363;
 RA Frees D., Ingmer H.T.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE ARSC FAMILY.
 CC
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 CC -----
 DR EMBL; AE006301; AAK04773.1; -;
 DR EMBL; AF058950; AAG43111.1; -;
 DR EMBL; AF028804; AAG37358.1; -;
 KM Oxidoreductase; Complete proteome.
 SQ SEQUENCE 132 AA; 15030 MW; F63EBAB8204136B3 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 132;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 207 ENGGAARL 213
 |||||

DB 122 ENGGAARL 128

RESULT 20
 YB02_AERPE STANDARD; PRT; 139 AA.
 ID YB02_AERPE
 AC 09YD10;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein APE1102.
 GN APE1102.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Desulfurococcaceae; Desulfurococcaceae;
 OC Aeropyrum.
 RX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anai A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.,
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1".
 RL DNA Res. 6:83-101(1999).
 RN [2]
 CC -1- SIMILARITY: BELONGS TO THE UPF0129 FAMILY.
 CC
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 CC -----
 DR EMBL; AP000060; BAA80087.1; -;
 DR InterPro; IPR002851; DUF133.
 DR Pfam; PF02000; DUF133; 1.
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 139 AA; 14804 MW; 0F16DEDDC88686 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 139;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 196 ORLAARL 202
 |||||
 DB 120 ORLAARL 126

RESULT 21
 YIGI_ECOLI STANDARD; PRT; 155 AA.
 ID YIGI_ECOLI
 AC P27845; P76761;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein yigI.
 GN YIGI OR B3820.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=92358234; PubMed=1379743;
 RA Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;

RT "Analysis of the Escherichia coli genome: DNA sequence of the region
 RT from 84.5 to 86.5 minutes."
 RL Science 257:771-778(1992).
 RN [2]
 RP REVISION TO 96.
 RC STRAIN-K12 / MG1655;
 RA MEDLINE=9742617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RA Chiori H.;
 RL Submitted (JAN-1993) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-42 FROM N.A.
 RX MEDLINE=85157492; PubMed=6397464;
 RA Homma H., Kobayashi T., Chiba N., Karasawa K., Mizushima H., Kudo I.,
 RA Inoue K., Ikeda H., Sekiguchi M., Nojima S.;
 RT "The DNA sequence encoding pldA gene, the structural gene for
 RT detergent-resistant phospholipase A of E. coli";
 RL J. Biochem. 96:1655-1664(1984).
 CC -----
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 CC -----
 DR EMBL: M87049; AAA67616.1; ALT_INIT.
 DR EMBL: AE000457; AAC76823.1; ALT_INIT.
 DR EMBL: U02122; AAD15042.1; ALT_INIT.
 DR EMBL: X02143; -; NOT_ANNOTATED_CDS.
 DR PIR: S30710; S30710.
 DR PIR: S30747; S30747.
 DR Ecogene: EG11467; Y1G1.
 DR InterPro: IPR003736; DUF157.
 DR Pfam: PF02584; DUF157; 1.
 DR Hypothetical protein; Complete proteome.
 KW CONFLICT 96 L -> V (IN REF. 1).
 FT CONFLICT 96
 SQ SEQUENCE 155 AA; 17163 MW; 96790B719B1E0609 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 155;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 192 DELRORL 198
 DB 90 DELRORL 96
 |||||||

RESULT 22
 Y1G1_SALTY STANDARD; PRT; 155 AA.
 AC P40725; O9L6P0;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein Y1G1.
 GN Y1G1 OR STM3956 OR STM31.34 OR STY3603.
 OS Salmonella typhimurium, and
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxId=602, 601;
 RN [1]

RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvanev E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2."
 RL Nature 413:852-856(2001).
 RN [2]
 RP SEQUENCE OF 1-25 FROM N.A.
 RC SPECIES=S.typhimurium;
 RX MEDLINE=94131966; PubMed=8300539;
 RA Brok R.G.P.M., Brinkman E., van Bortel R., Bekkers A.C.A.P.,
 RA Verheij H.M., Tommassen J.;
 RT "Molecular characterization of enterobacterial pldA genes encoding
 RT outer membrane phospholipase A."
 RL J. Bacteriol. 176:861-870(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhi; STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagals K.,
 RA Krog A., Larsen T.S., Leather S., Moulé S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skellern J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18."
 RL Nature 413:848-852(2001).
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 CC -----
 DR EMBL: AF233324; AAF3436.1; -;
 DR EMBL: AE000884; AAL2800.1; ALT_INIT.
 DR EMBL: X76900; -; NOT_ANNOTATED_CDS.
 DR EMBL: AL627278; CAD07936.1; -;
 DR StGene: SG10461; Y1G1.
 DR Hypothetical protein; Complete proteome.
 KW StGene; SG10461; Y1G1.
 SQ SEQUENCE 155 AA; 17043 MW; 546D5A3840701F2B CRC64;

Query Match 2.6%; Score 7; DB 1; Length 155;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 192 DELRORL 198
 DB 90 DELRORL 96
 |||||||

RESULT 23
 LOLB_ACTAC STANDARD; PRT; 207 AA.
 ID LOLB_ACTAC
 AC O52727;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Outer membrane lipoprotein lolB precursor.
 GN LOLB OR HEMM.
 OS Actinobacillus actinomycetemcomitans (Haemophilus
 OS actinomycetemcomitans).

CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Actinobacillus;
 CC NCBI_TaxID=714;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN-SUNY 465;
 CC Mintz K.P.;
 CC Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PLAYS A CRITICAL ROLE IN THE INCORPORATION OF
 CC LIPID PROTEINS IN THE OUTER MEMBRANE AFTER THEY ARE RELEASED BY
 CC THE LOA PROTEIN (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
 CC anchor (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE LOA FAMILY.
 CC -1- CAUTION: WAS ORIGINALLY THOUGHT TO BE INVOLVED IN DELTA-
 CC AMINOEVULINIC ACID BIOSYNTHESIS.
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 CC -----
 CC EMBL: AF045460; AAC04857.1;
 CC DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
 CC KW Chaperone; Outer membrane; Lipoprotein; Transport; Protein transport;
 CC Signal.
 CC FT SIGNAL 1 19 BY SIMILARITY.
 CC FT CHAIN 20 207 OUTER-MEMBRANE LIPOPROTEIN LOA.
 CC FT LIPID 20 20 N-ACYL DIGLYCERIDE (BY SIMILARITY).
 CC FT SEQUENCE 207 AA; 24219 MW; 5CE534F72F0C8B8D CRC64;
 CC
 CC Query Match 2.6%; Score 7; DB 1; Length 207;
 CC Best Local Similarity 100.0%; Pred. No. 30;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 8 LAVLELT 14
 CC ID EUTL_ECOLI
 CC ID EUTL_ECOLI STANDARD: PRT; 219 AA.
 CC AC P76541;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Ethanolamine utilization protein eutL.
 CC GN EUTL OR B2439.
 CC OS Escherichia coli.
 CC OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC OC Escherichia.
 CC OX NCBI_TaxID=562;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-K12 / MG1655;
 CC RA MEDLINE=97426617; PubMed=9278503;
 CC RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 CC RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
 CC RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 CC RA Mau B., Shao Y.;
 CC RT "The complete genome sequence of Escherichia coli K-12.";
 CC RL Science 277:1453-1474(1997).
 CC CC -1- FUNCTION: MAY BE INVOLVED IN THE FORMATION OF A SPECIFIC
 CC MICROCOMPARTMENT IN THE CELL IN WHICH THE METABOLISM OF
 CC POTENTIALLY TOXIC BY-PRODUCTS TAKES PLACE.
 CC CC -1- PATHWAY: ETHANOLAMINE UTILIZATION.
 CC CC -1- SIMILARITY: DISTANTLY RELATED TO THE CCHA/CKMK/CSOSI/PDUA FAMILY.
 CC -----

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 CC -----
 CC EMBL: AE000331; AAC75492.1;
 CC DR Ecogene: EGI4171; eutL.
 CC KW Complete proteome.
 CC SEQUENCE 219 AA; 22788 MW; 1A5417565256243E CRC64;
 CC
 CC Query Match 2.6%; Score 7; DB 1; Length 219;
 CC Best Local Similarity 100.0%; Pred. No. 32;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 12 FLTGSQA 18
 CC ID EUTL_SALTY
 CC ID EUTL_SALTY STANDARD: PRT; 219 AA.
 CC AC Q92FV9;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 01-MAR-2002 (Rel. 41, Last sequence update)
 CC DE Ethanolamine utilization protein eutL.
 CC GN EUTL OR STM2456 OR STY2693.
 CC OS Salmonella typhimurium, and
 CC OS Salmonella typhi.
 CC OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC OC Salmonella.
 CC OX NCBI_TaxID=602, 601;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES-S. typhimurium; STRAIN=LT2;
 CC RA MEDLINE=99355039; PubMed=10464203;
 CC RA Kofoid E.C., Rappleye C.A., Stojiljkovic I., Roth J.R.;
 CC RT "The 17-gene ethanolamine (eut) operon of Salmonella typhimurium
 CC RT encodes five homologues of carboxysome shell proteins.";
 CC RL J. Bacteriol. 181:5317-5329(1999).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES-S. typhimurium; STRAIN=LT2 / SSGC1412 / ATCC 700720;
 CC RA MEDLINE=21534948; PubMed=11677609;
 CC RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 CC RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 CC RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 CC RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 CC RA Waterston R., Wilson R.K.;
 CC RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 CC RT LT2.";
 CC RL Nature 413:852-856(2001).
 CC RN [3]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES-S. typhi; STRAIN=CT18;
 CC RA MEDLINE=21534947; PubMed=11677608;
 CC RA Parikh H.J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 CC RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 CC RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 CC RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 CC RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
 CC RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 CC RA Whitehead S., Barrett B.G.;
 CC RT "Complete genome sequence of a multiple drug resistant Salmonella
 CC RT enterica serovar Typhi CT18.";
 CC RL Nature 413:848-853(2001).
 CC CC -1- FUNCTION: MAY BE INVOLVED IN THE FORMATION OF A SPECIFIC
 CC -----

CC MICROCOMPARTMENT IN THE CELL IN WHICH THE METABOLISM OF
 CC POTENTIALLY TOXIC BY-PRODUCTS TAKES PLACE.
 CC -1- PATHWAY: ETHANOLAMINE UTILIZATION.
 CC -1- SIMILARITY: DISTANTLY RELATED TO THE CCHA/CCMK/CSOS1/PDUA FAMILY.
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 CC -----
 CC EMBL; AF093749; AAC78125.1; -
 CC DR EMBL; AE008810; AAL21350.1; -
 CC DR EMBL; AL627274; CAD07687.1; -
 CC DR StyGene; SG10631; eutL.
 CC Complete proteome.
 CC SEQUENCE 219 AA; 22695 MW; DA50BEDF6FCD858 CRC64;
 SQ
 Query Match 2.6%; Score 7; DB 1; Length 219;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 12 FLTGSQA 18
 |||||
 Db 189 FLTGSQA 195
 RESULT 26
 VGIX_ECOLI
 ID VGIX_ECOLI STANDARD: PRT: 219 AA.
 AC P52076;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Probable transcriptional regulatory protein ygiX.
 GN YgiX OR B3025.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 CC -1- FUNCTION: PROBABLE MEMBER OF A TWO-COMPONENT REGULATORY SYSTEM
 CC YgiX/YgiY.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- PTM: PHOSPHORYLATED BY YgiY (POTENTIAL).
 CC -1- SIMILARITY: STRONG TO H1N1 INFLUENZA H1N1/08.
 CC -1- SIMILARITY: CONTRAINS 1 RESPONSE REGULATORY DOMAIN.
 CC -----
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 CC -----
 CC EMBL; U28377; AAA69193.1; -
 CC DR EMBL; AE000384; AAC76061.1; -
 CC DR HSSP; P08402; 1B00.
 CC EcoGene; Egi3026; ygiX.
 CC InterPro; IPR001789; Response_reg.

DR InterPro: IPR001867; Trans_reg_C.
 DR Pfam; PF00072; response_reg_1.
 DR Pfam; PF00486; trans_reg_C_1.
 DR SMART; SM00446; REC_1.
 DR PROSITE; PS50110; RESPONSE_REGULATORY_1.
 DR Hypothetical protein; Sensor transduction; Phosphorylation;
 DR Transcription regulation; DNA-binding; Complete proteome.
 FT DOMAIN 1 116
 FT MOD_RES 51 51
 FT SEQUENCE 219 AA; 24677 MW; 9408B2B7261E042E CRC64;
 SQ
 Query Match 2.6%; Score 7; DB 1; Length 219;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 199 AARLEAL 205
 |||||
 Db 109 AARLEAL 115
 RESULT 27
 CHIT_DIOXA
 ID CHIT_DIOXA STANDARD: PRT: 250 AA.
 AC P80052;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Acidic endochitinase (EC 3.2.1.14).
 OS Diocorea japonica (Yam).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Dioscoreales; Dioscoreaceae;
 OC Diocorea.
 OX NCBI_TaxID=4673;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Aerial tuber;
 RX MEDLINE=93015853; PubMed=1400311;
 RA Araki T., Funatsu J., Kuramoto M., Konno H., Torikata T.;
 RT "The complete amino acid sequence of yam (Dioscorea japonica)
 RT chitinase. A newly identified acidic class I chitinase.";
 RL J. Biol. Chem. 267:19944-19947(1992).
 RN [2]
 RP SEQUENCE OF 1-53.
 RC TISSUE-Aerial tuber;
 RX MEDLINE=9232966; PubMed=1623187;
 RA Araki T., Funatsu J., Kuramoto M., Torikata T.;
 RT "Amino acid sequence of the N-terminal domain of yam (Dioscorea
 RT japonica) aerial tuber acidic chitinase. Evidence for the presence of
 RT a wheat germ agglutinin domain in matured acidic chitinase from
 RT unstressed tuber.";
 RL Plant Mol. Biol. 19:351-354(1992).
 CC -1- FUNCTION: DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
 CC acetyl-D-glucosamine polymers of chitin.
 CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO
 CC CLASS 1B IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
 CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
 CC HYDROLASES).
 CC PIR; A40173; A40173.
 DR HSSP; P10969; 1MGT.
 DR InterPro; IPR001002; Chitin_bind.
 DR InterPro; IPR000726; Glyco_hydro_19.
 DR Pfam; PF00187; chitin_binding_1.
 DR Pfam; PF00182; Glyco_hydro_19; 1.
 DR PRODOM; PD000574; Glyco_hydro_19; 1.
 DR PRODOM; PD000609; Chitin_bind; 1.
 DR SMART; SM00270; ChnBD1_1.
 DR PROSITE; PS00026; CHITIN_BINDING_1.
 DR PROSITE; PS00773; CHITINASE_19_1; 1.
 DR PROSITE; PS00774; CHITINASE_19_2; 1.
 DR Hydrolase; Glycosidase; Chitin degradation; Chitin-binding.
 FT MOD_RES 1 1
 FT PYRROLIDONE CARBOXYLIC ACID.

FT DOMAIN 1 36 CHITIN-BINDING (BY SIMILARITY).
 FT DISULFID 3 12 BY SIMILARITY.
 FT DISULFID 5 18 BY SIMILARITY.
 FT DISULFID 11 25 BY SIMILARITY.
 FT DISULFID 29 34 BY SIMILARITY.
 SQ SEQUENCE 250 AA; 27908 MW; 958E0816553C4985 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 250;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 VTQEFWD 97
 |||||
 DB 50 VTQEFWD 56

RESULT 28
 SC65_YEAST STANDARD; PRT; 273 AA.
 ID SC65_YEAST
 AC P29478;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Signal recognition particle SEC65 subunit.
 GN SEC65 OR YML105C OR YM6339.14C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92220169; PubMed=1313948;
 RX Stirling C.J., Hewitt E.W.;
 RT "The S. cerevisiae SEC65 gene encodes a component of yeast signal
 RT recognition particle with homology to human SRP19.";
 RL Nature 356:534-537(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=5288C / AB972;
 RC Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL submitted (May-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP CHARACTERIZATION.
 RA MEDLINE=92220168; PubMed=1313947;
 RX Hann B.C., Stirling C.J., Walter P.;
 RT "SEC65 gene product is a subunit of the yeast signal recognition
 RT particle required for its integrity.";
 RL Nature 356:532-533(1992).
 CC -1- FUNCTION: SIGNAL-RECOGNITION-PARTICLE ASSEMBLY HAS A CRUCIAL ROLE
 CC IN TARGETING SECRETORY PROTEINS TO THE ROUGH ENDOPLASMIC RETICULUM
 CC MEMBRANE. IT MUST BE INVOLVED INTIMATELY IN THE TRANSLLOCATION OF A
 CC WIDE VARIETY OF PROTEIN SUBSTRATES.
 CC -1- SUBUNIT: YEAST SIGNAL RECOGNITION PARTICLE CONSISTS OF A 7S RNA
 CC MOLECULE (SCR1) AND AT LEAST SEVEN PROTEIN SUBUNITS: SRP72, SRP68,
 CC SRP54, SEC65, SRP21, SRP14 AND SRP7.
 CC -1- SIMILARITY: BELONGS TO THE SRP19 FAMILY.
 CC -----
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 CC -----
 CC EMBL; X65783; CAA46666.1; -;
 DR EMBL; Z49210; CAA89113.1; -;
 DR PIR; S21731; S21731;
 DR SGD; S0004573; SEC65.
 DR InterPro; IPR002778; SRP19.
 DR Pfam; PF01922; SRP19; 1.
 DR ProDom; PD006609; SRP19; 1.

KW Signal recognition particle; RNA-binding; Ribonucleoprotein.
 SQ SEQUENCE 273 AA; 31170 MW; 4F4A6CBB9225E385 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 273;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 KDLEEVK 118
 |||||
 DB 90 KDLEEVK 96

RESULT 29
 VAT1_HUMAN STANDARD; PRT; 300 AA.
 ID VAT1_HUMAN
 AC Q99536; Q13035;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Synaptic vesicle membrane protein VAT-1 homolog.
 GN VAT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97092865; PubMed=8938427;
 RX Smith T.M., Lee M.K., Szabo C.I., Jerome N., McEuen M., Taylor M.,
 RA Hood L., King M.-C.;
 RT "Complete genomic sequence and analysis of 117 kb of human DNA
 RT containing the gene BRCA1.";
 RL Genome Res. 6:1029-1049(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95293380; PubMed=7774926;
 RX Friedman L.S., Ostermeyer E.A., Lynch E.D., Szabo C.I., Meza J.E.,
 RA Anderson L.A., Dowd P., Lee M.K., Rowell S.E., Ellison J.,
 RA Boyd J., King M.-C.;
 RT "22 genes from chromosome 17q21: cloning, sequencing, and
 RT characterization of mutations in breast cancer families and tumors.";
 RL Genomics 25:256-263(1995).
 CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY. QUINONE OXIDOREDUCTASE SUBFAMILY. STRONG, TO TORPEDO
 CC CALIFORNICA VAT-1.
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 CC -----
 CC EMBL; L78833; AAC37596.1; -;
 DR EMBL; U18009; AAA95990.1; ALF_INIT.
 DR MIM; 604631; -;
 DR InterPro; IPR002085; Ach_zn_family.
 DR InterPro; IPR002364; QOR_zeta_crystal.
 DR Pfam; PF00107; ach_zinc.1.
 DR PROSITE; PS01162; QOR_ZETA_CRYSTAL; 1.
 KW Oxidoreductase; Zinc; Synapse; Membrane.
 FT CONFLICT 10 10 L -> R (IN REF. 2).
 FT CONFLICT 20 20 E -> M (IN REF. 2).
 FT CONFLICT 30 30 E -> G (IN REF. 2).
 FT CONFLICT 40 40 R -> D (IN REF. 2).
 FT CONFLICT 114 115 QL -> HV (IN REF. 2).
 FT CONFLICT 299 300 ON -> ES (IN REF. 2).
 SQ SEQUENCE 300 AA; 32558 MW; F81DDBF18BD7E4 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 300;

Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 203 EALKENG 209
Db 134 EALKENG 140

RESULT 30
RPOA_BACSU STANDARD; PRT; 314 AA.
ID RPOA_BACSU
AC P20429;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (Transcriptase
alpha chain) (RNA polymerase alpha subunit).
GN RPOA.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=89213940; PubMed=2496109;
RX Boylan S.A., Sun J.-W., Thomas S.M., Price C.W.,
RA "Gene encoding the alpha core subunit of Bacillus subtilis RNA
RT polymerase is cotranscribed with the genes for initiation factor 1
RT and ribosomal proteins B, S13, S11, and L17."
RL J. Bacteriol. 171:2553-2562(1989).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=168 / MARBURG;
RC MEDLINE=96186897; PubMed=8635744;
RX Sun J.W., Boylan S.A., Oh S.H., Price C.W.,
RA "Genetic and transcriptional organization of the Bacillus subtilis
RT spc-alpha region."
RL Gene 169:17-23(1996).
[3]
RN SEQUENCE OF 1-65 FROM N.A.
RP MEDLINE=87008431; PubMed=3093467;
RX Sun J.-W., Boylan S.A., Price C.W.,
RA "Gene for the alpha subunit of Bacillus subtilis RNA polymerase maps
RT in the ribosomal protein gene cluster."
RL J. Bacteriol. 168:65-71(1986).
-1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
CC -1- SUBUNIT: CONSISTS OF A SIGMA FACTOR AND THE RNAP CORE ENZYME WHICH
CC IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, 1 BETA' CHAIN AND 1
CC OMEGA CHAIN.
CC -1- DOMAIN: THE AMINO-TERMINAL PORTION IS INVOLVED IN THE ASSEMBLY OF
CC CORE RNAP, WHEREAS THE C-TERMINAL IS INVOLVED IN INTERACTION WITH
CC TRANSCRIPTIONAL REGULATORS.
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE ALPHA CHAIN FAMILY.
CC
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CC
CC EMBL; M26414; AAA22217.1; -
DR EMBL; L47971; AAB06826.1; -
DR EMBL; M13957; AAA22708.1; -
DR EMBL; 299104; CAB11919.1; -
DR PIR; E32307; E32307.
DR PIR; C24972; C24972.
DR HSP; P00574; IBDP.

DR Subtilist; BG10732; rpoA.
DR InterPro: IPR001700; RNA_POL_A_bac.
DR Pfam: PF01000; RNA_POL_A_bac; 1.
DR Pfam: PF03118; RNA_POL_A_CTD; 1.
DR ProDom: PD001179; RNA_POL_A_bac; 1.
KW Transferrase; Transcription; DNA-directed RNA polymerase;
KW Complete proteome.
SQ SEQUENCE 314 AA; 34799 MW; 9ADCAD891C0BCD67 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 114 LEEVAK 120
Db 296 LEEVAK 302

RESULT 31
Y034_TREPA STANDARD; PRT; 316 AA.
ID Y034_TREPA
AC 083077;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative periplasmic metal-binding protein TP0034 precursor.
GN TP0034.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=NICHOLS;
RC MEDLINE=98332770; PubMed=9665876;
RX Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete."
RL Science 281:375-388(1998).
-1- FUNCTION: PART OF AN ATP-DRIVEN TRANSPORT SYSTEM
CC TP0034/TP0035/TP0036 FOR A METAL. METAL-BINDING COMPONENT.
CC -1- SUBCELLULAR LOCATION: Periplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL SOLUTE-BINDING PROTEIN FAMILY
CC 9.
CC
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CC
CC EMBL; AE001188; AAC65029.1; -
DR TIGR; TP0034; -
DR InterPro: IPR001987; Lipoprotein_4.
DR Pfam: PF01297; Lipoprotein_4; 1.
KW Hypothetical protein; Transport; Periplasmic; Metal-binding; Signal;
KW Complete proteome.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 316 PUTATIVE PERIPLASMIC METAL-BINDING
FT PROTEIN TP0034.
SQ SEQUENCE 316 AA; 35433 MW; 16051C2199BC81AB CRC64;

Query Match 2.6%; Score 7; DB 1; Length 316;
Best Local Similarity 100.0%; Pred. No. 44;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 AARLEAL 205
 |||||
 Db 184 AARLEAL 190

RESULT 32
 EXL2_HUMAN STANDARD; PRT; 330 AA.
 AC 09UB06;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Exostosin-like 2 (EXT-related protein 2).
 GN EXT2 OR EXT2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9811853; PubMed=9450183;
 RA Wvits W., Van Hul W., Hendrickx J., Speleman F., Wauters J.,
 RA de Boullie K., Van Roy N., Van Agtamel T., Bossuyt P., Willems P.J.;
 RT "Identification and characterization of a novel member of the EXT gene
 family, EXT2.";
 RL Eur. J. Hum. Genet. 5:382-389(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98139867; PubMed=9473480;
 RA Saito T., Seki N., Yamauchi M., Tsuji S., Hayashi A., Kozuma S.,
 RA Hori T.A.;
 RT "Structure, chromosome location, and expression profile of EXT1 and
 EXT2, new members of the multiple exostosins gene family.";
 RL Biochem. Biophys. Res. Commun. 243:61-66(1998).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
 CC reticulum (By similarity).
 CC -1- TISSUE SPECIFICITY: URIDUINOUS.
 CC -1- SIMILARITY: BELONGS TO THE EXOSTOSIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF000416; AAC02898.1; -;
 CC EMBL: AB009284; BAA24081.1; -;
 CC MIM: 602411; -;
 CC InterPro: IPR004263; Exostosin.
 CC Pfam: PF03016; Exostosin; 1.
 KW Multigene family; Transmembrane; Signal-anchor.
 FT TRANSMEM 23 43
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 74 74
 FT SEQUENCE 330 AA; 37465 MW; 6976BE7EC6F588C8 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 330;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DNLEKET 103
 |||||
 Db 270 DNLEKET 276

RESULT 33
 DIA2_MOUSE STANDARD; PRT; 349 AA.
 ID DIA2_MOUSE

AC 070566;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Diaphanous protein homolog 2 (Diaphanous-related formin 2) (DPR2)
 DE (mdia3) (Fragment).
 GN DIAPH2 OR DIAP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE=96163437; PubMed=9497258;
 RA Bione S., Sala C., Manzini C., Arrigo G., Zuffardi O., Banfi S.,
 RA Borsani G., Jouveaux P., Philippe C., Zuccotti M., Ballabio A.,
 RA Toniolo D.;
 RT "A human homologue of the Drosophila melanogaster diaphanous gene is
 RT disrupted in a patient with premature ovarian failure: evidence for
 RT conserved function in oogenesis and implications for human
 RT sterility.";
 RL Am. J. Hum. Genet. 62:533-541(1998).
 CC -1- FUNCTION: MAY BE INVOLVED IN OOGENESIS.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN LIVER, HEART, KIDNEY, OVARY AND
 CC TESTIS, AT E16, P6 AND P16.
 CC -1- DOMAIN: DRES ARE REGULATED BY INTRAMOLECULAR GBD-DAD BINDING WHERE
 CC RHO-GTP ACTIVATES THE DRES BY DISRUPTING THE GBD-DAD INTERACTION
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 FORMIN HOMOLOG 2 (FH2) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DRE AUTOREGULATORY DOMAIN (DAD).
 CC -1- SIMILARITY: BELONGS TO THE FORMIN HOMOLOG FAMILY. DIAPHANOUS
 CC SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: Y15910; CAA75871.1; -;
 CC MGD: MGI:1856500; Diap2.
 CC InterPro: IPR003104; FH2.
 CC Pfam: PF02181; FH2; 1.
 CC SMART: SMO0498; FH2; 1.
 KW Coiled coil.
 FT NON_TER 1 1
 FT DOMAIN <1 319
 FT DOMAIN 250 301
 FT DOMAIN 302 316
 FT DOMAIN 320 323
 FT DOMAIN 286 289
 FT SEQUENCE 349 AA; 40557 MW; B79C15CE0E04F758 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 349;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 LEALKEN 208
 |||||
 Db 251 LEALKEN 257

RESULT 34
 REPB_THIFE STANDARD; PRT; 352 AA.
 ID REPB_THIFE
 AC P27186;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE DNA primase (EC 2.7.7.-) (Replication primase).
 GN Rep.
 OS Thiolobacillus ferrooxidans.
 OC Plasmid pPF-FC2.
 CC Bacteria; Proteobacteria; gamma subdivision; Acidithiobacillus.
 RX NCBI_TaxID=920;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92104508; PubMed=1761233;
 RA Dorrington R.A., Bardien S., Rawlings D.E.;
 RT "The broad-host-range plasmid pPF-FC2 requires a primase-like protein
 for autonomous replication in Escherichia coli.";
 RL Gene 108:7-14(1991).
 CC -1- FUNCTION: FUNCTIONS AS A PRIMEASE WITH RESPECT TO REPLICATION AT
 CC THE ORIGIN OF REPLICATION (VEGETATIVE) OF PTF-FC2.
 CC -1- SIMILARITY: SOME TO REPB, PRIMEASE OF PLASMID INCO RSF1010.
 CC -----
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 CC -----
 CC EMBL: M64981; AAA27386.1; -.
 DR PIR: J50637; J50637.
 KW DNA replication; Transferrase; DNA-directed RNA polymerase; Plasmid.
 SQ SEQUENCE 352 AA; 40156 MW; 6B5E63D06FA59E24 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 KAKPALE 236
 Db 216 KAKPALE 222
 |||||

RESULT 35
 CILD_MOUSE STANDARD; PRT; 359 AA.
 AC 09D019;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein c11orf13 homolog.
 GN c11orf13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi S., Yamakata S.,
 RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata S.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glass C., King B., Kochiwa H.,
 RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Bonfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch X.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 CC -----
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 CC -----
 CC EMBL: AK02243; BAB21960.1; -.
 DR EMBL: BC01131; AAH1131.1; -.
 DR InterPro: IPR000159; RA.
 DR SMART: SM00314; RA: 1.
 KW Coiled coil.
 FT DOMAIN 135 154 PRO-RICH.
 FT DOMAIN 180 208 COILED COIL (POTENTIAL).
 FT DOMAIN 242 301 COILED COIL (POTENTIAL).
 FT DOMAIN 309 328 PRO-RICH.
 FT CONFLICT 53 53 L -> P (IN REF. 1).
 FT CONFLICT 350 350 V -> F (IN REF. 1).
 FT CONFLICT 353 359 MISSING (IN REF. 1).
 SQ SEQUENCE 359 AA; 39246 MW; 39F0BCA1D8500F1 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 359;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 199 AARLEAL 205
 Db 209 AARLEAL 215
 |||||

RESULT 36
 P53_PLAFE STANDARD; PRT; 366 AA.
 AC 012946;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cellular tumor antigen p53 (tumor suppressor p53).
 GN TP53 OR P53.
 OS Platycthyus flesus (European flounder).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 OC Pleuronectidae; Pleuronectidae; Platycthyus.
 OX NCBI_TaxID=8260;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99138245; PubMed=9972298;
 RA Cachot J., Galgani F., Vincent F.;
 RT "cDNA cloning and expression analysis of flounder p53 tumour
 suppressor gene.";
 RL Comp. Biochem. Physiol. 121B:235-242(1998).
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2

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CC      EXPRESSION (BY SIMILARITY).
CC      -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Nuclear.
CC      -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC      -----
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CC      -----
DR      EMBL: Y08919; CAA70123.1; -.
DR      HSP: P04637; 1YCS.
DR      InterPro: IPR002117; P53.
DR      Pfam: PF00870; P53; 1.
DR      PRINTS: PR00386; P53SUPPRESSR.
DR      PRODOM: PD002881; P53; 1.
DR      PROSITE: PS00348; P53; 1.
KW      Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW      Nuclear protein; Phosphorylation; Apoptosis.
FT      DOMAIN 1 41 TRANSSCRIPTION ACTIVATION (ACIDIC).
FT      DNA BIND 80 267 BY SIMILARITY.
FT      DOMAIN 305 336 OLIGOMERIZATION.
FT      DOMAIN 341 362 BASIC (REPRESSION OF DNA-BINDING).
FT      DOMAIN 282 298 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT      MOD_RES 365 365 PHOSPHORYLATION (BY SIMILARITY).
SQ      SEQUENCE 366 AA; 40619 MW; 40DE4CA20B22BB88 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 SVTSPFS 82
Db 99 SVTSPFS 105

RESULT 37
YCCZ_ECOLI
ID YCCZ_ECOLI STANDARD: PRT; 379 AA.
AC P75881.
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Putative polysaccharide export protein yccz precursor.
GN YCCZ OR B0983 OR Z1400 OR ECS1139.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
OX RN
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655.
RA MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto S., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,

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RA Yano M., Horiiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RL [3]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potomousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
RL [4]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -1- FUNCTION: MAY BE INVOLVED IN POLYSACCHARIDE TRANSPORT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
CC (By similarity).
CC -1- SIMILARITY: BELONGS TO THE BEXD/CYPA/VEXA FAMILY.
CC -----
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CC      -----
DR      EMBL: AE000200; AAC74068.1; -.
DR      EMBL: D90735; BAA35748.1; -.
DR      EMBL: D90736; BAA36123.1; -.
DR      EMBL: AE005292; AAG55531.1; -.
DR      EMBL: AP002554; BAB34562.1; -.
DR      EcoGene: EG33728; YCCZ.
DR      InterPro: IPR003715; Poly-export.
DR      Pfam: PF02563; Poly-export; 1.
DR      PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW      Hypothetical protein; Polysaccharide transport; Transport;
KW      Outer membrane; Transmembrane; Lipoprotein; Porin; Signal;
FT      SIGNAL 1 20 POTENTIAL.
FT      CHAIN 21 379 PUTATIVE POLYSACCHARIDE EXPORT PROTEIN
FT      LIPID 21 21 YCCZ.
FT      LIPID 21 21 N-ACYL DIGLYCERIDE (BY SIMILARITY).
SQ      SEQUENCE 379 AA; 41740 MW; 36A5F5B9B5C5E842 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 379;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VLTAVL 11
Db 10 VLTAVL 16

RESULT 38
DXX_NEIMA
ID DXX_NEIMA STANDARD: PRT; 394 AA.
AC Q9JX33.
DT 16-OCT-2001 (Rel. 40, Created)

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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE 1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267) (DXP
DE reductoisomerase) (1-deoxyxylulose-5-phosphate reductoisomerase).
CN DXP OR NMA0083.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
ON NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holtroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajadaram M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."
RL Nature 404:502-506(2000).
CC -1- FUNCTION: CATALYZES THE NADP-DEPENDENT REARRANGEMENT AND REDUCTION
CC OF 1-DEOXY-D-XYLULOSE-5-PHOSPHATE (DXP) TO 2-C-METHYL-D-ERYTHRITOL
CC 4-PHOSPHATE (MEP) (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+)
CC = 1-deoxy-D-xylulose 5-phosphate + NADPH.
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; second
CC step.
CC -1- SIMILARITY: BELONGS TO THE DXR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AL162752; CAB83399.1;
DR InterPro: IPR003821; DXP_reductoisomerase.
DR Pfam: PF02670; DXP_reductoisom.1.
KW Isoprene biosynthesis; Oxidoreductase; NADP; Complete proteome.
FT NP_BIND 9 16 NADPH (POTENTIAL).
SQ SEQUENCE 394 AA; 41912 MW; B5D361B224806DBB CRC64;

Query Match 2.6%; Score 7; DB 1; Length 394;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 AARLEAL 205
DB 64 AARLEAL 70

RESULT 39
DXR_NEIMB
ID DXR_NEIMB STANDARD; PRT; 394 AA.
AC 09K1G8;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE 1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267) (DXP
DE reductoisomerase) (1-deoxyxylulose-5-phosphate reductoisomerase).
CN DXP OR NMB0184.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
ON NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

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RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwin M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischman R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blat E., Clifton H., Clark E.B.,
RA Cotton M.D., Gutterbarb T.R., Kouri H., Qin H., Yamachyan J.,
RA Gill J., Scariato V., Maignani V., Piza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappunli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
CC -1- FUNCTION: CATALYZES THE NADP-DEPENDENT REARRANGEMENT AND REDUCTION
CC OF 1-DEOXY-D-XYLULOSE-5-PHOSPHATE (DXP) TO 2-C-METHYL-D-ERYTHRITOL
CC 4-PHOSPHATE (MEP) (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+)
CC = 1-deoxy-D-xylulose 5-phosphate + NADPH.
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; second
CC step.
CC -1- SIMILARITY: BELONGS TO THE DXR FAMILY.
CC -----
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CC -----
DR EMBL: AE002375; AAF40641.1;
DR TIGR: NMB0184;
DR InterPro: IPR003821; DXP_reductoisomerase.
DR Pfam: PF02670; DXP_reductoisom.1.
KW Isoprene biosynthesis; Oxidoreductase; NADP; Complete proteome.
FT NP_BIND 9 16 NADPH (POTENTIAL).
SQ SEQUENCE 394 AA; 41920 MW; AAB5397E5BE7BD2E CRC64;

Query Match 2.6%; Score 7; DB 1; Length 394;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 AARLEAL 205
DB 64 AARLEAL 70

RESULT 40
HYFL_ALCEU
ID HYFL_ALCEU STANDARD; PRT; 394 AA.
AC P45805;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Hydrogenase maturation protein hyfL.
CN HYFL OR HYPF.
OS Alkaligenes eutrophus (Ralstonia eutropha).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
ON NCBI_TaxID=510;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H16 / ATCC 17699;
RX MEDLINE=93356597; PubMed=8352644;
RA Drenth J., Elfinger M., Friedrich B.;
RT "Analysis of a pleiotropic gene region involved in formation of
RT catalytically active hydrogenases in Alkaligenes eutrophus H16."
RT Arch. Microbiol. 159:545-553(1993).
RN [2]
RP REVISIONS.
RC STRAIN=H16 / ATCC 17699;
RA Elfinger T.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN THE HYDROGENASE MATURATION PROCESS.

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CC -1- SIMILARITY: BELONGS TO THE HYPF FAMILY.
 CC -----
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 CC -----
 DR EMBL: X70183; CAA49731.1; -
 DR HSSP: P02647; 1ODR.
 KW Plasmid.
 SQ SEQUENCE 394 AA; 40677 MW; 268E9CF0C9B3E64B CRC64;
 QY 196 ORLAARL 202
 Db 85 ORLAARL 91
 Query Match 2.68; Score 7; DB 1; Length 394;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 41
 ID APA4_HUMAN STANDARD; PRT; 396 AA.
 AC P06727;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV).
 GN APOA4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 ON NCBL_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=89194198; PubMed=2930771;
 RA Yang C., Gu Z.W., Xiong W., Rosseneu M., Yang H.X., Lee B.M.,
 RA Goto A.M., Jr., Chan L.;
 RL "The primary structure of human apolipoprotein A-IV.";
 RL Biochim. Biophys. Acta 1002:231-237(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87041474; PubMed=3095836;
 RA Karathanasis S.K., Oeltgen P., Haddad I.A., Antonarakis S.E.;
 RL "Structure, evolution, and polymorphisms of the human apolipoprotein
 RL A4 gene (APOA4).";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8457-8461(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86296629; PubMed=3755616;
 RA Karathanasis S.K., Yunis I.;
 RL "Structure, evolution, and tissue-specific synthesis of human
 RL apolipoprotein AIV.";
 RL Biochemistry 25:3962-3970(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87250378; PubMed=3036793;
 RA Elshoutdady N.A., Walker D.W., Paik Y.K., Boguski M.S., Freeman M.,
 RA Gordon J.I., Taylor J.M.;
 RL "Structure and expression of the human apolipoprotein A-IV gene.";
 RL J. Biol. Chem. 262:7973-7981(1987).
 RN [5]
 RP SEQUENCE OF 21-396 FROM N.A.
 RX MEDLINE=86111885; PubMed=3080432;
 RA Elshoutdady N.A., Walker D.W., Boguski M.S., Gordon J.I., Taylor J.M.;
 RL "The nucleotide and derived amino acid sequence of human
 RL apolipoprotein A-IV mRNA and the close linkage of its gene to the

RT genes of apolipoproteins A-I and C-III.";
 RL J. Biol. Chem. 261:1998-2002(1986).
 RN [6]
 RP SIGNAL SEQUENCE CLEAVAGE SITE.
 RX MEDLINE=84161950; PubMed=6706947;
 RA Gordon J.I., Bisgaier C.L., Sims H.F., Sachdev O.P., Glickman R.M.,
 RA Strauss A.W.;
 RL "Biosynthesis of human preapolipoprotein A-IV.";
 RL J. Biol. Chem. 259:468-474(1984).
 RN [7]
 RP REVIEW ON POLYMORPHISM.
 RA Lohse P., Brewer H.B., Jr.;
 RL "Genetic polymorphism of apolipoprotein A-IV.";
 RL Curr. Opin. Lipidol. 2:90-95(1991).
 RN [8]
 RP VARIANT A-IV*2.
 RX MEDLINE=90277616; PubMed=2351649;
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B., Jr.;
 RL "Genetic polymorphism of human plasma apolipoprotein A-IV is due to
 RL nucleotide substitutions in the apolipoprotein A-IV gene.";
 RL J. Biol. Chem. 265:10061-10064(1990).
 RN [9]
 RP VARIANTS A-IV*0 AND A-IV*3.
 RX MEDLINE=90324273; PubMed=1973689;
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B., Jr.;
 RL "Human plasma apolipoproteins A-IV-0 and A-IV-3. Molecular basis for
 RL two rare variants of apolipoprotein A-IV.";
 RL J. Biol. Chem. 265:12734-12739(1990).
 RN [10]
 RP VARIANTS.
 RX MEDLINE=91310615; PubMed=1677358;
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B., Jr.;
 RL "Three genetic variants of human plasma apolipoprotein A-IV: apoA-IV-
 RL 1(Thr-347-->Ser), apoA-IV-0(Lys-167-->Glu, Glu-360-->His), and apoA-IV-
 RL 3(Glu-165-->Lys).";
 RL J. Biol. Chem. 266:13513-13518(1991).
 RN [11]
 RP ERRATUM.
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B., Jr.;
 RL J. Biol. Chem. 266:19866-19866(1991).
 RN [12]
 RP VARIANT MET-13.
 RX MEDLINE=92238494; PubMed=1349197;
 RA von Eckardstein A., Funke H., Schulte M., Erren M., Schulte H.,
 RA Assmann G.;
 RL "Nonsynonymous polymorphic sites in the apolipoprotein (apo) A-IV
 RL gene are associated with changes in the concentration of apo B- and
 RL apo A-I-containing lipoproteins in a normal population.";
 RL Am. J. Hum. Genet. 50:1115-1128(1992).
 RN [13]
 RP VARIANT SER-147.
 RX MEDLINE=92144647; PubMed=1737067;
 RA Tenkunen H., Koskinen P., Metso J., Baumann M., Lukka M.,
 RA Kauppinen-Makelin R., Kontula K., Taskiran M.R., Manttari M.,
 RA Manninen V., Ehnholm C.;
 RL "A novel polymorphism of apolipoprotein A-IV is the result of an
 RL asparagine to serine substitution at residue 127.";
 RL Biochim. Biophys. Acta 1138:27-33(1992).
 RN [14]
 RP VARIANT A-IV*5.
 RX MEDLINE=93136374; PubMed=1487136;
 RA Kanboh M.I., Williams E.R., Law J.C., Aston C.E., Bunker C.H.,
 RA Ferrell R.E., Pollitzer W.S.;
 RL "Molecular basis of a unique African variant (A-IV 5) of human
 RL apolipoprotein A-IV and its significance in lipid metabolism.";
 RL Genet. Epidemiol. 9:379-388(1992).
 RN [15]
 RP VARIANTS LYS-44 (BUDAPEST-2); CYS-305 AND SER-367 (BUDAPEST-1).
 RX MEDLINE=95245341; PubMed=7728150;
 RA Menzel H.J., Dieplinger H., Sandholzer C., Karadi I., Utermann G.,
 RA Caszaz A.;
 RL "Apolipoprotein A-IV polymorphism in the Hungarian population: gene
 RL frequencies, effect on lipid levels, and sequence of two new

KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal;
 KW Polymorphism.
 FT NON_TER 1 1
 FT SIGNAL <1 4 POTENTIAL.
 FT CHAIN 5 401 APOLIPROTEIN A-IV.
 FT DOMAIN 17 314 13 X 22 AA APPROXIMATE TANDEM REPEATS.
 FT REPEAT 17 38 1.
 FT REPEAT 44 65 2.
 FT REPEAT 66 87 3.
 FT REPEAT 99 120 4.
 FT REPEAT 121 142 5.
 FT REPEAT 143 164 6.
 FT REPEAT 165 186 7.
 FT REPEAT 187 208 8.
 FT REPEAT 209 230 9.
 FT REPEAT 231 252 10.
 FT REPEAT 253 270 11.
 FT REPEAT 271 292 12.
 FT REPEAT 293 314 13.
 FT DOMAIN 356 394 GLU/GLN-RICH.
 FT VARIANT 80 80 K -> E (IN ISOFORM E).
 SQ SEQUENCE 401 AA; 46538 MW; 0A76D1284AA9837F CRC64;

Query Match 2.6%; Score 7; DB 1; Length 401;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 193 ELRORLA 199
 DB 246 ELRORLA 252

RESULT 43
 AATC_BOVIN STANDARD; PRT; 412 AA.
 AC P33977; Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Aspartate aminotransferase, cytoplasmic (EC 2.6.1.1) (Transaminase A)
 DE (Glutamate oxaloacetate transaminase-1).
 GN GOT1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=94039977; PubMed=8224363;
 RA Aurilia V., Palmisano A., Ferrara L., Cubellis M.V., Sanna G.,
 RA Marino G.;
 RT "Cloning and sequence analysis of A cDNA encoding bovine cytosolic
 aspartate aminotransferase.";
 RT Int. J. Biochem. 25:1505-1509(1993).
 RL -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
 L-glutamate.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
 ONE AND A MITOCHONDRIAL ONE.
 CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 AMINOTRANSFERASES.
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 CC -----
 DR EMBL; X66020; CAA46818.1; -.
 DR PIR; S21560; S21560.
 DR HSSP; P00503; IASJ.
 DR InterPro; IPR001511; Aminotran_1
 DR InterPro; IPR000796; Aminotransfse-sub.
 DR Pfam; PF00155; aminotran_1_2; 1.
 DR PRINTS; PR00799; TRANSAMINASE.
 DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
 KW Transferrase; Aminotransferase; Pyridoxal phosphate.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT BINDING 258 258 PYRIDOXAL PHOSPHATE.
 SQ SEQUENCE 412 AA; 46281 MW; 1F7DACCC1D7FBC62 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 412;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 200 ARLEALK 206
 DB 339 ARLEALK 345

RESULT 44
 AATC_HORSE STANDARD; PRT; 412 AA.
 AC P08906;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Aspartate aminotransferase, cytoplasmic (EC 2.6.1.1) (Transaminase A)
 DE (Glutamate oxaloacetate transaminase-1).
 GN GOT1.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87169770; PubMed=3104605;
 RA Doonan S., Martini F., Angelaccio S., Pascarella S., Barra D.,
 RA Bossa F.;
 RT "The complete amino acid sequences of cytosolic and mitochondrial
 aspartate aminotransferases from horse heart, and inferences on
 evolution of the isoenzymes.";
 RT J. Mol. Evol. 23:328-335(1986).
 RL [2]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=84281020; PubMed=6466688;
 RA Martini F., Angelaccio S., Barra D., Doonan S., Bossa F.,
 RT "Partial amino-acid sequence and cysteine reactivities of cytosolic
 aspartate aminotransferase from horse heart.";
 RT Biochim. Biophys. Acta 789:51-56(1984).
 RL -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
 L-glutamate.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
 ONE AND A MITOCHONDRIAL ONE.
 CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 AMINOTRANSFERASES.
 CC PIR; A26341; A26341.
 DR PIR; A05067; A05067.
 DR HSSP; P00503; IASJ.
 DR InterPro; IPR001511; Aminotran_1.
 DR InterPro; IPR000796; Aminotransfse-sub.
 DR Pfam; PF00155; aminotran_1_2; 1.
 DR PRINTS; PR00799; TRANSAMINASE.
 DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
 KW Transferrase; Aminotransferase; Pyridoxal phosphate; Acetylation.

FT MOD_RES 1 1 ACETYLATION.
 BINDING 258 258 PYRIDOXAL PHOSPHATE.
 SQ SEQUENCE 412 AA; 46213 MW; 299757858492003D CRC64;

Query Match 2.6%; Score 7; DB 1; Length 412;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 200 ARLEALK 206
 |||||
 Db 339 ARLEALK 345

RESULT 45
 AATC_HUMAN STANDARD; PRT; 412 AA.
 ID AATC_HUMAN
 AC P17174;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Aspartate aminotransferase, cytoplasmic (EC 2.6.1.1) (Transaminase A)
 DE (Glutamate oxaloacetate transaminase-1).
 GN GOT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID:9606;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=91054353; PubMed=2241899;
 RA Doyle J.M., Schlinn M.E., Bossa F., Doonan S.;
 RT "The amino acid sequence of cytosolic aspartate aminotransferase from
 human liver.";
 RL Biochem. J. 270:651-657(1990).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=90344765; PubMed=1974457;
 RA Bousquet-Lemerle B., Pol S., Pave-Preux M., Hanoune J., Barouki R.;
 RT "Properties of human liver cytosolic aspartate aminotransferase mRNAs
 generated by alternative polyadenylation site selection.";
 RL Biochemistry 29:5293-5299(1990).
 RN (3)
 RP SEQUENCE FROM N.A.
 RA Wang C.Y., Huang Y.Q., Shi J.D., Marron M.P., Ruan Q.G.,
 RA Hawkins-Lee B., Ochoa B., She J.X.;
 RT "Genomic structure and mutation analysis of GOT1 in the urofacial
 (Ochoa) syndrome gene critical region on chromosome 10.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Yu W., Sarajin J., Gibbs R.A.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
 L-glutamate.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
 CC ONE AND A MITOCHONDRIAL ONE.
 CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
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CC EMBL: M37400; AAC35563.1; -
 DR EMBL: AF080467; AAC32851.1; -
 DR EMBL: AF080459; AAC32851.1; JOINED.
 DR EMBL: AF080460; AAC32851.1; JOINED.
 DR EMBL: AF080461; AAC32851.1; JOINED.
 DR EMBL: AF080462; AAC32851.1; JOINED.
 DR EMBL: AF080463; AAC32851.1; JOINED.
 DR EMBL: AF080464; AAC32851.1; JOINED.
 DR EMBL: AF080465; AAC32851.1; JOINED.
 DR EMBL: AF080466; AAC32851.1; JOINED.
 DR EMBL: AF052153; AAC28622.1; -
 DR PIR: S13035; S13035.
 DR HSSP: P00503; IATS.
 DR MIM: 138180; -
 DR InterPro: IPR001511; AminoTran.1.
 DR InterPro: IPR00796; AminoTranFree-sub.
 DR Pfam: PF00155; AminoTran_1_2; 1.
 DR PRINTS: PR00799; TRANSAMINASE.
 DR PROSITE: PS00105; AA-TRANSFER_CLASS_1; 1.
 KW Transferase; AminoTransferase; Pyridoxal phosphate.
 FT INIT_MET 0
 FT BINDING 258 258 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 FT CONFLICT 214 214 H -> R (1N REF. 1).
 SQ SEQUENCE 412 AA; 46116 MW; 9863F47FBCD055AF CRC64;

Query Match 2.6%; Score 7; DB 1; Length 412;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 200 ARLEALK 206
 |||||
 Db 339 ARLEALK 345

RESULT 46
 AATC_MOUSE STANDARD; PRT; 412 AA.
 ID AATC_MOUSE
 AC P05201;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Aspartate aminotransferase, cytoplasmic (EC 2.6.1.1) (Transaminase A)
 DE (Glutamate oxaloacetate transaminase-1).
 GN GOT1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87057413; PubMed=3782150;
 RA Obaru K., Nomiya H., Shimada K., Nagashima F., Morino Y.;
 RT "Cloning and sequence analysis of mRNA for mouse aspartate
 RT aminotransferase isoenzymes.";
 RL J. Biol. Chem. 261:16976-16983(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88245178; PubMed=3739636;
 RA Obaru K., Suzuki T., Setoyama C., Shimada K.;
 RT "Structural organization of the mouse aspartate aminotransferase
 RT isoenzyme genes. Introns antedate the divergence of cytosolic and
 RT mitochondrial isoenzyme genes.";
 RL J. Mol. Biol. 200:13-22(1988).
 CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
 L-glutamate.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
 CC ONE AND A MITOCHONDRIAL ONE.
 CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT

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CC -----
DR EMBL: J02623; AAA37263.1; -
DR EMBL: X07302; CAA30275.1; -
DR EMBL: X07303; CAA30275.1; JOINED.
DR EMBL: X07304; CAA30275.1; JOINED.
DR EMBL: X07305; CAA30275.1; JOINED.
DR EMBL: X07306; CAA30275.1; JOINED.
DR EMBL: X07307; CAA30275.1; JOINED.
DR EMBL: X07308; CAA30275.1; JOINED.
DR EMBL: X07309; CAA30275.1; JOINED.
DR PIR: S01076; S01076.
DR PIR: B25349; B25349.
DR HSSP: P00503; LAJS.
DR SWISS-2DPAGE: P05201; MOUSE.
DR MGD: MGI:95791; Got1.
DR InterPro: IPR001511; Aminotran_1.
DR InterPro: IPR000796; Aminotransfere_sub.
DR Pfam: PF00155; aminotran_1_2; 1.
DR PRINTS: PR00799; TRANSAMINASE.
DR PROSITE: PS00105; AA_TRANSFERR_CLASS_1; 1.
KW Transferase: Aminotransferase; Pyridoxal phosphate.
FT INIT MET 0
FT BINDING 258 258 PYRIDOXAL PHOSPHATE.
FT CONFLICT 290 290 I -> N (IN REF. 2).
SQ SEQUENCE 412 AA; 46100 MW; 97BBIFFED83EE6AA23 CRC64;

Query Match 2.6%; Score 7; DB 1; Length 412;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 200 ARLEALK 206
Db 339 ARLEALK 345

RESULT 47
AATC_PIG STANDARD; PRT; 412 AA.
AC P00503:
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Aspartate aminotransferase, cytoplasmic (EC 2.6.1.1) (Transaminase A)
DE (Glutamate oxaloacetate transaminase-1).
GN GOT1.
OS Sus scrofa (Pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RX MEDLINE=89229121; PubMed=2653435;
RA Nagashima F., Tanase S., Fukumoto Y., Joh T., Nomiyama H.,
RA Tsunuki T., Shimada K., Kufamitsu S., Kagamiyama H., Morino Y.;
RT "cDNA cloning and expression of pig cytosolic aspartate
RT aminotransferase in Escherichia coli: amino-terminal heterogeneity of
RT expressed products and lack of its correlation with enzyme
RT function."
RL Biochemistry 28:1153-1160(1989).
RN [2]
RP SEQUENCE.
RC TISSUE=Heart muscle;
RA Ovchinnikov Y.A., Egorov T.A., Aidanova N.A., Feigina M.Y.,

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RA Lipkin V.M., Abdulaev N.G., Grishin E.V., Kiselev A.P.,
RA Modyanov N.N., Braunstein A.E., Polyakov O.L., Nosikov V.V.;
RT "The complete amino acid sequence of cytoplasmic aspartate
RT aminotransferase from pig heart."
RL FEBS Lett. 29:31-34(1973).
RN [3]
RP EXPERIMENTAL DETAILS.
RA Ovchinnikov Y.A., Egorov T.A., Aidanova N.A., Feigina M.Y.,
RA Lipkin V.M., Abdulaev N.G., Grishin E.V., Kiselev A.P.,
RA Modyanov N.N., Braunstein A.E., Polyakov O.L., Nosikov V.V.;
RT "The complete primary structure of cytoplasmic aspartate amino-
RT transferase from pig heart muscle."
RL Izv. Akad. Nauk SSSR, Ser. Khim. 1974:1189-1196(1974).
RN [4]
RP SEQUENCE.
RX MEDLINE=76087776; PubMed=1239277;
RA Doonan S., Doonan H.J., Hanford R., Vernon C.A., Walker J.M.,
RA Alrold L.P., Da S., Bossa F., Barra D., Carloni M., Fasella P.,
RA Riva F.;
RT "The primary structure of aspartate aminotransferase from pig heart
RT muscle. Digestion with a proteinase having specificity for lysine
RT residues."
RL Biochem. J. 149:497-506(1975).
RN [5]
RP ACTIVE SITE.
RX MEDLINE=73044407; PubMed=4634443;
RA Polyakov O.L., Demidkina T.V., Egorov C.A.;
RT "The position of an essential tyrosine residue in the polypeptide
RT chain of aspartate transaminase."
RL FEBS Lett. 23:262-264(1972).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=69285398; PubMed=5809231;
RA Morino Y., Watanabe T.;
RT "Primary structure of pyridoxal phosphate binding site in the
RT mitochondrial and extramitochondrial aspartate aminotransferases from
RT pig heart muscle. Chymotryptic peptides."
RL Biochemistry 8:3412-3417(1969).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.74 ANGSTROMS).
RX MEDLINE=97362209; PubMed=9211866;
RA Rhee S., Silva M.M., Hyde C.C., Rogers P.H., Metzler C.M.,
RA Metzler D.E., Arnone A.;
RT "Refinement and comparisons of the crystal structures of pig
RT cytosolic aspartate aminotransferase and its complex with
RT 2-methylaspartate."
RL J. Biol. Chem. 272:17293-17302(1997).
CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
CC L-glutamate.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC ONE AND A MITOCHONDRIAL ONE.
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -1- DATABASE: NAME=worthington enzyme manual;
CC WWW=http://www.worthington-biochem.com/manual/A/GOT.html".
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DR EMBL: M24088; AAA3531.1; -
DR PIR: A00592; XNPGDC.
DR PIR: A30138; A30138.
DR PDB: LAJS; 20-AUG-97.
DR PDB: LAJS; 20-AUG-97.
DR InterPro: IPR001511; Aminotran_1.

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DR      InterPro: IPR000796; AminoTransferse.sub.
DR      Pfam: PF00155; aminotran_1.2; 1.
DR      PRINTS: PR00799; TRANSAMINASE.
DR      PROSITE: PS00105; AA-TRANSFER-CLASS_1; 1.
KW      Transferase; AminoTransferase; Pyridoxal phosphate; 3D-structure.
FT      INIT_MET 0
FT      AC1_SITE 40 40
FT      IN THE PRESENCE OF SUBSTRATES, REACTS
FT      WITH TETRANITROMETHANE WITH CONCOMITANT
FT      INACTIVATION OF THE ENZYME.
FT      BINDING 258 258
FT      CONFLICT 144 144
FT      CONFLICT N -> D (IN REF. 2).
SO      SEQUENCE 412 AA; 46343 MW; 15FB716D2492E893 CRC64;

Query Match      2.6%; Score 7; DB 1; Length 412;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      200 ARLEALK 206
DB      339 ARLEALK 345

RESULT 48
AATC_RAT
ID      AATC_RAT      STANDARD;      PRT;      412 AA.
AC      P13221; 06A570; (Rel. 13, Created)
DT      01-JAN-1990 (Rel. 13, Last sequence update)
DT      01-JAN-1990 (Rel. 13, Last annotation update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      Aspartate aminotransferase, cytoplasmic (EC 2.6.1.1) (Transaminase A)
DE      (Glutamate oxaloacetate transaminase-1).
GN      GORT.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89034271; PubMed=3182856;
RA      Pave-Pieux M., Ferry N., Bouguet J., Hanoune J., Barouki R.;
RT      "Nucleotide sequence and glucocorticoid regulation of the mRNAs for
RT      the isoenzymes of rat aspartate aminotransferase."
RL      J. Biol. Chem. 263:17459-17466(1988).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89033975; PubMed=3053674;
RA      Morino Y., Tanaka T., Taketoshi M., Nagashima F., Tanase S.,
RT      "Rat cytosolic aspartate aminotransferase: molecular cloning of cDNA
RT      and expression in Escherichia coli."
RL      J. Biochem. 103:797-804(1988).
RN      [3]
RP      SEQUENCE OF 1-38 FROM N.A.
RX      MEDLINE=90170950; PubMed=2307672;
RA      Pave-Pieux M., Aegerter M., Veyssier C., Bousquet-Lemerrier B.,
RA      Hanoune J., Barouki R.;
RT      "Hormonal discrimination among transcription start sites of aspartate
RT      aminotransferase."
RL      J. Biol. Chem. 265:4444-4448(1990).
RN      [4]
RP      CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
RN      L-glutamate.
CC      -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC      -1- SUBUNIT: HOMODIMER.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMS: A CYTOPLASMIC
CC      ONE AND A MITOCHONDRIAL ONE.
CC      -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
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CC      -----
DR      EMBL: J04171; AAA0769.1; -
DR      EMBL: D00252; BAA00183.1; -
DR      EMBL: J05263; AAA40842.1; -
DR      PIR: A32120; A32120.
DR      PIR: J0439; J0439.
DR      HSP: P00503; 1A25.
DR      InterPro: IPR001511; AminoTran_1.
DR      InterPro: IPR000796; AminoTransferse.sub.
DR      Pfam: PF00155; aminotran_1.2; 1.
DR      PRINTS: PR00799; TRANSAMINASE.
DR      PROSITE: PS00105; AA-TRANSFER-CLASS_1; 1.
KW      Transferase; AminoTransferase; Pyridoxal phosphate.
FT      INIT_MET 0
FT      BINDING 258 258
FT      CONFLICT 54 54
FT      CONFLICT 99 99
FT      CONFLICT 108 108
FT      CONFLICT 120 120
FT      CONFLICT 124 124
FT      CONFLICT 253 253
FT      CONFLICT 365 365
FT      CONFLICT L -> F (IN REF. 2).
SO      SEQUENCE 412 AA; 46197 MW; 5255D8F02B7334AB CRC64;

Query Match      2.6%; Score 7; DB 1; Length 412;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      200 ARLEALK 206
DB      339 ARLEALK 345

RESULT 49
AP04_MACFA
ID      AP04_MACFA      STANDARD;      PRT;      429 AA.
AC      P33621;
DT      01-FEB-1994 (Rel. 28, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      Apolipoprotein A-IV precursor (Apo-AIV).
DE      Apolipoprotein A-IV precursor (Apo-AIV).
GN      APOA4.
OS      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9541;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93192330; PubMed=8448212;
RA      Osada J., Pocovi M., Nicolosi R.J., Schaefer E.J., Ordovas J.M.;
RT      "Nucleotide sequences of the Macaca fascicularis apolipoprotein C-III
RT      and A-IV genes."
RL      Biochim. Biophys. Acta 1172:335-339(1993).
RN      [2]
RP      FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
RN      CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
RN      LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
RN      COMPONENT OF HDL AND CHYLOMICRONS.
CC      -1- SUBCELLULAR LOCATION: Extracellular.
CC      -1- TISSUE SPECIFICITY: SECRETED IN PLASMA.
CC      -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
CC      22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
CC      MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
CC      HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
CC      THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL
CC      ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
CC      -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.

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CC -----
DR EMBL; X68361; CAA48421.1; -
DR PIR; S29565; S29565.
DR PIR; S30195; S30195.
DR HSSP; P02649; INEO.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal.
FT SIGNAL 1 20
FT CHAIN 21 429
FT DOMAIN 33 330 13 X 22 AA APPROXIMATE TANDEM REPEATS.
FT REPEAT 33 54 1.
FT REPEAT 60 81 2.
FT REPEAT 82 103 3.
FT REPEAT 115 136 4.
FT REPEAT 137 158 5.
FT REPEAT 159 180 6.
FT REPEAT 181 202 7.
FT REPEAT 203 224 8.
FT REPEAT 225 246 9.
FT REPEAT 247 268 10.
FT REPEAT 269 286 11.
FT REPEAT 287 308 12.
FT REPEAT 309 330 13.
FT DOMAIN 372 420
SO SEQUENCE 429 AA; 49876 MW; 3D458F551D0DB60C CRC64;

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Query Match
Best Local Similarity 2.6%; Score 7; DB 1; Length 429;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 193 ELRORLA 199
DB 262 ELRORLA 268

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RESULT 50
YJUT_ECOLI
ID YJUT_ECOLI STANDARD; PRT; 443 AA.
AC P39410;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yjJ7.
GN YJUT OR BA385.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655.
RA MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes.";
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [2]
RP SEQUENCE OF 1-49 FROM N.A.
RC STRAIN-K12.
RA MEDLINE=87259990; PubMed=3299264;
RA Larsen J.E.L., Albrechtsen B., Valentin-Hansen P.;
RT "Analysis of the terminator region after the deoCABD operon of

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RT Escherichia coli K-12 using a new class of single copy number operon-
RT fusion vectors.";
RL Nucleic Acids Res. 15:5125-5140(1987).
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CC -----
DR EMBL; U14003; AAA97281.1; -
DR EMBL; AE000508; AAC77338.1; -
DR EMBL; X05629; CAA29115.1; ALT_SEQ.
DR Ecogene; EG12342; yjJ7.
KW Hypothetical protein; Complete proteome.
SO SEQUENCE 443 AA; 49756 MW; 38B78B6921CEAC91 CRC64;

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Query Match
Best Local Similarity 2.6%; Score 7; DB 1; Length 443;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 193 ELRORLA 199
DB 17 ELRORLA 23

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Search completed: September 22, 2002, 12:27.09
Job time: 229 sec

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OM protein - protein search, using sw model

Run on: September 22, 2002, 12:02:49 : Search time 51.49 Seconds
(without alignments)
80.644 Million cell updates/sec

Title: US-09-803-918a-2_COPY_25_194
Perfect score: 885
Sequence: 1 DEPPQSPWDRVKDLATYVD.....KRAHVDAIRLTHLAPYDEL 170

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues
Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	885	100.0	264	1	US-08-448-606-6
2	885	100.0	267	1	US-07-959-946-3
3	885	100.0	267	1	US-08-333-577-3
4	885	100.0	267	4	US-08-952-796-2
5	885	100.0	267	5	PCT-US92-08634-3
6	650	73.4	200	4	US-08-952-796-15
7	328	37.1	64	2	US-08-292-870-1
8	227	25.6	44	2	US-08-292-870-2
9	153	18.4	32	2	US-08-292-870-3
10	138	15.6	317	4	US-08-949-135-6
11	124	14.0	25	2	US-08-292-870-4
12	119.5	13.5	896	1	US-08-095-737-2
13	119.5	13.5	896	1	US-08-480-145-2
14	119.5	13.5	896	2	US-08-477-389-2
15	118.5	13.4	897	1	US-08-095-737-4
16	118.5	13.4	897	1	US-08-480-145-4
17	118.5	13.4	897	2	US-08-477-389-4
18	116.5	13.2	317	1	US-07-709-949-2
19	107.5	12.1	900	2	US-08-630-822A-62
20	107.5	12.1	900	2	US-09-005-069-62
21	106.5	12.0	107	1	US-08-182-175A-105
22	106.5	12.0	107	1	US-08-474-633A-92
23	106.5	12.0	107	5	PCT-US92-06412-105
24	106	12.0	515	3	US-08-705-660-46
25	106	12.0	515	3	US-08-989-045-46
26	101	11.4	424	2	US-08-951-148-9
27	101	11.4	424	2	US-09-165-234-9

28	101	11.4	424	3	US-09-274-570-9	Sequence 9, Appl
29	100	11.3	110	1	US-07-849-389-7	Sequence 7, Appl
30	100	11.3	220	2	US-08-726-306A-29	Sequence 29, Appl
31	97.5	11.0	683	6	5210183-3	Patent No. 5210183
32	96	10.8	337	1	US-08-317-223-3	Sequence 3, Appl
33	96	10.8	337	3	US-09-059-849A-3	Sequence 3, Appl
34	96	10.8	337	3	US-09-213-632-3	Sequence 3, Appl
35	96	10.8	337	5	PCT-US95-12675-3	Sequence 3, Appl
36	96	10.8	311	2	US-08-460-309-4	Sequence 4, Appl
37	96	10.8	311	2	US-08-125-077-4	Sequence 4, Appl
38	95.5	10.8	428	1	US-07-882-790-4	Sequence 4, Appl
39	95	10.7	337	1	US-08-445-135-4	Sequence 4, Appl
40	95	10.7	1093	4	US-09-315-793-52	Sequence 52, Appl
41	94	10.6	344	6	5210183-2	Patent No. 5210183
42	93	10.5	288	2	US-08-961-858-6	Sequence 6, Appl
43	93	10.5	288	3	US-09-089-593-6	Sequence 6, Appl
44	93	10.5	288	3	US-08-950-925-4	Sequence 4, Appl
45	92	10.4	420	2	US-08-592-126-142	Sequence 142, App

ALIGNMENTS

RESULT 1
US-08-448-606-6
; Sequence 6, Application US/08448606
; Patent No. 5721114
GENERAL INFORMATION:
APPLICANT: Adrahams n, Lars
APPLICANT: Holmgren, Erik
APPLICANT: Kalder n, Christina
APPLICANT: Lake, Mats
APPLICANT: Mikaelsson, sa
APPLICANT: Sejlitz, Torsten
TITLE OF INVENTION: Expression System For Producing
NUMBER OF SEQUENCES: 7
TITLE OF INVENTION: Apolipoprotein AI-M
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pollock, Vande Sande & Priddy
STREET: 1990 M Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,606
FILING DATE: 25-AUG-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE93/01061
FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9203753-0
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Amernick, Burton A.
REGISTRATION NUMBER: 24,852
REFERENCE/DOCKET NUMBER: 0151/00121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)331-7111
TELEFAX: (202) 293-6229
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-448-606-6

Query Match	100.0%;	Score 885;	DB 1;	Length 264;
Best Local Similarity	100.0%;	Pred. No. 5e-72;		
Matches 170; Conservative	0;	Mismatches	0;	Indels 0;

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Oy      1 DEPQSPWDRKDLATYYVDVLKDSDGRDYVSQFEESALGKLNLKLLDNWDVSTFSKL    60
          |||||
Db     22 DEPQSPWDRKDLATYYVDVLKDSGRDYVSQFEESALGKLNLKLLDNWDVSTFSKL    81
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Dy 61 REQLGPVTEGFWDNEKEKETEGLRQEMSKDLEEVAKAVQPYLDDFQKKWQEEMELLYRQVE 120
DB 82 REQLGPVTEGFWDNEKEKETEGLRQEMSKDLEEVAKAVQPYLDDFQKKWQEEMELLYRQVE 141

QY 121 PLRAELGEGARÖKLHELQEKSLPGEEMDRARAHDALRTHLAPYSDEL 1700
| | | | |
Db 142 PLRAELGEGARÖKLHELQEKSLPGEEMDRARAHDALRTHLAPYSDEL 1911

RESULT 2
US-07-959-946-3
; Sequence 3, Application US/07959946
Data: US 5400038

GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Witzlum, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:

ADDRESS: Dressier, Goldsmith, Snore, Suckee
ADDRESS: Milnamov, Ltd.
STREET: 180 No. 5408038th Stetson, Suite 4700
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,946
FILING DATE: 19921008

Query Match	100.0%	Score 885;	DB 1;	Length 267;
Best Local Similarity	100.0%	Pred. No. 5.1e-72;		
Matches 1/1;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0

0Y 1 DEPPSPWDRVKDLATYYVDV LKDSGRDYVSQFECSALGKQLNLKLLDNWDSVTITFSKL 60

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Db      25 DEEPQSPMDRVDLATVYVDVLKDSGRDYVQFEGSALGQNLKLLDNNDVSITSFSL 84

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QY 61 REQLSPVTEFFWMDNTEKETEGIRQEMSKDL EEVKAKVPYLDDPQKKWQEMEL YRQVE 120
|||
85 REQLGPVTGEFWDNLKEKETEGIRQEMSKDLEEVKAKVPYLLDPQKKWQEMEL YRQVE 144

QY 121 PLRAELQEGARQKHLHELQEKLSPLGCEMRDRARAHYDALRTHLAPYSDEL 170
 |||||
 DB 145 PLRAELQEGARQKHLHELQEKLSPLGCEMRDRARAHYDALRTHLAPYSDEL 194

RESULT 3
US-08-333-577-3
: Sequence 3, Application US/08333577

```

1 GENERAL INFORMATION:
2 APPLICANT: Smith, Richard K.
3 APPLICANT: Koduri, Raju
4 APPLICANT: Young, Stephen G.
5 APPLICANT: Witzlum, Joseph L.
6 APPLICANT: Curtiss, Linda K.
7 TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
8 TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
9 NUMBER OF SEQUENCES: 20
10 CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Dressler, Goldsmith, Shore, Sutker
 ADDRESSEE: Mllamow, Ltd.
 STREET: 180 No. 5786206th Steetson, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/333,577
 FILING DATE:

Query Match	100.0%;	Score 885;	DB 1;	Length 267;
Best Local Similarity	100.0%;	Pred. No. 5.1e-72;		
Matches 170; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy 1 DEPOSMDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKLNLKLLDNWDSVSTFSKL 60
| | | | |
Db 25 DEPOSMDRVKDLATVYVDVLKDSGRDYVSQFEGSALGKLNLKLLDNWDSVSTFSKL 84

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QY      61 REQLGPVTQGFWDNLEKETEGTRQEMSKDLEEVAKAVQPLDDFOKKWQEEMLYRKVE 120
        |||||||
Db       85 REQLGPTVQGFWDNLEKETEGTRQEMSKDLEEVAKAVQPLDDFOKKWQEEMLYRKVE 144
```

QY 121 PLRAELQEGARQKHLHELQEKLSPIGGEEMDRARAHAVALRTHLAPYSDEL 170
 |||||
 145 PLRAELQEGARQKHLHELQEKLSPIGGEEMDRARAHAVALRTHLAPYSDEL 194
 Db

APPLICANT: DUBERGER, Nicolas
APPLICANT: FRUCHART, Jean-Charles
APPLICANT: LUC, Gerald
APPLICANT: TURPIN, Gerard
APPLICANT: ASSMANN, Gerd
APPLICANT: FUNKE, Harald
TITLE OF INVENTION: NOVEL VARIANTS OF APOLOPROTEIN A-1
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcoia Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,796
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/06061
FILING DATE: 22-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/00747
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fehner Esq., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: S795031-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-952-796-15

Query Match 73.4%; Score 650; DB 4; Length 200;
Best Local Similarity 99.2%; Pred. No. 4,1e-51;
Matches 126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 44 LKLDNMDSVTSTFSKLRQLGPTQEFMDNLEKETEGLRQMSKDLDEVKAKVQPYIDD 103
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DB 1 LKLDNMDSVTSTFSKLRQLGPTQEFMDNLEKETEGLRQMSKDLDEVKAKVQPYIDD 60
QY 104 FQKKWOEEMELTQKVEPLRAELQEGAROKLHLEQKLSPLGEEMRDARAVDRLTHL 163
|||||
DB 61 FQKKWOEEMELTQKVEPLRAELQEGAROKLHLEQKLSPLGEEMRDARAVDRLTHL 120

QY 164 APYSDLEL 170
|||||
DB 121 APYSDLEL 127

RESULT 7
US-08-292-870-1
Sequence 1, Application US/08292870
Patent No. 5814467
GENERAL INFORMATION:
APPLICANT: Curtiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Bonnet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS

TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 NO. 5814467th Torrey Pines Road., TPC 8
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,761
FILING DATE: 07-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,333
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-292-870-1

Query Match 37.1%; Score 328; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 7e-23;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 EMSKDLDEEVAKVQPYLDDFQKKWOEEMELTQKVEPLRAELQEGAROKLHLEQKLSPL 144
|||||
DB 1 EMSKDLDEEVAKVQPYLDDFQKKWOEEMELTQKVEPLRAELQEGAROKLHLEQKLSPL 60
QY 145 GEEM 148
|||||
DB 61 GEEM 64

RESULT 8
US-08-292-870-2
Sequence 2, Application US/08292870
Patent No. 5814467
GENERAL INFORMATION:
APPLICANT: Curtiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Bonnet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
METHODS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
;
; US-08-292-870-2

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Query Match 25.6%; Score 227; DB 2; Length 44;
 Best Local Similarity 100.0%; Pred. No. 4.9e-14;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 RQEMSKDLEEVKAKVQPYLDPOKKQWEMELYRQKVEPLRAEL 126
 Db 1 RQEMSKDLEEVKAKVQPYLDPOKKQWEMELYRQKVEPLRAEL 44

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; RESULT 9
; Sequence 3, Application US/08292870
; Patent No. 5814467
;
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
;
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Region
; LOCATION: 11
; OTHER INFORMATION: /note="Xaa can be either E (Glu)
; OR OTHER INFORMATION: or F (Phe)"
;
; US-08-292-870-3

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Query Match 18.4%; Score 163; DB 2; Length 32;
 Best Local Similarity 96.9%; Pred. No. 1.8e-08;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 94 KAKVQPYLDPOKKQWEMELYRQKVEPLRAE 125
 Db 1 KAKVQPYLDPOKKQWEMELYRQKVEPLRAE 32

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; RESULT 10
; Sequence 6, Application US/08949155
; Patent No. 6271436
;
; GENERAL INFORMATION:
; APPLICANT: Piedrahita, Jorge A
; APPLICANT: Bazer, Fuller W
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Generation of Transgenic Animal Species
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE AND DURKEE
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210-4433
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,155
; FILING DATE: Concurrently Herewith

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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,338
FILING DATE: 11-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,094
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK.177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-949-155-6

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Query Match	15.6%;	Score 138;	DB 4;	Length 317;
Best Local Similarity	21.2%;	Pred. No. 5.5e-05;		
Matches	43;	Conservative	42;	Mismatches 78; Indels 40; Gaps 3;

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Dz      93 EELEAOLGVEYTOQARLSKELOAAQAARVAGADMEDVANRLVLVRSVHNMGLCOTT EELRS   15
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QY      96  KVDPIYDDPQKKMOEMELLYRQKVEPIRAELQEGARQKHLHEQKISPL-----144
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Db     153  RLASHLRKLEKRLRLPTEDLQRLAVYAGLRQEGERSVSLRREKRLPLVEQGRRLATY 212

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QY 145 ---GEEMDRARAHVDALRTHL 163
      | : : | | | | |
Db 213 STRAGQPLBERAEAWGQKLRGL 235
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RESULT 11
 US-08-292-870-4
 : Sequence 4, Application US/08292870
 : Patent No. 5814467
 : GENERAL INFORMATION:
 : APPLICANT: Curtiss, Linda K
 : APPLICANT: Banka, Carole L
 : APPLICANT: Bonnet, David J
 : APPLICANT: Smith, Richard S
 : TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
 : TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
 : METHODS
 : NUMBER OF SEQUENCES: 4
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: The Scripps Research Institute, Office of
 : STREET: Patent Counsel
 : STREET: 10666 No. 5814467ch Torrey Pines Road., TPC 8
 : CITY: La Jolla
 : STATE: California
 : COUNTRY: US
 : ZIP: 92037
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentln Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/292,870
 : FILING DATE: 17-AUG-1994

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1 CLASSIFICATION: 436
2
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: US 07/534,761
5 FILING DATE: 07-JUN-1990
6
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: US 07/711,333
9 FILING DATE: 06-JUN-1991
10
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: PCT/US 91/04038
13 FILING DATE: 07-JUN-1991
14
15 ATTORNEY/AGENT INFORMATION:
16 NAME: Fitting, Thomas
17
18 REGISTRATION NUMBER: 34,163
19
20 REFERENCE/DOCKET NUMBER: TSKI 210.1 D1
21
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: 619-554-2937
24 TELEFAX: 619-554-6312
25
26 INFORMATION FOR SEQ. ID NO.: 4:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 25 amino acids
29 TYPE: amino acid
30 TOPOLOGY: linear
31
32 MOLECULE TYPE: peptide
33
34 FRAGMENT TYPE: internal
35
36 US-08-292-870-4

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	Query Match	Similarity	Score	DB 2:	Length	25:			
Best Local	96.0%	Pred. No.	4.1e-05						
Matches	2;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	87	SKDLEFVKAVOPYLDDFOKKWEE	111						
Db	1	SKDLEFVKAVOPYLDDFOKKWEE	25						

RESULT 12
 US-08-095-737-2
 Sequence 2, Application US/08095737
 Patent No. 5487979
 GENERAL INFORMATION:
 APPLICANT: DiFiore, Pier P
 APPLICANT: Fazioli, Francesca
 TITLE OF INVENTION: A Substrate for the Epidermal Growth
 FACTOR RECEPTOR KINASE
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson & Bear
 STREET: 620 Newport Center Drive, Sixteenth Floor
 CITY: Newport Beach
 STATE: California
 COUNTRY: United States of America
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/095,737
 FILING DATE: 19930722
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Israel, Ned A
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER: NIH060.001A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 896 amino acids
 TYPE: amino acid

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US-08-477-389-2
: Sequence 2, Application US/08477389
: Patent No. 5872219
:
: GENERAL INFORMATION:
: APPLICANT: DiFiore, Pier P
: APPLICANT: Fazioli, Francesca
: TITLE OF INVENTION: A Substrate for the Epidermal Growth
: TITLE OF INVENTION: Factor Receptor Kinase
: NUMBER OF SEQUENCES: 4
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Knobbe, Martens, Olson & Bear
: STREET: 620 Newport Center Drive, Sixteenth Floor
: City: Newport Beach
: STATE: California
: COUNTRY: United States of America
: ZIP: 92660
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/477,389
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/095,737
: FILING DATE: 22-JUL-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Israelson, Ned A
: REGISTRATION NUMBER: 29,655
: REFERENCE/DOCKET NUMBER: NIH060.001A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 235-8550
: TELEFAX: (619) 235-0176
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 896 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-477-389-2
:
Query Match 13.5%; Score 119.5; DB 2; Length 896;
Best Local Similarity 24.0%; Pred. NO. 0.0091;
Matches 47; Conservative 40; Mismatches 66; Indels 43; Gaps 8;
QY 3 PPSMDRYKDLATVYVDLKDSDRDVYSQESGALSGLKLNLTKLDDVSTFSKLE 62
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 309 PF-----SDRASLQKNI---GSSPYADFSALKELDTLNELVLDIQRKNNVEDDLK 358
Y 63 QLGPV-----TQEFWDNLEKETEGLR-----QEMSKDLEEVKAKVPIYLDPFQK 107

```

Db 359 KEDTITKQRTSEVQDDQDEYQRENTNIOKQAOQOVQELLDDEQKAQLEQKAEVKK 418

QY 108 KOEEMELIYQKVEPLRAEL--QEG-----AROKLHELQKLSPLGEMDRARA 154

Db 419 CAEEAOL---ISSIKAEITSOESQISTYEELAKARELSRLQOETAEL-EESVESGKA 473

QY 155 HYDALRTHLAPYSDEL 170

Db 474 QLEPILQOHLQDSQOET 489

RESULT 15

US-08-095-737-4

; Sequence 4, Application US/08095737

; Patent No. 5487979

; GENERAL INFORMATION:

; APPLICANT: Difiore, Pier P

; APPLICANT: Fazio, Francesca

; TITLE OF INVENTION: A Substrate for the Epidermal Growth

; TITLE OF INVENTION: Factor Receptor Kinase

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knodbe, Martens, Olson & Bear

; STREET: 620 Newport Center Drive, Sixteenth Floor

; CITY: Newport Beach

; STATE: California

; COUNTRY: United States of America

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/095,737

; FILING DATE: 19930722

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Israelson, Ned A

; REGISTRATION NUMBER: 29,655

; REFERENCE/DOCKET NUMBER: NIH060.001A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 235-8550

; TELEFAX: (619) 235-0176

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 897 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-095-737-4

Query Match

Best Local Similarity 13.4%; Score 118.5; DB 1; Length 897;

Matches 49; Conservative 43; Mismatches 65; Indels 47; Gaps 9;

QY 2 EPPQS-----PMDRVKDLATVYVDVLKDSGRDYSOPFSGSALQKQNLKLLDNMDSVT 54

Db 298 DPHSLTPEMIPPSDR-----SSLOKNI---TGSSPVADPSAIKELDTLNNETVDLQRIKN 350

QY 55 STFSKLEQOLGPV-----TOEFMDLKEKTEGLR-----OEMSKDLEEVAKVOP 99

Db 351 NVEQDLKEKEDYKQRTSEVQDDQDEYQRENTNIOKQAOQOVQELLDDEQKAQLEQKAEVKK 410

QY 100 YLDDFOKKWOEMELIYQKVEPLRAEL--QEG-----AROKLHELQKLSPLIGE 146

Db 411 QLOEVRKKCAEEAOL---ISSIKAEITSOESQISTYEELAKARELSRLQOETAOL-E 465

QY 147 EMDRARAHVVDLRTHLAPYSDEL 170

Db 466 ESVEGSGKAQLEPILQOHLQDSQOET 489

Search completed: September 22, 2002, 12:02:50
Job time: 250 sec

10

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2002, 11:58:40 ; Search time 51.49 seconds
(without alignments)
126.658 Million cell updates/sec

Title: US-09-803-918a-2
Perfect score: 1362
Sequence: 1 MKAAVLTIAVLFTGSQARH.....SEKVSFLSALEETKTKLNTQ 267

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/2/1aa/58.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/58.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/68.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1362	100.0	267	1 US-07-959-946-3	Sequence 3, Appl1
2	1362	100.0	267	1 US-08-333-577-3	Sequence 3, Appl1
3	1362	100.0	267	4 US-08-952-796-2	Sequence 2, Appl1
4	1362	100.0	267	5 PCT-US92-08634-3	Sequence 3, Appl1
5	1240.5	91.1	264	1 US-08-448-606-6	Sequence 6, Appl1
6	1006	73.9	200	4 US-08-952-796-15	Sequence 15, Appl1
7	328	24.1	64	2 US-08-292-870-1	Sequence 1, Appl1
8	227	16.7	44	2 US-08-292-870-2	Sequence 2, Appl1
9	190	14.0	317	4 US-08-949-155-6	Sequence 6, Appl1
10	171.5	12.6	317	1 US-07-709-949-2	Sequence 2, Appl1
11	163	12.0	32	2 US-08-292-870-3	Sequence 3, Appl1
12	129	9.5	900	2 US-08-630-822A-62	Sequence 62, Appl1
13	129	9.5	900	2 US-09-005-069-62	Sequence 29, Appl1
14	126	9.3	220	2 US-08-726-306A-29	Sequence 4, Appl1
15	124	9.1	25	2 US-08-292-870-4	Sequence 4, Appl1
16	123.5	9.1	683	6 5210183-3	Patent No. 5210183
17	122.5	9.0	896	1 US-08-095-737-2	Sequence 2, Appl1
18	122.5	9.0	896	1 US-08-480-145-2	Sequence 2, Appl1
19	122.5	9.0	896	1 US-08-477-389-2	Sequence 2, Appl1
20	122	9.0	1588	5 PCT-US93-07261-11	Sequence 11, Appl1
21	122	9.0	1663	5 PCT-US93-07261-16	Sequence 16, Appl1
22	121.5	8.9	897	1 US-08-095-737-4	Sequence 4, Appl1
23	121.5	8.9	897	1 US-08-480-145-4	Sequence 4, Appl1
24	121.5	8.9	897	2 US-08-477-389-4	Sequence 4, Appl1
25	121	8.9	1184	4 US-09-541-782-2	Sequence 2, Appl1
26	119	8.7	337	1 US-08-445-135-4	Sequence 4, Appl1
27	118	8.7	337	1 US-08-317-223-3	Sequence 3, Appl1

28	118	8.7	337	3 US-09-059-849A-3	Sequence 3, Appl1
29	118	8.7	337	3 US-09-213-632-3	Sequence 3, Appl1
30	118	8.7	337	5 PCT-US95-12675-3	Sequence 3, Appl1
31	118	8.7	3111	2 US-08-460-309-4	Sequence 4, Appl1
32	117.5	8.6	428	1 US-07-882-790-4	Sequence 4, Appl1
33	117.5	8.6	515	2 US-08-705-660-46	Sequence 46, Appl1
34	117.5	8.6	515	3 US-08-989-045-46	Sequence 46, Appl1
35	117.5	8.6	1786	4 US-08-973-462-8	Sequence 8, Appl1
36	117	8.6	3248	4 US-08-353-700-1	Sequence 1, Appl1
37	117	8.6	3248	5 PCT-US95-16216-1	Sequence 1, Appl1
38	117	8.5	1093	4 US-09-315-793-52	Sequence 52, Appl1
39	116	8.5	2101	1 US-08-466-390-4	Sequence 4, Appl1
40	116	8.5	2101	1 US-08-470-950-4	Sequence 4, Appl1
41	116	8.5	2101	1 US-08-467-781-4	Sequence 4, Appl1
42	116	8.5	2101	1 US-08-195-487-4	Sequence 4, Appl1
43	116	8.5	2101	2 US-08-483-924-4	Sequence 4, Appl1
44	116	8.5	2101	2 US-09-452-294-1	Sequence 1, Appl1
45	116	8.5	2101	4 US-09-452-294-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-07-959-946-3
; Sequence 3, Application US/07959946
; Patent No. 5408038
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Wiltzium, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Dressler, J.
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 No. 5408038th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,946
; FILING DATE: 19921008
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,706
; FILING DATE: 18-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5460
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-959-946-3
Query Match 100.0%; Score 1362; DB 1; Length 267;

US-08-952-96-2

Query Match 100.0%; Score 1362; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 3, 1e-109;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAATLAVLFLTGSQARHFWQDEPPQSPMDRVKDLATVYVDYKDSGRDYVSQFEGS 60
DB 1 MKAATLAVLFLTGSQARHFWQDEPPQSPMDRVKDLATVYVDYKDSGRDYVSQFEGS 60
QY 61 ALGQNLKLLDNDVSTSTFSKLRQGLPVTOEFMDNLEKETEGLRQMSKDLSEYKAK 120
DB 61 ALGQNLKLLDNDVSTSTFSKLRQGLPVTOEFMDNLEKETEGLRQMSKDLSEYKAK 120
QY 121 VQPYLDDFOKKWQEMELRYKQVEPLRAELQEGAROKLHELOEKLSPJGEMRDRAAHV 180
DB 121 VQPYLDDFOKKWQEMELRYKQVEPLRAELQEGAROKLHELOEKLSPJGEMRDRAAHV 180
QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQ 240
DB 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQ 240
QY 241 GLPVLSEFKVSFLSALSEYTKKLTNQ 267
DB 241 GLPVLSEFKVSFLSALSEYTKKLTNQ 267

RESULT 4

PCT-US92-08634-3

Sequence 3, Application PC/TUS9208634

GENERAL INFORMATION:

APPLICANT: Smith, Richard K.

APPLICANT: Koduri, Raju

APPLICANT: Young, Stephen G.

APPLICANT: Witzum, Joseph L.

APPLICANT: Curtiss, Linda K.

TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &

STREET: 180 North Steetson, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/08634

FILING DATE: 19921009

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,706

FILING DATE: 18-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Gamsen, Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)616-5400

TELEFAX: (312)616-5460

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US92-08634-3

Query Match 100.0%; Score 1362; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 3, 1e-109;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAATLAVLFLTGSQARHFWQDEPPQSPMDRVKDLATVYVDYKDSGRDYVSQFEGS 60
DB 1 MKAATLAVLFLTGSQARHFWQDEPPQSPMDRVKDLATVYVDYKDSGRDYVSQFEGS 60
QY 61 ALGQNLKLLDNDVSTSTFSKLRQGLPVTOEFMDNLEKETEGLRQMSKDLSEYKAK 120
DB 61 ALGQNLKLLDNDVSTSTFSKLRQGLPVTOEFMDNLEKETEGLRQMSKDLSEYKAK 120
QY 121 VQPYLDDFOKKWQEMELRYKQVEPLRAELQEGAROKLHELOEKLSPJGEMRDRAAHV 180
DB 121 VQPYLDDFOKKWQEMELRYKQVEPLRAELQEGAROKLHELOEKLSPJGEMRDRAAHV 180
QY 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQ 240
DB 181 DALRTHLAPYSDELRLQRLAARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQ 240
QY 241 GLPVLSEFKVSFLSALSEYTKKLTNQ 267
DB 241 GLPVLSEFKVSFLSALSEYTKKLTNQ 267

RESULT 5

US-08-448-606-6

Sequence 6, Application US/08448606

Patent No. 5721114

GENERAL INFORMATION:

APPLICANT: Abrahams n, Lars

APPLICANT: Holmgren, Erik

APPLICANT: Kalder n, Christina

APPLICANT: Lake, Mats

APPLICANT: Mikaelsson, sa

APPLICANT: Sejlitz, Torsten

TITLE OF INVENTION: Expression System For Producing

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pollock, Vande Sande & Priddy

STREET: 1990 M Street, N.W., Suite 800

CITY: Washington

STATE: D.C.

COUNTRY: U.S.

ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/448,606

FILING DATE: 25-AUG-1995

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/SE93/01061

FILING DATE: 09-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9203753-0

FILING DATE: 11-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Amernick, Burton A.

REGISTRATION NUMBER: 24,852

REFERENCE/DOCKET NUMBER: 0151/00121

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)331-7111

TELEFAX: (202)293-6229

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 264 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-448-606-6

Query Match 91.1%; Score 1240.5; DB 1; Length 264;
 Best Local Similarity 92.2%; Pred. No. 7.8e-99;
 Matches 249; Conservative 3; Mismatches 9; Indels 9; Gaps 2;

QY 1 MKAAYTLAVL---FLTSSQARHEWQDEPPQSPWDKVKDLATVYVDVLDKSGRDYVSQF 57
 1 MKRTAIAVALAGATVANA-----DEPPQSPWDKVKDLATVYVDVLDKSGRDYVSQF 54
 QY 58 ESSALGKOLNKLNDMDSVTSTFSKLRQLGPTQGFMDLKEKTEGLRQMSKDLIEV 117
 55 ESSALGKOLNKLNDMDSVTSTFSKLRQLGPTQGFMDLKEKTEGLRQMSKDLIEV 114
 QY 118 KAKVQPYLDDFOKKWOEEMELYRQKVEPLRAELQEGAROKLHELQEKLSPLGEEMRDRAR 177
 115 KAKVQPYLDDFOKKWOEEMELYRQKVEPLRAELQEGAROKLHELQEKLSPLGEEMRDRAR 174
 QY 178 AHVDLRTHLAPYSDLRQRLAELKENGARLAETHAHAKATEHLSTSEKAKPALED 237
 175 AHVDLRTHLAPYSDLRQRLAELKENGARLAETHAHAKATEHLSTSEKAKPALED 234
 QY 238 LRQGLLPVLESFKVSFLSALFEYTKKLTNQ 267
 235 LRQGLLPVLESFKVSFLSALFEYTKKLTNQ 264
 Db

RESULT 6
 US-08-952-796-15

; Sequence 15, Application US/08952796

; Patent No. 6258596

; GENERAL INFORMATION:

; APPLICANT: BENOTT, Patrick

; APPLICANT: BRUCKERT, Eric

; APPLICANT: DENEFFLE, Patrice

; APPLICANT: DUBERGER, Nicolas

; APPLICANT: FRUCHART, Jean-Charles

; APPLICANT: LUC, Gerald

; APPLICANT: TURPIN, Gerard

; APPLICANT: ASSMANN, Geird

; APPLICANT: FUNKE, Harald

; TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPROTEIN A-I

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Road, Mailstop 3043

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/952,796

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 95/06061

; FILING DATE: 22-MAY-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO FR96/00747

; FILING DATE: 20-MAY-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Fehlner Esq., Paul F.

; REGISTRATION NUMBER: 35,135

REFERENCE/DOCKET NUMBER: ST95031-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3839
 TELEFAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 200 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-952-796-15

Query Match 73.9%; Score 1006; DB 4; Length 200;
 Best Local Similarity 99.5%; Pred. No. 6.5e-79;
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 68 LKLLDNDVSTSTFSKLRQLGPTQGFMDLKEKTEGLRQMSKDLIEVRAKVPYDLD 127
 1 LKLLDNDVSTSTFSKLRQLGPTQGFMDLKEKTEGLRQMSKDLIEVRAKVPYDLD 60
 Db
 QY 128 FOKKWOEEMELYRQKVEPLRAELQEGAROKLHELQEKLSPLGEEMRDRARAHVDAIRTHL 187
 61 FOKKWOEEMELYRQKVEPLRAELQEGAROKLHELQEKLSPLGEEMRDRARAHVDAIRTHL 120
 Db
 QY 188 APYSDLRQRLAELKENGARLAETHAHAKATEHLSTSEKAKPALEDLRQGLLPVLE 247
 121 APYSDLRQRLAELKENGARLAETHAHAKATEHLSTSEKAKPALEDLRQGLLPVLE 180
 Db
 QY 248 SFKVSFLSALFEYTKKLTNQ 267
 181 SFKVSFLSALFEYTKKLTNQ 200
 Db

RESULT 7

US-08-292-870-1

; Sequence 1, Application US/08292870

; Patent No. 5814467

; GENERAL INFORMATION:

; APPLICANT: Curtiss, Linda K

; APPLICANT: Banks, Carole L

; APPLICANT: Bonnet, David J

; APPLICANT: Smith, Richard S

; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS

; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute, Office of

; ADDRESSEE: Patent Counsel

; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8

; CITY: La Jolla

; STATE: California

; COUNTRY: US

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/292,870

; FILING DATE: 17-AUG-1994

; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/534,761

; FILING DATE: 07-JUN-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/711,333

; FILING DATE: 06-JUN-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US 91/04038

; FILING DATE: 07-JUN-1991

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-292-870-1

Query Match 24.1%; Score 328; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.6e-21;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 EMSKDLSEVAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQSGARQKLTLEQKLSPL 168
|||||

Db 1 EMSKDLSEVAKVQPYLDDFQKKWQEMELYRQKVEPLRAELQSGARQKLTLEQKLSPL 60
QY 169 GDEM 172
|||||
Db 61 GDEM 64

RESULT 8
US-08-292-870-2
Sequence 2, Application US/08292870
Patent No. 5814467

GENERAL INFORMATION:
APPLICANT: Curtiss, Linda K
APPLICANT: Banks, Carole L
APPLICANT: Bonnet, David J
TITLE OF INVENTION: APO A1 POLYPEPTIDES, DIAGNOSTIC METHODS
TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO A1, AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292.870
FILING DATE: 17-AUG-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,761
FILING DATE: 07-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/11,333
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 210.1 D1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-292-870-2

Query Match 16.7%; Score 227; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 RQMSKDLSEVAKVQPYLDDFQKKWQEMELYRQKVEPLRAEL 150
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Db 1 RQMSKDLSEVAKVQPYLDDFQKKWQEMELYRQKVEPLRAEL 44
QY 9
US-08-949-155-6
Sequence 6, Application US/08949155
Patent No. 6271436

GENERAL INFORMATION:
APPLICANT: Piedrahita, Jorge A
APPLICANT: Bazer, Fuller W
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Generation of Transgenic Animal Species
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD WHITE AND DURKEE
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,155
FILING DATE: Concurrently Herewith
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,338
FILING DATE: 11-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,094
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hidler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-949-155-6

Query Match 14.0%; Score 190; DB 4; Length 317;
Best Local Similarity 21.9%; Pred. No. 9e-09;
Matches 68; Conservative 60; Mismatches 112; Indels 70; Gaps 8;

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QY 1 MKAATLAVLTGSGAAR-----HFMOOPEPO--SPMDRVKDLATVYVLDKDS 49
Db 1 MKVLVALVTLTGCRFEDDEGPPEPEVHWMEPKWOGSPWEOALGRFVDYLRWYSL 60
QY 50 GADYVSOEGSALGKOLNKLKLDNDVSTFSSKIREOLGVPYQEFMDNLEKETEGRLDE 109
Db 61 SDVOVEELLSTKVQELTELIEESMKYKAYREELQGLGVTOETQARLSKELQAAQAR 120
QY 110 MSKDL-----EEVAKVOPYLDDFOKKMOEMELVROKVEPLR 147
Db 121 VGADVEDVRNRLVLYRSVHNMIGOTTEELSLRSLHRLKRLKLDVDELOKRLAVYQ 180
QY 148 AELQGANOKLHELOEKLSP-----GEMDRARAHVADLRTHLAFYSID 192
Db 181 AGLREGARSVSALRERLGLPEQGRLEAATLSTRAGQPLRERAEAMGOKLRGL-----E 236
QY 193 ELRRLARLALKENGARLAELHAKATEHLSTLSEKA-----KPALEDLRQ- 240
Db 237 EMGSRTRDLDEMR-----OLEVRYVEEGSQLRLQAGEFHALLKGWFEPLVEDIRQ 292
QY 241 --GLLPVLES 248
Db 293 WAGLVERMQS 302

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RESULT 10
US-07-709-949-2
; Sequence 2, Application US/07709949
; Patent No. 5472858
; GENERAL INFORMATION:
; APPLICANT: Attie, Alan D
; APPLICANT: Gretch, Daniel G
; APPLICANT: Sturley, Stephen L
; APPLICANT: Beckage, Nancy E
; TITLE OF INVENTION: Production of Recombinant Proteins in
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: P.O. Box 2113
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/709,949
; FILING DATE: 19910604
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 9629691801
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-709-949-2

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Query Match 12.6%; Score 171.5; DB 1; Length 317;
Best Local Similarity 20.1%; Pred. No. 3,5e-07;
Matches 65; Conservative 64; Mismatches 121; Indels 73; Gaps 6;

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QY 1 MKAATLAVLTGSGAARHFMOOPEPOSP-----MDRVKDLAT 40
Db 1 MKVLVALVTLTGCRFEDDEGPPEPEVHWMEPKWOGSPWEOALGRFVDYLRWYSL 60
QY 41 VYVDVLDKSDGRDVSOEGSALGKOLNKLKLDNDVSTFSSKIREOLGVPYQEFMDNLE 100
Db 61 LSPQVOEELLSSGYTQ-----ELRALMDETMKELAKYKSELEOLTPVAETRARLS 112
QY 101 KETEGRLQENSKDL-----EEVAKVOPYLDDFOKKMOEMEL 138
Db 113 KELDTQARLIGADMEDVCGRLVQYRGEVQAMLGOSTEELRLVRLASHLRLKRLRDPDD 172
QY 139 YROKVEPLRAELQEGAROKLHELOEKLSP-----GEMDRARAHVADLR 183
Db 173 LQKRLVAYAGAREGARELSAIRERLGLPVQGRVRAATVGSILAGOPLOEAAQAMGERL 232
QY 184 RTHLAPYSELQRRLAARLEALKENGARLAELHAKATEHLSTLSEKAKPALEDLRQGL 243
Db 233 RARM-----EMGSRTRDLDEYKE-----QVAEVRAKLEBQAOQIRLQAEATQARLSWFE 284
QY 244 PVLESFVSLALDEYTKKLT 266
Db 285 PVEDMQRWAGLVERVQAAGVT 307

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RESULT 11
US-08-292-870-3
; Sequence 3, Application US/08292870
; Patent No. 5814467
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 3:

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? SEQUENCE CHARACTERISTICS:
? LENGTH: 32 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? FRAGMENT TYPE: internal
? FEATURE:
? NAME/KEY: Region
? LOCATION: 11
? OTHER INFORMATION:
? OTHER INFORMATION: /note="Xaa can be either E (Glu)
? or F (Phe)"
US-08-292-870-3

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Db 508 E-HNOKLKQAVELRYAQSATEQLNNELOETMOGL-QTORDALQOQVASTLOQKLSQERS 565
QY 189 -PYSDELRORLARLEALK-----ENGARLALEYHAKTEHLSLSEAKRALE 236
Db 566 RSOASDMQLEAKLALHELEHVRNCEKVTQDNROLLEISTL-EKECASTLE 619

RESULT 14
US-08-726-306A-29

; Sequence 29, Application US/08726306A
; Patent No. 5958684
; GENERAL INFORMATION:
; APPLICANT: van Leeuwen, Frederik Willem
; APPLICANT: Burbach, Johannes Peter Henri
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
; NUMBER OF SEQUENCES: 189
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1 Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726.306A
; FILING DATE: 02-Oct-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 95/20080.4
; FILING DATE: 02-Oct-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/009,832
; FILING DATE: 01-Jan-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-726-306A-29

Query Match 9.3%; Score 126; DB 2; Length 220;
Best Local Similarity 22.2%; Pred. No. 0.0017;
Matches 51; Conservative 34; Mismatches 95; Indels 50; Gaps 3;

QY 1 MKAAVLTIAVLFLTSSQARHFQNDPEPQSP-----WDRYKDLAT 40
Db 21 MKVLAALVFLFLAGCOAKVEQAVTEPEPELRQOTEMQSGQRMELALGRWDYLRWVOT 80
QY 41 VVVDVLKDSGRDYVSQFESALGKQLNKLIDNMDSVTSTFSKLRQGLPTVTOEFMDLE 100
Db 81 LSEQVQELSSQYQ-----ELRALMDETMKEIAAYSELEEQULTPVAEETRAALS 132
QY 101 KETESLRQEMSKDLSEYAKAVQPYLDLDFOKKQWEMELYLROKVEPLRAELQEGAROKLHE 160
Db 133 KLTQTAQAALGADMDVCGRLVQY-----REYVQAMLGQSTEE 170
QY 161 LOEKLSPLGEERBARARAHVADALRTHLAPYSDELRORLARLEALKENG 210

Db 171 LRVLASLRKLRKRLRLLRDPDDQLKRLAVYQAGARBEAGSLAIRRLG 220

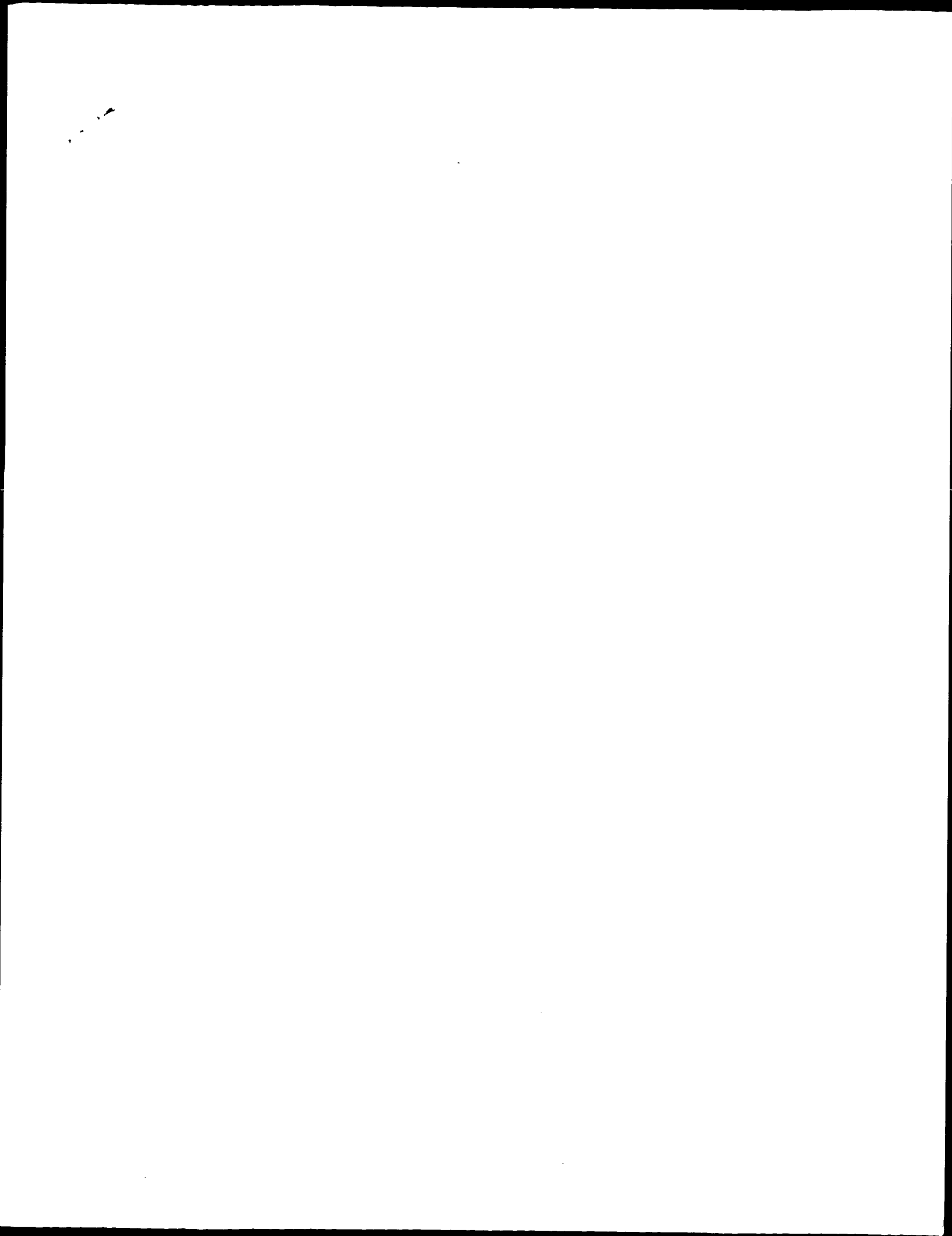
RESULT 15
US-08-292-870-4

; Sequence 4, Application US/08292870
; Patent No. 5814467
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Linda K
; APPLICANT: Banka, Carole L
; APPLICANT: Bonnet, David J
; APPLICANT: Smith, Richard S
; TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
; TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,870
; FILING DATE: 17-AUG-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/534,761
; FILING DATE: 07-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/711,333
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 91/04038
; FILING DATE: 07-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-292-870-4

Query Match 9.1%; Score 124; DB 2; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.00014;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 111 SKDLEEVKAVQPYLDLDFOKKQWEE 135
Db 1 SKDLEEVKAVQPYLDLDFOKKQWEE 25

Search completed: September 22, 2002, 12:02:49
Job time: 249 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2002, 12:16:40 : Search time 13.02 seconds
(without alignments)
500.894 Million cell updates/sec

Title: US-09-803-918A-2

Perfect score: 267
Sequence: 1 MKAAYLFLAVFLTGSGARH.....SFKVFLSLALEYTKKLNTQ 267

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size: 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database:

Issued Patents-AA:*
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2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	267	100.0	267	1	US-07-959-946-3
2	267	100.0	267	1	US-08-333-577-3
3	267	100.0	267	4	US-08-952-796-2
4	267	100.0	267	5	PCT-US92-08634-3
5	172	64.4	264	1	US-08-448-606-6
6	107	40.1	200	4	US-08-952-796-15
7	64	24.0	64	2	US-08-292-870-1
8	44	16.5	44	2	US-08-292-870-2
9	21	7.9	32	2	US-08-292-870-3
10	17	6.4	25	2	US-08-292-870-4
11	16	6.0	16	1	US-07-959-946-5
12	16	6.0	16	1	US-08-333-577-5
13	16	6.0	16	5	PCT-US92-08634-5
14	9	3.4	13	5	PCT-US94-01234-47
15	8	3.0	8	2	US-08-630-645-6
16	8	3.0	8	5	PCT-US96-10220-6
17	8	3.0	8	5	PCT-US96-10220-6
18	7	2.6	7	4	US-08-952-796-11
19	7	2.6	13	3	US-08-448-606-2
20	7	2.6	70	3	US-09-101-146-4
21	7	2.6	229	4	US-09-188-930-315
22	7	2.6	233	4	US-09-188-930-139
23	7	2.6	315	4	US-09-180-827-6
24	7	2.6	343	1	US-08-336-891-2
25	7	2.6	343	5	PCT-US95-13795-4
26	7	2.6	482	4	US-08-637-8238-32
27	7	2.6	483	4	US-08-637-8238-4

ALIGNMENTS

28	7	2.6	484	4	US-08-637-8238-2	Sequence 2, Appli
29	7	2.6	547	3	US-08-903-139B-7	Sequence 7, Appli
30	7	2.6	548	2	US-08-676-279-50	Sequence 50, Appl
31	7	2.6	548	3	US-08-903-139B-8	Sequence 8, Appli
32	7	2.6	548	3	US-08-903-139B-9	Sequence 9, Appli
33	7	2.6	548	3	US-08-903-139B-28	Sequence 28, Appli
34	7	2.6	548	3	US-08-637-8238-25	Sequence 25, Appl
35	7	2.6	549	2	US-08-676-279-57	Sequence 57, Appl
36	7	2.6	550	4	US-08-637-8238-30	Sequence 30, Appl
37	7	2.6	556	4	US-08-637-8238-27	Sequence 27, Appl
38	7	2.6	584	4	US-08-637-8238-28	Sequence 28, Appl
39	7	2.6	629	4	US-09-300-809-19	Sequence 19, Appl
40	7	2.6	882	4	US-09-413-814-78	Sequence 78, Appl
41	7	2.6	2254	2	US-08-677-010-3	Sequence 18, Appl
42	7	2.6	2254	2	US-08-790-519-3	Sequence 3, Appli
43	7	2.6	2509	1	US-08-469-005A-10	Sequence 10, Appl
44	7	2.6	2511	4	US-09-261-907-2	Sequence 2, Appli
45	7	2.6	5087	4	US-09-144-085-1	Sequence 1, Appli
46	6	2.2	7	1	US-08-704-170-43	Sequence 1, Appli
47	6	2.2	7	1	US-08-474-741-1	Sequence 43, Appl
48	6	2.2	7	2	US-09-187-859-1184	Sequence 1184, Ap
49	6	2.2	7	5	PCT-US94-02631-43	Sequence 43, Appl
50	6	2.2	8	4	US-09-187-859-1189	Sequence 1189, Ap
51	6	2.2	10	4	US-09-187-859-1150	Sequence 1150, Ap
52	6	2.2	10	4	US-09-187-859-1192	Sequence 1192, Ap
53	6	2.2	12	1	US-08-117-362-28	Sequence 28, Appl
54	6	2.2	12	1	US-08-486-924-28	Sequence 28, Appl
55	6	2.2	15	1	US-08-218-025A-144	Sequence 144, App
56	6	2.2	17	4	US-08-954-395A-4	Sequence 4, Appli
57	6	2.2	18	3	US-08-940-095-208	Sequence 208, App
58	6	2.2	18	3	US-08-940-093-208	Sequence 208, App
59	6	2.2	18	3	US-08-940-096-208	Sequence 208, App
60	6	2.2	18	4	US-09-465-719-208	Sequence 208, App
61	6	2.2	18	4	US-09-453-605-208	Sequence 208, App
62	6	2.2	20	1	US-08-484-631-140	Sequence 140, App
63	6	2.2	20	1	US-08-484-631-140	Sequence 140, App
64	6	2.2	20	2	US-08-827-570-140	Sequence 140, App
65	6	2.2	20	2	US-08-484-635-134	Sequence 134, App
66	6	2.2	22	1	US-08-484-635-144	Sequence 144, App
67	6	2.2	22	1	US-08-484-631-134	Sequence 134, App
68	6	2.2	22	2	US-08-484-631-144	Sequence 144, App
69	6	2.2	22	2	US-08-827-570-134	Sequence 134, App
70	6	2.2	22	2	US-08-827-570-144	Sequence 144, App
71	6	2.2	22	2	US-08-940-095-102	Sequence 102, App
72	6	2.2	22	3	US-08-940-095-109	Sequence 109, App
73	6	2.2	22	3	US-08-940-095-190	Sequence 190, App
74	6	2.2	22	3	US-08-940-093-102	Sequence 102, App

RESULT 1
US-07-959-946-3
Sequence 3, Application US-07959946
Patent No. 5408038

GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Wiltz, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
Dressler, Ltd.
ADDRESS: 180 No. 5408038th Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA

ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,946
FILING DATE: 19921008
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gamsou, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-959-946-3

Query Match 100.0%; Score 267; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.7e-250;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAAYTLAVLFLTSGQARHFQWODEPPQSPMDRVKDLATVYVDVLKDSGRDYVSQFECS 60
DB 1 MKAAYTLAVLFLTSGQARHFQWODEPPQSPMDRVKDLATVYVDVLKDSGRDYVSQFECS 60
QY 61 ALGKQNLKLLDNDVSTSTFSKRLQGLGYVQEFMDNLEKETEGRLQEMSKDLEEVYAK 120
DB 61 ALGKQNLKLLDNDVSTSTFSKRLQGLGYVQEFMDNLEKETEGRLQEMSKDLEEVYAK 120
QY 121 VQPYLDLDFQKKQWEMELYRQKVEPLRAELQEGAROKLHELOEKSLPLGEEMDRARAHV 180
DB 121 VQPYLDLDFQKKQWEMELYRQKVEPLRAELQEGAROKLHELOEKSLPLGEEMDRARAHV 180
QY 181 DALRTHLAPYSDLRORLAARLEALKENGARLAIEYHAKATEHLSTLSEKAKPALEDLRQ 240
DB 181 DALRTHLAPYSDLRORLAARLEALKENGARLAIEYHAKATEHLSTLSEKAKPALEDLRQ 240
QY 241 GLPVLSEFVSVFLSALEETTKLNTQ 267
DB 241 GLPVLSEFVSVFLSALEETTKLNTQ 267

RESULT 2
US-08-333-577-3

; Sequence 3, Application US/08333577
; Patent No. 5786206

; GENERAL INFORMATION:

; APPLICANT: Smith, Richard K.
; APPLICANT: Koduri, Raju
; APPLICANT: Young, Stephen G.
; APPLICANT: Witzum, Joseph L.
; APPLICANT: Curtiss, Linda K.
; TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sukter &
; ADDRESS: Milnamow, Ltd.
; STREET: 180 No. 5786206th Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois

COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,577
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gamsou, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: SCRF 234.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-333-577-3

Query Match 100.0%; Score 267; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.7e-250;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAAYTLAVLFLTSGQARHFQWODEPPQSPMDRVKDLATVYVDVLKDSGRDYVSQFECS 60
DB 1 MKAAYTLAVLFLTSGQARHFQWODEPPQSPMDRVKDLATVYVDVLKDSGRDYVSQFECS 60
QY 61 ALGKQNLKLLDNDVSTSTFSKRLQGLGYVQEFMDNLEKETEGRLQEMSKDLEEVYAK 120
DB 61 ALGKQNLKLLDNDVSTSTFSKRLQGLGYVQEFMDNLEKETEGRLQEMSKDLEEVYAK 120
QY 121 VQPYLDLDFQKKQWEMELYRQKVEPLRAELQEGAROKLHELOEKSLPLGEEMDRARAHV 180
DB 121 VQPYLDLDFQKKQWEMELYRQKVEPLRAELQEGAROKLHELOEKSLPLGEEMDRARAHV 180
QY 181 DALRTHLAPYSDLRORLAARLEALKENGARLAIEYHAKATEHLSTLSEKAKPALEDLRQ 240
DB 181 DALRTHLAPYSDLRORLAARLEALKENGARLAIEYHAKATEHLSTLSEKAKPALEDLRQ 240
QY 241 GLPVLSEFVSVFLSALEETTKLNTQ 267
DB 241 GLPVLSEFVSVFLSALEETTKLNTQ 267

RESULT 3

US-08-952-796-2

; Sequence 2, Application US/08952796
; Patent No. 6258596

; GENERAL INFORMATION:

; APPLICANT: BENOIT, Patrick
; APPLICANT: BRUCKERT, Eric
; APPLICANT: DENEUFLE, Patrice
; APPLICANT: DUBBERGER, Nicolas
; APPLICANT: FRUCHART, Jean-Charles
; APPLICANT: LUC, Gerald
; APPLICANT: TURPIN, Gerard
; APPLICANT: ASSMANN, Gerd
; APPLICANT: FUNK, Harald
; TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPROTEIN A-1
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3c43
; CITY: Collegeville
; STATE: PA

COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,796
FILING DATE:
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: FR 95/06061
FILING DATE: 22-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/00747
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fehner Esq., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: ST95031-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-952-796-2

Query Match 100.0%; Score 267; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.7e-250; Indels 0; Gaps 0;
Matches 267; Conservative 0; Mismatches 0;

QY 1 MKAIVLTAVLFLTGSQARHFMOODEPPOSMDRVKDLATVYVDVLKDSGRVYSQFEGS 60
DB 1 MKAIVLTAVLFLTGSQARHFMOODEPPOSMDRVKDLATVYVDVLKDSGRVYSQFEGS 60
QY 61 ALGKOLNKLKLDNDVSTFSKRLREGLVPTQEFMDNLEKETEGLRQMSKDLSEVAK 120
DB 61 ALGKOLNKLKLDNDVSTFSKRLREGLVPTQEFMDNLEKETEGLRQMSKDLSEVAK 120
QY 121 VQPLDFOKKWQEMELRYQKVEPLRAELQEGAROKLHELOKLSPLGEMRDRARAHV 180
DB 121 VQPLDFOKKWQEMELRYQKVEPLRAELQEGAROKLHELOKLSPLGEMRDRARAHV 180
QY 181 DALRTHLAPYSDELRORLARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQ 240
DB 181 DALRTHLAPYSDELRORLARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQ 240
QY 241 GILPVLESFKVSLSALEYTKKLNTQ 267
DB 241 GILPVLESFKVSLSALEYTKKLNTQ 267

RESULT 4
PCT-US92-08634-3
Sequence 3, Application PC/TUS9208634
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Kouduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Witzum, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
DRESSIER, Dressier, Goldsmith, Shore, Sukter &
ADDRESSEE: Milinow, Ltd.

STREET: 180 North Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08634
FILING DATE: 19921009
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-08634-3

Query Match 100.0%; Score 267; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.7e-250; Indels 0; Gaps 0;
Matches 267; Conservative 0; Mismatches 0;

QY 1 MKAIVLTAVLFLTGSQARHFMOODEPPOSMDRVKDLATVYVDVLKDSGRVYSQFEGS 60
DB 1 MKAIVLTAVLFLTGSQARHFMOODEPPOSMDRVKDLATVYVDVLKDSGRVYSQFEGS 60
QY 61 ALGKOLNKLKLDNDVSTFSKRLREGLVPTQEFMDNLEKETEGLRQMSKDLSEVAK 120
DB 61 ALGKOLNKLKLDNDVSTFSKRLREGLVPTQEFMDNLEKETEGLRQMSKDLSEVAK 120
QY 121 VQPLDFOKKWQEMELRYQKVEPLRAELQEGAROKLHELOKLSPLGEMRDRARAHV 180
DB 121 VQPLDFOKKWQEMELRYQKVEPLRAELQEGAROKLHELOKLSPLGEMRDRARAHV 180
QY 181 DALRTHLAPYSDELRORLARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQ 240
DB 181 DALRTHLAPYSDELRORLARLEALKENGARLAELYHAKATEHLSTLSEKAKPALEDLRQ 240
QY 241 GILPVLESFKVSLSALEYTKKLNTQ 267
DB 241 GILPVLESFKVSLSALEYTKKLNTQ 267

RESULT 5
US-08-448-606-6
Sequence 6, Application US/08448606
Patent No. 5721114
GENERAL INFORMATION:
APPLICANT: Abrahams n, Iars
APPLICANT: Holmgren, Erik
APPLICANT: Kalder n, Christina
APPLICANT: Lake, Mats
APPLICANT: Mikaelsson, sa
APPLICANT: Seijltz, Torsten
TITLE OF INVENTION: Expression System For Producing
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pollock, Vande Sande & Priddy
STREET: 1990 M Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,606
FILING DATE: 25-AUG-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE93/01061
FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9203753-0
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Amernick, Burton A.
REGISTRATION NUMBER: 24,852
REFERENCE/DOCKET NUMBER: 0151/00121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 331-7111
TELEFAX: (202) 293-6229
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-448-606-6

Query Match 64.4%; Score 172; DB 1; Length 264;
Best Local Similarity 100.0%; Pred. NO. 2.2e-158;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 DEPOSMDRVKDLATVYVDVLKSGRDYVSQFEGSALGKOLNKLDMNDVSSTFSKL 84
DB 22 DEPOSMDRVKDLATVYVDVLKSGRDYVSQFEGSALGKOLNKLDMNDVSSTFSKL 81
QY 85 REQGLPVTQWMDNLEKTEGLRQEMSKDLEEVAKVQPYLDDPQKKWQEMELRYQKVE 144
DB 82 REQGLPVTQWMDNLEKTEGLRQEMSKDLEEVAKVQPYLDDPQKKWQEMELRYQKVE 141
QY 145 PLRAELQEGAROKLHELOEKLSPLGEEWRDRARAHVDAIRTHLAPYSDELQ 196
DB 142 PLRAELQEGAROKLHELOEKLSPLGEEWRDRARAHVDAIRTHLAPYSDELQ 193

RESULT 6
US-08-952-796-15
Sequence 15, Application US/08952796
Patent No. 6258596
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: BROCKERT, Eric
APPLICANT: DENEFFLE, Patrice
APPLICANT: DUBERGER, Nicolas
APPLICANT: FRUCHART, Jean-Charles
APPLICANT: LUC, Gerald
APPLICANT: TURPIN, Gerard
APPLICANT: ASSMANN, Gerd
APPLICANT: FUNKE, Harald
TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPOPROTEIN A-I
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Wallstop 3c43

CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,796
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/06061
FILING DATE: 22-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/00747
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fehlner Esq., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: ST95031-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-952-796-15

Query Match 40.1%; Score 107; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. NO. 1.1e-95;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 LKLDMDVSTSTFSKLRQLGPTQWMDNLEKTEGLRQEMSKDLEEVAKVQPYLDD 127
DB 1 LKLDMDVSTSTFSKLRQLGPTQWMDNLEKTEGLRQEMSKDLEEVAKVQPYLDD 60
QY 128 FQKKWQEMELRYQKVEPLRAELQEGAROKLHELOEKLSPLGEEWRD 174
DB 61 FQKKWQEMELRYQKVEPLRAELQEGAROKLHELOEKLSPLGEEWRD 107

RESULT 7
US-08-292-870-1
Sequence 1, Application US/08292870
Patent No. 5814467
GENERAL INFORMATION:
APPLICANT: Curtiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Bonnet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
STREET: Patent Counsel
STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,761
FILING DATE: 07-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,333
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-292-870-1

Query Match 24.0% Score 64; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.3e-54; Indels 0; Gaps 0;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 109 EMSKDLSEVAKAKVQPYLDLDFQKKQEMELLYRQKVEPLRAELQEGARQKLHLEQKLSPL 168
|||||
DB 1 EMSKDLSEVAKAKVQPYLDLDFQKKQEMELLYRQKVEPLRAELQEGARQKLHLEQKLSPL 60

OY 169 GEEM 172
|||||
DB 61 GEEM 64

RESULT 8
US-08-292-870-2
Sequence 2, Application US/08292870
Patent No. 5814467
GENERAL INFORMATION:
APPLICANT: Curtiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Bonnet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
NUMBER OF INVENTION: METHODS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994

CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,761
FILING DATE: 07-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,333
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-292-870-2

Query Match 16.5% Score 44; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.9e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 107 RQMSKDLSEVAKAKVQPYLDLDFQKKQEMELLYRQKVEPLRAEL 150
|||||
DB 1 RQMSKDLSEVAKAKVQPYLDLDFQKKQEMELLYRQKVEPLRAEL 44

RESULT 9
US-08-292-870-3
Sequence 3, Application US/08292870
Patent No. 5814467
GENERAL INFORMATION:
APPLICANT: Curtiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Bonnet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
NUMBER OF INVENTION: METHODS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,761
FILING DATE: 07-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,333
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Region
LOCATION: 11
OTHER INFORMATION: /note="Xaa can be either E (Glu)
US-08-292-870-3

Query Match 7.9%; Score 21; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 2,4e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 129 OKKWOEMELYRQKVEPLRAE 149
DB 12 OKKWOEMELYRQKVEPLRAE 32
|||||

RESULT 10
US-08-292-870-4
Sequence 4, Application US/08292870
Patent No. 5814467
GENERAL INFORMATION:
APPLICANT: Curtiss, Linda K
APPLICANT: Banka, Carole L
APPLICANT: Bonnet, David J
APPLICANT: Smith, Richard S
TITLE OF INVENTION: APO AI POLYPEPTIDES, DIAGNOSTIC METHODS
TITLE OF INVENTION: AND SYSTEMS FOR QUANTIFYING APO AI, AND THERAPEUTIC
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5814467th Torrey Pines Road., TPC 8
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,870
FILING DATE: 17-AUG-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,761
FILING DATE: 07-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/711,333
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 91/04038
FILING DATE: 07-JUN-1991
ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 210.1 D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-292-870-4

Query Match 6.4%; Score 17; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 1,4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 111 SKDLEEVKAKVQPYLDD 127
DB 1 SKDLEEVKAKVQPYLDD 17
|||||

RESULT 11
US-07-959-946-5
Sequence 5, Application US/07959946
Patent No. 5408038
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Witzum, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
ADDRESSEE: Milnamow, Ltd.
STREET: 180 No. 5408038th Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,946
FILING DATE: 19921008
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gansson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-959-946-5

Query Match 6.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 KVQPYLDPFQKKMOEE 135
|||||
DB 1 KVQPYLDPFQKKMOEE 16

RESULT 12
US-08-333-577-5
Sequence 5, Application US/08333577
Patent No. 5786206

GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Wiltz, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
ADDRESSEE: Milnamow, Ltd.
STREET: 180 No. 5786206th Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,577
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gansson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: SCRF 234.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-333-577-5

Query Match 6.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 KVQPYLDPFQKKMOEE 135
|||||
DB 1 KVQPYLDPFQKKMOEE 16

RESULT 13
PCT-US92-08634-5
Sequence 5, Application PC/TUS9208634

GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Wiltz, Joseph L.

APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
ADDRESSEE: Milnamow, Ltd.
STREET: 180 North Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08634
FILING DATE: 19921009
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gansson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-08634-5

Query Match 6.0%; Score 16; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 KVQPYLDPFQKKMOEE 135
|||||
DB 1 KVQPYLDPFQKKMOEE 16

RESULT 14
PCT-US94-01234-47
Sequence 47, Application PC/TUS9401234
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE
TITLE OF INVENTION: BINDING SITES
NUMBER OF SEQUENCES: 76
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01234
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,542
FILING DATE: 28-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,566
FILING DATE: 02-FEB-1993
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
PCT-US94-01234-47

Query Match 3.4%; Score 9; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 127 DPQKWOEE 135
Db 5 DFQKWOEE 13

RESULT 15
US-08-630-645-6
Sequence 6, Application US/08630645
Patent No. 5948763
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BADMANN, Marc
APPLICANT: FRANGIONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,645
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YON, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-630-645-6

Query Match 3.0%; Score 8; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 DLATYVVD 44
Db 1 DLATYVVD 8

RESULT 16
PCT-US96-10220-6
Sequence 6, Application PC/TUS9610220
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10220
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-10220-6

Query Match 3.0%; Score 8; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 DLATYVVD 44
Db 1 DLATYVVD 8

RESULT 17
US-08-949-155-6
Sequence 6, Application US/08949155
Patent No. 6271436
GENERAL INFORMATION:
APPLICANT: Piedrahita, Jorge A
APPLICANT: Bazer, Fuller W
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Generation of Transgenic Animal Species
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESSES:
ADDRESSEE: ARNOLD, WHITE AND DURKEE
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,155
CLASSIFICATION: 800
FILING DATE: Concurrently Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,338
FILING DATE: 11-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,094
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TMMK:177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-949-155-6

Query Match 3.0%; Score 8; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 QLGPTQ 94
|111111|
DB 98 QLGPTQ 105

RESULT 18
US-08-952-796-11
Sequence 11, Application US/08952796
Patent No. 6258596
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: BRUCKERT, Eric
APPLICANT: DENEPIE, Patrice
APPLICANT: DUBERGER, Nicolas
APPLICANT: FRUCHART, Jean-Charles
APPLICANT: LUC, Gerald
APPLICANT: TURPIN, Gerard
APPLICANT: ASSMANN, Gerd
APPLICANT: FUNKE, Harald
TITLE OF INVENTION: NOVEL VARIANTS OF APOLIPOPROTEIN A-I
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcoia Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,796
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 95/06061
FILING DATE: 22-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/00747
FILING DATE: 20-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fehlner Esq., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: ST95031-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-952-796-11

Query Match 2.6%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 MRDRARA 178
|111111|
DB 1 MRDRARA 7

RESULT 19
US-08-448-606-2
Sequence 2, Application US/08448606
Patent No. 5721114
GENERAL INFORMATION:
APPLICANT: Abrahams n, Lars
APPLICANT: Holmgren, Erik
APPLICANT: Kalder n, Christina
APPLICANT: Lake, Mats
APPLICANT: Mikaelsson, sa
APPLICANT: Sejlitz, Torsten
TITLE OF INVENTION: Expression System For Producing
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pollock, Vande Sande & Priddy
STREET: 1990 M Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,606
FILING DATE: 25-AUG-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE93/01061
FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9203753-0
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Amernick, Burton A.
REGISTRATION NUMBER: 24,852
REFERENCE/DOCKET NUMBER: 0151/00121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)331-7111
TELEFAX: (202) 293-6229

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-448-606-2

Query Match 2.6%; Score 7; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 DEPOSP 31
DB 7 DEPOSP 13

RESULT 20
US-09-101-146-4
; Sequence 4, Application US/09101146
; Patent No. 6124125

; GENERAL INFORMATION:
; APPLICANT: Dartmouth College, St. Vincents Institute of
; APPLICANT: Medical Research, Kemp et al.
; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053

; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101,146
; FILING DATE: October 7, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PN7450
; FILING DATE: 8 JAN 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: DC-0050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70
; TYPE: Amino acid
; TOPOLOGY: Linear
US-09-101-146-4

Query Match 2.6%; Score 7; DB 3; Length 70;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 VITFSK 83
DB 26 VITFSK 32

RESULT 21
US-09-188-930-315
; Sequence 315, Application US/09188930A

; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 315
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Rat
US-09-188-930-315

Query Match 2.6%; Score 7; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 KDLEEVK 118
DB 10 KDLEEVK 16

RESULT 22
US-09-188-930-139
; Sequence 139, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 139
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Rat
US-09-188-930-139

Query Match 2.6%; Score 7; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 KDLEEVK 118
DB 10 KDLEEVK 16

RESULT 23
US-09-180-827-6
; Sequence 6, Application US/09180827
; Patent No. 6355464
; GENERAL INFORMATION:
; APPLICANT: Healy, Judith M.
; APPLICANT: Bodirova, Jana
; APPLICANT: Lam, Kelvin T.
; APPLICANT: Lesson, Andrea J.
; TITLE OF INVENTION: M. Tuberculosis RNA Polymerase Alpha

FILE OF INVENTION: Subunit
CURRENT APPLICATION NUMBER: US/09/180, 827
CURRENT FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: PCT/US97/22216
PRIOR FILING DATE: 1997-11-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 315
TYPE: PRT
ORGANISM: B. subtilis
US-09-180-827-6

Query Match 2.6%; Score 7; DB 4; Length 315;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 LEEVAK 120
Db 296 LEEVAK 302

RESULT 24
US-08-336-891-2
Sequence 2, Application US/08336891
Patent No. 5622842
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN A
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336, 891
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-891-2

Query Match 2.6%; Score 7; DB 1; Length 343;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 232 KPALEDL 238
Db 122 KPALEDL 128

RESULT 25
PCT-US95-13795-4
Sequence 4, Application PC/TUS9513795
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13795
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-13795-4

Query Match 2.6%; Score 7; DB 5; Length 343;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 232 KPALEDL 238
Db 122 KPALEDL 128

RESULT 26
US-08-637-823B-32
Sequence 32, Application US/08637823B
Patent No. 6184031
GENERAL INFORMATION:
APPLICANT: Gros, Philippe
TITLE OF INVENTION: DNA SEQUENCES THAT ENCODE A NATURAL
TITLE OF INVENTION: RESISTANCE TO INFECTION WITH INTRACELLULAR PARASITES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
STREET: 411 Hackensack Ave
CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,823B
FILING DATE: 05/08/96
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, David A.
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487 5800
TELEFAX: 201 343 1684
TELEX:
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 482 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-637-823B-32

Query Match 2.6%; Score 7; DB 4; Length 482;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 ORLAARL 202
DB 40 ORLAARL 46

RESULT 27
US-08-637-823B-4
Sequence 4, Application US/08637823B
Patent No. 6184031
GENERAL INFORMATION:
APPLICANT: Gros, Philippe
TITLE OF INVENTION: DNA SEQUENCES THAT ENCODE A NATURAL
TITLE OF INVENTION: RESISTANCE TO INFECTION WITH INTRACELLULAR PARASITES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
STREET: 411 Hackensack Ave
CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,823B
FILING DATE: 05/08/96
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, David A.
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487 5800
TELEFAX: 201 343 1684
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-637-823B-4

Query Match 2.6%; Score 7; DB 4; Length 483;

Best Local Similarity 100.0%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 ORLAARL 202
DB 40 ORLAARL 46

RESULT 28
US-08-637-823B-2
Sequence 2, Application US/08637823B
Patent No. 6184031
GENERAL INFORMATION:
APPLICANT: Gros, Philippe
TITLE OF INVENTION: DNA SEQUENCES THAT ENCODE A NATURAL
TITLE OF INVENTION: RESISTANCE TO INFECTION WITH INTRACELLULAR PARASITES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
STREET: 411 Hackensack Ave
CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,823B
FILING DATE: 05/08/96
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, David A.
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487 5800
TELEFAX: 201 343 1684
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-637-823B-2

Query Match 2.6%; Score 7; DB 4; Length 484;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 ORLAARL 202
DB 40 ORLAARL 46

RESULT 29
US-08-903-139B-7
Sequence 7, Application US/08903139B
Patent No. 6114118
GENERAL INFORMATION:
APPLICANT: Joe W. Templeton, Jianwei Peng, L. Garry Adams,
APPLICANT: Erwin Schurr, Philippe Gros, Donald S. Davis and Roger Smith
TITLE OF INVENTION: METHOD OF IDENTIFICATION OF ANIMALS
TITLE OF INVENTION: RESISTANT OR SUSCEPTIBLE TO DISEASES SUCH AS RUMINANT
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor


```

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,139B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031,443
FILING DATE: September 20, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 00162-3/V96171US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 547 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-903-139B-7

Query Match      2.6%; Score 7; DB 3; Length 547;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 ORLAARL 202
DB 104 ORLAARL 110

RESULT 30
US-08-676-279-50
Sequence 50, Application US/08676279
Patent No. 5869247
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MACROPHAGE NUCLEOTIDE SEQUENCE
NUMBER OF SEQUENCES: 63
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,279
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00095
APPLICATION NUMBER: GB 9400929.7
FILING DATE: 19-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9422021.7
FILING DATE: 31-OCT-1994
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-676-279-50

```

```

Query Match      2.6%; Score 7; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 ORLAARL 202
DB 104 ORLAARL 110

RESULT 31
US-08-903-139B-8
Sequence 8, Application US/08903139B
Patent No. 6114118
GENERAL INFORMATION:
APPLICANT: Joe W. Templeton, Jianwei Feng, L. Garry Adams,
Erwin Schurr, Philippe Gros, Donald S. Davis and Roger Smith
TITLE OF INVENTION: METHOD OF IDENTIFICATION OF ANIMALS
RESISTANT OR SUSCEPTIBLE TO DISEASES SUCH AS RUMINANT
TUBERCULOSIS, PARATUBERCULOSIS AND SALMONELLOSIS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th floor
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,139B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031,443
FILING DATE: September 20, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 00162-3/V96171US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-903-139B-8

Query Match      2.6%; Score 7; DB 3; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 ORLAARL 202
DB 104 ORLAARL 110

RESULT 32
US-08-903-139B-9
Sequence 9, Application US/08903139B
Patent No. 6114118
GENERAL INFORMATION:
APPLICANT: Joe W. Templeton, Jianwei Feng, L. Garry Adams,
Erwin Schurr, Philippe Gros, Donald S. Davis and Roger Smith
TITLE OF INVENTION: METHOD OF IDENTIFICATION OF ANIMALS
RESISTANT OR SUSCEPTIBLE TO DISEASES SUCH AS RUMINANT
TUBERCULOSIS, PARATUBERCULOSIS AND SALMONELLOSIS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th floor
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,139B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031,443
FILING DATE: September 20, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 00162-3/V96171US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-903-139B-8

```

TITLE OF INVENTION: BRUCELOSIS, TUBERCULOSIS, PARATUBERCULOSIS AND SALMONELLOSIS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,139B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031,443
FILING DATE: September 20, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 00162-3/V96171US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-903-139B-9

Query Match 2.6%; Score 7; DB 3; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 QRLAARL 202
Db 104 QRLAARL 110

RESULT 33
US-08-903-139B-28
Sequence 28, Application US/08903139B
Patent No. 6114118
GENERAL INFORMATION:
APPLICANT: Joe W. Templeton, Jianwei Feng, L. Garry Adams,
APPLICANT: Erwin Schurt, Philippe Gros, Donald S. Davis and Roger Smith
TITLE OF INVENTION: METHOD OF IDENTIFICATION OF ANIMALS
TITLE OF INVENTION: RESISTANT OR SUSCEPTIBLE TO DISEASES SUCH AS RUMINANT
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,139B
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031,443
FILING DATE: September 20, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 00162-3/V96171US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 amino acids
TYPE: peptide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-903-139B-28

Query Match 2.6%; Score 7; DB 3; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 QRLAARL 202
Db 104 QRLAARL 110

RESULT 34
US-08-637-823B-25
Sequence 25, Application US/08637823B
Patent No. 6184031
GENERAL INFORMATION:
APPLICANT: Gros, Philippe
APPLICANT: Skamene, Emil
TITLE OF INVENTION: DNA SEQUENCES THAT ENCODE A NATURAL
TITLE OF INVENTION: RESISTANCE TO INFECTION WITH INTRACELLULAR PARASITES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
STREET: 411 Hackensack Ave
CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,823B
FILING DATE: 05/08/96
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, David A.
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487 5800
TELEFAX: 201 343 1684
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-637-823B-25

Query Match 2.6%; Score 7; DB 4; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 QRLAARL 202
|||||||
DB 104 QRLAARL 110

RESULT 35

US-08-676-279-57

Sequence 57, Application US/08676279

Patent No. 5869247

GENERAL INFORMATION:

APPLICANT: TITLE OF INVENTION: MACROPHAGE NUCLEOTIDE SEQUENCE

NUMBER OF SEQUENCES: 63

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/676,279

FILING DATE:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/GB95/00095

FILING DATE: 19-JAN-1994

APPLICATION NUMBER: GB 9400929.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

FILING DATE: 31-OCT-1994

APPLICATION NUMBER: GB 9422021.7

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson, David A.

REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487 5800

TELEFAX: 201 343 1684

TELEX:

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 550 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-637-823B-30

Query Match 2.6%; Score 7; DB 4; Length 550;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 QRLAARL 202
|||||||
DB 107 QRLAARL 113

RESULT 37

US-08-637-823B-27

Sequence 27, Application US/08637823B

Patent No. 6184031

GENERAL INFORMATION:

APPLICANT: Gros, Philippe

TITLE OF INVENTION: DNA SEQUENCES THAT ENCODE A NATURAL

TITLE OF INVENTION: RESISTANCE TO INFECTION WITH INTRACELLULAR PARASITES

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSER: KLAUBER & JACKSON

STREET: 411 Hackensack Ave

CITY: Hackensack

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/637,823B

FILING DATE: 05/08/96

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson, David A.

REGISTRATION NUMBER: 26,742

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487 5800

TELEFAX: 201 343 1684

TELEX:

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 568 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-637-823B-27

Query Match 2.6%; Score 7; DB 4; Length 568;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 QRLAARL 202

Db 119 ORLAARL 125

RESULT 38

US-08-637-823B-28
Sequence 28, Application US/08637823B
Patent No. 6184031

GENERAL INFORMATION:

APPLICANT: GROS, Philippe
APPLICANT: Skamene, Emil
TITLE OF INVENTION: DNA SEQUENCES THAT ENCODE A NATURAL
NUMBER OF SEQUENCES: RESISTANCE TO INFECTION WITH INTRACELLULAR PARASITES
CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
STREET: 411 Hackensack Ave
CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,823B
FILING DATE: 05/08/96
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson, David A.
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487 5800
TELEFAX: 201 343 1684

INFORMATION FOR SEQ ID NO:

28:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Mus musculus
TISSUE TYPE: Blood
CELL TYPE: B-cell precursor
CELL LINE: 70/2
IMMEDIATE SOURCE:
CLONE: M1ramp-2
US-08-637-823B-28

Query Match

Best Local Similarity 2.6%; Score 7; DB 4; Length 584;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 ORLAARL 202

Db 135 ORLAARL 141

RESULT 39

US-09-300-909-19
Sequence 19, Application US/09300909
Patent No. 6306580

GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: PREPARATION OF HUMAN PAPILLOMAVIRUS EI HAVING
TITLE OF INVENTION: HELICASE ACTIVITY AND METHOD THEREFOR
NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/300,909
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/083,942
FILING DATE: 01-MAY-1998
INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 629 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-300-909-19

Query Match

Best Local Similarity 2.6%; Score 7; DB 4; Length 629;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 VSFLSAL 257

Db 434 VSFLSAL 440

RESULT 40

US-09-413-814-78
Sequence 78, Application US/09413814
Patent No. 6225064

GENERAL INFORMATION:

APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
APPLICANT: Bloeker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polypeptide or
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
EARLIER FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 78
LENGTH: 882
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-413-814-78

Query Match

Best Local Similarity 2.6%; Score 7; DB 4; Length 882;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 LAARLEA 204

Db 158 LAARLEA 164

RESULT 41

US-08-677-010-3
Sequence 3, Application US/08677010
Patent No. 5925805

GENERAL INFORMATION:
APPLICANT: Ohlrogge, John B.
APPLICANT: Roessler, Keith R.
APPLICANT: Shorrock, Basil S.
TITLE OF INVENTION: Structure and Expression of an
NUMBER OF SEQUENCES: 3
TITLE OF INVENTION: Arabidopsis Acetyl-coenzyme A Carboxylase Gene
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,010
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Dean F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 6550-00002CPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810)641-1600
TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2254 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-677-010-3

Query Match 2.6%; Score 7; DB 2; Length 2254;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 RORLAAR 201
DB 1501 RORLAAR 1507

RESULT 42
US-08-790-519-3
Sequence 3, Application US/08790519
Patent No. 5962767
GENERAL INFORMATION:
APPLICANT: Ohlrogge, John B.
APPLICANT: Roessler, Keith R.
APPLICANT: Shorrock, Basil S.
TITLE OF INVENTION: Structure and Expression of an
NUMBER OF SEQUENCES: 3
TITLE OF INVENTION: Arabidopsis Acetyl-coenzyme A Carboxylase Gene
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/790,519
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/248,630
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Dean F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 6550-00002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810)641-1600
TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2254 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-790-519-3

Query Match 2.6%; Score 7; DB 2; Length 2254;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 RORLAAR 201
DB 1501 RORLAAR 1507

RESULT 43
US-08-469-005A-10
Sequence 10, Application US/08469005A
Patent No. 565874
GENERAL INFORMATION:
APPLICANT: KUHADA, FRANCIS P.
APPLICANT: PASTERNAK, GARY A.
TITLE OF INVENTION: CANCER RELATED ANTIGEN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BORTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,005A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/188,426
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 08/096,908
FILING DATE: 26-JUL-1993
APPLICATION NUMBER: 07/917,716
FILING DATE: 24-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 062482-0113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 2509 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-469-005A-10

Query Match 2.6%; Score 7; DB 1; Length 2509;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 QEFWDNL 99
|||||
DB 20 QEFWDNL 26

RESULT 44
US-09-261-907-2
Sequence 2, Application US/09261907A
Patent No. 6294364
GENERAL INFORMATION:
APPLICANT: ELLIS, CATHERINE
APPLICANT: LONSDALE, JOHN
APPLICANT: BERGSM, DEK J.
APPLICANT: MOONEY, JEFFREY L.
APPLICANT: DEPIERA, MEGAN E.
APPLICANT: CHAPMAN, CONRAD
TITLE OF INVENTION: HUMAN FMS
FILE REFERENCE: GP-70603
CURRENT APPLICATION NUMBER: US/09/261,907A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 2511
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-261-907-2

Query Match 2.6%; Score 7; DB 4; Length 2511;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 QEFWDNL 99
|||||
DB 20 QEFWDNL 26

RESULT 45
US-09-144-085-1
Sequence 1, Application US/09144085
Patent No. 6280999
GENERAL INFORMATION:
APPLICANT: Gustafsson, Claes
APPLICANT: Betlach, Mary C.
APPLICANT: Ashley, Gary
APPLICANT: Jullien, Bryan
APPLICANT: Ziemann, Rainier
TITLE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES AND ENCODING DNA
FILE REFERENCE: 30062-20020.20
CURRENT APPLICATION NUMBER: US/09/144,085
CURRENT FILING DATE: 1998-08-31
EARLIER APPLICATION NUMBER: 09/010,809
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 5087
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-144-085-1

Query Match 2.6%; Score 7; DB 4; Length 5087;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 GGARLAE 215
|||||
DB 4467 GGARLAE 4473

RESULT 46
US-08-704-170-43
Sequence 43, Application US/08704170
Patent No. 5707626
GENERAL INFORMATION:
APPLICANT: Douvas, Angeline
APPLICANT: Takehana, Yoshi
APPLICANT: Ehresmann, Glenn
TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 No. 5707626th Figueroa Street, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,170
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/029,850
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Spitals, John P.
REGISTRATION NUMBER: 29,215
REFERENCE/DOCKET NUMBER: 1920-331
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
TELEFAX: (213) 977-1003
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-704-170-43

Query Match 2.2%; Score 6; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 SKIRRO 87
|||||
DB 1 SKIRRO 6

RESULT 47

US-08-474-741-1
; Sequence 1, Application US/08474741
; Patent No. 5837816
; GENERAL INFORMATION:
; APPLICANT: Ciardelli, Thomas L.
; APPLICANT: Johnson, Kirk
; TITLE OF INVENTION: METHODS OF PREPARING SOLUBLE, OLIGOMERIC
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street - R440
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,741
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D.
; REGISTRATION NUMBER: 31,259
; REFERENCE/DOCKET NUMBER: 1095,002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2706
; TELEFAX: (510) 655-3542
; TELEX: n/a
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-741-1

Query Match 2.2%; Score 6; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 LEALKE 207
|11111|
DB 1 LEALKE 6

RESULT 48
US-09-187-859-1184
; Sequence 1184, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086,407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1184
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence

US-09-187-859-1184

Query Match 2.2%; Score 6; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 LEEYTK 262
|11111|
DB 2 LEEYTK 7

RESULT 49
PCT-US94-02631-43
; Sequence 43, Application PC/TUS9402631
; GENERAL INFORMATION:
; APPLICANT: Douvas, Angeline
; APPLICANT: Takehana, Yoshi
; APPLICANT: Ehresmann, Glenn
; TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR
; TITLE OF INVENTION: IMMUNOINFECTION CLUSTER VIRUS INFECTIONS
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 North Figueroa Street, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02631
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,850
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spitals, John P.
; REGISTRATION NUMBER: 29,215
; REFERENCE/DOCKET NUMBER: 1920-331
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US94-02631-43

Query Match 2.2%; Score 6; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 SKLRQ 87
|11111|
DB 1 SKLRQ 6

RESULT 50
US-09-187-859-1147
; Sequence 1147, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.

/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
/ TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
/ FILE REFERENCE: 100086.407C1
/ CURRENT APPLICATION NUMBER: US/09/187,859A
/ CURRENT FILING DATE: 1998-11-06
/ NUMBER OF SEQ ID NOS: 4052
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1147
/ LENGTH: 8
/ TYPE: PRP
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Representative cyclic modulating agent based on
/ OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-187-859-1147

Query Match 2.28; Score 6; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 257 LEEYTK 262
|||||
DB 3 LEEYTK 8

Search completed: September 22, 2002, 12:23:14
Job time: 394 sec